

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2002, 09:10:06 ; Search time 755.55 Seconds  
(without alignments)  
428.707 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20  
Sequence: 1 cgaccacacagacagccccc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estda:\*  
2: em\_esthum:\*  
3: em\_estln:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.8	74.0	41	12	BG616493 602614656
2	14.2	71.0	85	17	AZ428622 1M0212N10
3	13.8	69.0	40	9	AA877262 ng94d06.s
4	13.8	69.0	49	9	A1815199 wk72c04.x
5	13.8	69.0	50	9	AU104946 AU104946
6	13.8	69.0	76	9	A1601162 ar89e02.x

7	13.8	69.0	79	14	H42857	H42857 y010e01.s1
8	13.8	69.0	93	17	AZ949869	AZ949869 2M0213107
9	13.8	69.0	100	12	BG213902	BG213902 RST33525
10	13.6	68.0	61	9	A1015169	A1015169 oet4905.s
11	13.6	68.0	64	9	A1061438	A1061438 an29a06.x
12	13.6	68.0	66	17	AQ254888	AQ254888 EP(3)0464
13	13.6	68.0	70	9	A1856414	A1856414 sb41h10.x
14	13.6	68.0	73	17	AQ254591	AQ254591 PR(3)0593
15	13.6	68.0	82	14	T25069	T25069 EST644 Humu
16	13.6	67.0	92	9	AA866273	AA866273 OJ38f06.s
17	13.4	67.0	88	9	AA270168	AA270168 va58h01.r
18	13.4	67.0	97	14	BQ614622	BQ614622 1K99e01.Y
19	13.2	66.0	45	17	AZ954608	AZ954608 2M0220B24
20	13.2	66.0	61	9	A1612903	A1612903 tY33d04.x
21	13.2	66.0	61	14	H39535	H39535 y168d08.r1
22	13.2	66.0	66	17	AF219041	AF219041 AF218041
23	13.2	66.0	72	14	BQ271752	BQ271752 1K17h10.x
24	13.2	66.0	73	13	BM128826	BM128826 1f17b08.x
25	13.2	66.0	81	9	A1828860	A1828860 tA81q12.x
26	13.2	66.0	84	10	BE566379	BE566379 601339975
27	13.2	66.0	84	14	W21701	W21701 ZEST00787 M
28	13.2	66.0	86	13	BM312177	BM312177 1941b10.x
29	13.2	66.0	90	13	BM531195	BM531195 1976h05.x
30	13.2	66.0	97	10	BE463686	BE463686 hx79b04.x
31	13.2	66.0	98	13	B1324964	B1324964 1c20d11.x
32	13.2	66.0	99	10	AW583476	AW583476 1a05d12.x
33	13.2	66.0	99	13	BM272195	BM272195 1940d11.x
34	13.2	66.0	99	14	BQ272071	BQ272071 1K17h10.Y
35	13.2	66.0	99	17	BH230402	BH230402 1006157G0
36	12.8	64.0	34	17	AZ387869	AZ387869 1M0147N23
37	12.8	64.0	52	17	AZ511071	AZ511071 1M0355M21
38	12.8	64.0	73	9	A1941442	A1941442 sD89h10.Y
39	12.8	64.0	74	9	A1274464	A1274464 qv61b05.x
40	12.8	64.0	79	17	AZ433977	AZ433977 1M0220G09
41	12.8	64.0	79	9	A1571011	A1571011 t025d09.x
42	12.8	64.0	83	14	BQ764538	BQ764538 EBca01.SQ
43	12.8	64.0	87	14	F32349	F32349 HSPD25000 H
44	12.8	64.0	94	13	BM310585	BM310585 1950d02.x
45	12.8	64.0	100	17	AZ819462	AZ819462 2M0091A10

#### ALIGNMENTS

RESULT 1  
LOCUS BG616493 41 bp mRNA linear EST 18-APR-2001  
DEFINITION 602614656F1 NIH\_MGC\_76 Homo sapiens cDNA clone IMAGE:4733796 5',  
ACCESSION BG616493  
VERSION BG616493.1 GI:13667864  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 41)  
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: CLONETECH Laboratories, Inc.  
CDNA Library Preparation: CLONETECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM1595 row: O column: 13.  
location/Qualifiers  
1. .41  
/organism="Homo sapiens"

#### FEATURES

source

/db\_xref="taxon:9606"  
/clone\_image="4733796"  
/clone\_lib="NIH\_MGC\_76"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site\_1:  
SfiI (ggcgctcgcc); Site\_2: SfiI (ggccatgccc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CAGCGCATATGACC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGGCGCGCATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.85  
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

BASE COUNT 10 a 23 c 5 g 3 t

ORIGIN

Query Match 74.0%; Score 14.8; DB 12; Length 41;  
Best Local Similarity 88.9%; Pred. No. 1.7e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCCCAGACAGCCCCC 20  
Db 11 ACCCCAGACAGCCCCC 28

RESULT 2  
LOCUS AZ428622 85 bp DNA linear GSS 03-OCT-2000  
DEFINITION M0212N10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0212N10 F, DNA sequence.  
ACCESSION AZ428622  
VERSION AZ428622.1 GI:10552635  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 85)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah  
Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0212 row: N column: 10  
Seq primer: CTTCTAAACGACGCGCAGT  
Class: plasmid  
High quality sequence stop: 85.  
Location/Qualifiers  
1. 85

FEATURES  
Source  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0212N10"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (q11473211419b1AF129072.1), a copy-number  
inducible derivative of plasmid RI. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 18 a 37 c 15 g 15 t

ORIGIN

Query Match 71.0%; Score 14.2; DB 17; Length 85;  
Best Local Similarity 84.2%; Pred. No. 3.3e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACCCAGACAGCCCCC 20  
Db 15 GAACCTCAGACAGCCCCC 33

RESULT 3  
LOCUS AA877262/c 40 bp mRNA linear EST 31-MAR-1998  
DEFINITION ng94d06.s1 NCI\_CGAP\_C010 Homo sapiens cDNA clone IMAGE:115979 3'  
similar to gb:M16038 TYROSINE-PROTEIN KINASE LYX (HUMAN);, mRNA  
sequence.  
ACCESSION AA877262  
VERSION AA877262.1 GI:2986339  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 40)  
NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cga@bcrf@mail.nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI\_CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bdrp/image/image.html

Trace considered overall poor quality  
Insert Length: 1388 Std Error: 0.00  
Seq primer: -40m13 fwd. Et from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. 40

FEATURES  
Source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="115979"  
/clone\_lib="NCI\_CGAP\_C010"  
/tissue\_type="Colon tumor RER+"  
/lab\_host="DH10B"  
/note="Organ: Colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; 1st strand cDNA was prepared from  
RER+ colon tumor, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT73



vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4). "

BASE COUNT 4 a 11 c 18 g 7 t

Query Match 69.0%; Score 13.8; DB 9; Length 40;  
Best Local Similarity 88.2%; Pred. No. 4.3e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CGACCCACAGACGCC 17  
Db 38 CGACCCACAGACGCC 22

RESULT 4  
LOCUS A1815199 49 bp mRNA linear EST 07-MAR-2000  
DEFINITION WK72C04.X1 NCI-CGAP\_Pan1 Homo sapiens cDNA clone IMAGE:2420934 3'

similar to SW:PPP4\_HUMAN P10163 SALIVARY PROLINE-RICH PROTEIN PO  
PRECURSOR ;, mRNA sequence.

ACCESSION A1815199  
VERSION A1815199.1 GI:5426404  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 49)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-rcmail.nih.gov

Life Technologies catalog #: 11548-013  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bdrp/image/image.html

Trace considered overall poor quality  
Insert Length: 300 Std Error: 0.00  
Seq Primer: -40UP from Gldpc  
High quality sequence stop: 1.

FEATURES  
source 1..49  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2420934"  
/clone\_1lb="NCI-CGAP\_Pan1"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/note="Organ: pancreas; Vector: PCMV-SPORT6; site\_1: SalI;  
site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.72 kb. Life Technologies catalog #:  
11548-013"

BASE COUNT 17 a 22 c 6 g 4 t  
ORIGIN

Query Match 69.0%; Score 13.8; DB 9; Length 49;  
Best Local Similarity 88.2%; Pred. No. 4.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCCACAGACAGCCCCC 20  
Db 26 CCCCAAGAAAGCCCCC 42

RESULT 5  
LOCUS AUI04946 50 bp mRNA linear EST 30-AUG-2001  
DEFINITION AUI04946 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
HRC05670, mRNA sequence.

ACCESSION AUI04946  
VERSION AUI04946.1 GI:13554467  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata  
'H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okudo,K., Sakaki  
'Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

TITLE  
JOURNAL  
MEDLINE  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp

21270072  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
'S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="HRC05670"  
/clone\_1lb="Sugano Homo sapiens cDNA library"  
/note="Differential display comparison of untreated and  
dimethylfumarate treated U937 cells"

BASE COUNT 4 a 10 c 29 g 7 t  
ORIGIN

Query Match 69.0%; Score 13.8; DB 9; Length 50;  
Best Local Similarity 88.2%; Pred. No. 4.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCCACAGACAGCCCCC 20  
Db 38 CCCCGACAGACCCCCC 22

RESULT 6  
LOCUS A1601162 76 bp mRNA linear EST 21-APR-1999  
DEFINITION ar89e02.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone  
IMAGE:2152442 3' similar to TR:Q62901 Q62901 ATROPHIN-1 RELATED  
PROTEIN ;, mRNA sequence.

ACCESSION A1601162  
VERSION A1601162.1 GI:4610368  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 76)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Haller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,  
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin  
'J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theisling,B.,  
White,Y., Wylie,T., Waterston,R. and Wilson,R.  
WashU-NCI human EST Project  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu

This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
possible reversed clone: similarity on wrong strand



```

/clone="UUGC2M0213107"
/clone_lib="Mouse 10kb plasmid UUGC2M Library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-".
/Note="Vector: pMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1147321149b/AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT      14 a      14 c      34 g      31 t
ORIGIN
Query Match      69.0%; Score 13.8; DB 17; Length 93;
Best Local Similarity 88.2%; Pred. No. 4.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 ACCCCACAGACAGCCCC 19
Db 71 ACCCCATATACAGCCCC 55

RESULT 9
LOCUS      BG213902      100 bp      mRNA      linear      EST 21-APR-2001
DEFINITION BG213902 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
ACCESSION  BG213902
VERSION     BG213902.1 GI:13735589
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 100)
AUTHORS    Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
            Lerner,L., Costanzo,D., McElligott,K., Bozzer,S., Mays,R., Smith
            ,E., Veloso,N., Kilka,A., Hess,J., Cochren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
TITLE      Creation of genome-wide protein expression libraries using random
            activation of gene expression
JOURNAL    Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE    21227151
COMMENT    Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scaln@athersys.com.

FEATURES
            source
            1..100
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="Athersys RAGE Library"
            /cell_line="HT1080"
            /note="See 'Creation of Genome-wide Protein Expression
            Libraries using Random Activation of Gene Expression',
            Nature Biotechnology, in press. Note that even though the
            cell type indicated is HT1080, since a random activation
            method was used, these sequence tags are not necessarily

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expressed in HT1080 under normal circumstances."

BASE COUNT      32 a      31 c      20 g      17 t
ORIGIN
Query Match      69.0%; Score 13.8; DB 12; Length 100;
Best Local Similarity 88.2%; Pred. No. 4.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 ACCCCACAGACAGCCCC 19
Db 46 ACCCCAAAGAGAGCCCC 62

RESULT 10
LOCUS      A1015169      61 bp      mRNA      linear      EST 16-JUN-1998
DEFINITION A1015169 0c74g05.s1 Soares_total_fetus_hb2HF8_9w Homo sapiens CDNA clone
            IMAGE:1622552 3' similar to TR:P94915 P94915
            GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE HOMOLOG. ;, mRNA sequence.
ACCESSION  A1015169
VERSION     A1015169.1 GI:3229505
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 61)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.lnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: -40m13 fwd. BT from Amersham
            High quality sequence stop: 1.

FEATURES
            source
            1..61
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="IMAGE:1622552"
            /dev_stage="8-9 weeks"
            /lab_host="DH10B"
            /note="Vector: pT73D-Pac (Pharmacia) with a modified
            polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
            was prepared from mRNA obtained from pooled 8-9 week
            (total) fetus material with a Not I - oligo(dT) primer [5'
            TGTTACCAATCTGAACTGGAGCGGCGCTTATTTTCTTTT 3'].
            Double-stranded cDNA was ligated to Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not I
            and Eco RI sites of the modified pT73 vector. Library
            went through one round of normalization, and was
            constructed by Bento Soares and M. Felima Bernaldo. "

BASE COUNT      12 a      25 c      21 g      3 t
ORIGIN
Query Match      68.0%; Score 13.6; DB 9; Length 61;
Best Local Similarity 80.0%; Pred. No. 5.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CGACCCACAGACAGCCCC 20
Db 3 CGGACCCACAGCGGCCCC 22

RESULT 11
LOCUS      A1061438      64 bp      mRNA      linear      EST 22-JUL-1998
DEFINITION A1061438 an29a06.x1 Gessler Wilms tumor Homo sapiens CDNA clone
            IMAGE:1700050 3' similar to SW:CA1B_HUMAN P12107 COLLAGEN ALPHA

```



**COMMENT**

Other ESTs:sp41h10.y1  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand this clone is  
 available through: RASgen, Invitrogen Corp. 2130 South Memorial  
 Parkway Huntsville, AL 35801 For further information call: (800  
 )-533-4363 or contact via email: c@uterasgen.com  
 Seq primer: primer name ambguous  
 High quality sequence stop: 1.

BASE COUNT	9 a	33 c	27 g	1 e
ORIGIN				

Query Match	68.0%;	Score 13.6;	DB 9;	Length 70;
Best Local Similarity	80.0%;	Pred. No. 5.7e+04;		
Matches 16; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

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QY      1 CGACCCACAGACAGCCCC 20
        | | | | | | | | | |
Db      43 CCACCCACACACACCCCGC 62
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RESULT 14				
A0254591				
LOCUS				
DEFINITION	A0254591	73 bp	DNA	linear
	EP(3.0593-3prime			GSS 23-AUG-2000
	Drosophila			
	melanogaster			
	EP line			
	Drosophila			

ACCESSION	AO256591	
VERSION	AO256591.1	GI:3738454
KEYWORDS	GSS.	
SOURCE	fruit fly.	
ORGANISM	Drosophila	melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidae; Drosophilidae; Drosophila.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 73)	Liao, G.-C., Rehm, E. J. and Rubin, G. M.	Insertion site preferences of the P transposable element in

**COMMENT**  
Contact: Gerald Rubin  
Berkeley Drosophila Genome Project  
University of California, Berkeley  
LSA Building, Berkeley, CA 94720-3200, USA  
Fax: 5106439947

Email: gerry@fruitfly.berkeley.edu  
Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P element

The P element insertion position is base 001 in the 73 bases. This insertion position refers to the first base of the 8 base target recognition sequence.  
Class: transposon-tagged.

FEATURES	Location/Qualifiers
source	1. .73

BASE COUNT	ORIGIN
18 a	25 c
18 g	12 t

Query Match	68.08;	Score 13.6;	DB 17;	Length 73;
Best Local Similarity	80.08;	Pred. No. 5.7e+04;		
Matches 16; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0

QY	1	CGACCCACAGACGCCCC	20
Db	45	CGACCCACAGCCCGGCC	64

RESULT 15	
T25069/c	
LOCUS	82 bp mRNA linear EST_24-AUG-1995
DEFINITION	EST644 Human colorectal cancer Homo sapiens cDNA clone 30B12, mRNA sequence.

ACCESSION	T25069	GI:534694
VERSION	T25069.1	
KEYWORDS	EST.	
SOURCE	human.	

ORGANISM

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 82)  
Frigerio, J.-M., Berthezene, P., Garrido, P., Ortiz, E., Barthelmy, S.  
Vasseur, S., Sastre, B., Seleznieff, I., Dagorn, J.-C. and Iovanna  
, J.-L.

TITLE	Analysis of 2166 clones from a human colorectal cancer cDNA library
JOURNAL	Hum. Mol. Genet. 4, 37-43 (1995)
MEDLINE	95227175
COMMENT	Contact: Iovanna JL

Fax: (33) 91 26 62 19  
Email: [daegon@arthur.cit12.fr](mailto:daegon@arthur.cit12.fr)  
This sequence is one of a series obtained by systematic sequencing of a colorectal cancer cDNA library.  
Seq primer: M13 Forward.

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FEATURES
source
location/Qualifiers
1.82
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="30B12"
/clone_1lb="Human colorectal cancer"
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```
/lab_host="E. coli NM522"  
/note="Vector: pT7T3D; Site_1: Eco RI; Site_2: Not I; mRNA  
was purified from a colorectal tumour of an adult male.  
cDNA was constructed and cloned into the pT7T3D phagemid  
following the manufacturer instructions (Pharmacia)."  
BASE COUNT      9 a      23 c      35 g      15 t  
ORIGIN
```

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Query Match      68.0%; Score 13.6; DB 14; Length 82;  
Best Local Similarity 80.0%; Pred. No. 5.8e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CGACCCACAGACAGCCCC 20  
   ||| |||| ||||| |||  
DB 64 CGGCTCCACGACAGCACC 45
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Search completed: November 26, 2002, 04:08:13  
Job time : 766.8 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:54:41 : Search time 17.25 Seconds  
(without alignments)  
439.108 Million cell updates/sec

Title: US-09-296-264-12  
Perfect score: 20  
Sequence: 1 cgacccacagacagaccccc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 195614

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published.Applications.NA.\*  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	13.2	66.0	90	10	US-09-864-761-19125
2	12.8	64.0	80	10	US-09-764-877-400
3	12.8	64.0	82	9	US-10-079-623-80
4	12.6	63.0	25	10	US-09-866-108-5565
5	12.6	63.0	25	10	US-09-866-108-5566
6	12.6	63.0	25	10	US-09-866-108-5567
7	12.6	63.0	25	10	US-09-866-108-5568
8	12.6	63.0	25	10	US-09-866-108-5569
9	12.6	63.0	25	10	US-09-866-108-5570
10	12.6	63.0	25	10	US-09-866-108-5571
11	12.6	63.0	31	10	US-09-374-671-77
12	12.6	63.0	38	10	US-09-884-877-4
13	12.6	63.0	40	10	US-09-931-184-6
14	12.6	63.0	72	10	US-09-922-261-118
15	12.6	63.0	90	10	US-09-922-261-116
16	12.2	61.0	17	10	US-09-866-108-2636
17	12.2	61.0	20	10	US-09-350-259-79
18	12.2	61.0	25	10	US-09-866-108-5572
19	12.2	61.0	25	10	US-09-866-108-5573

c 20	12.2	61.0	26	10	US-09-350-259-67	Sequence 67, Appl
c 21	12.2	61.0	31	10	US-09-801-274-410	Sequence 410, Appl
c 22	12.2	61.0	89	10	US-09-864-761-20205	Sequence 20205, A
c 23	12.2	61.0	100	9	US-10-047-542-40	Sequence 40, Appl
c 24	12	60.0	18	10	US-09-768-436-34	Sequence 34, Appl
c 25	11.8	59.0	93	10	US-09-878-574-9664	Sequence 9664, Ap
c 26	11.8	59.0	23	10	US-09-216-393-220	Sequence 220, Appl
c 27	11.8	59.0	23	10	US-09-832-723-2	Sequence 2, Appl1
c 28	11.8	59.0	25	10	US-09-866-073-8	Sequence 8, Appl1
c 29	11.8	59.0	31	10	US-09-801-274-237	Sequence 237, App
c 30	11.8	59.0	47	9	US-09-953-526-282	Sequence 282, App
c 31	11.8	59.0	47	10	US-09-901-484A-282	Sequence 282, App
c 32	11.8	59.0	100	10	US-09-983-965-4933	Sequence 4933, Ap
c 33	11.6	58.0	20	10	US-09-735-995-92	Sequence 92, Appl
c 34	11.6	58.0	25	10	US-09-866-108-5564	Sequence 5564, Ap
c 35	11.6	58.0	31	10	US-09-801-274-1698	Sequence 1698, Ap
c 36	11.6	58.0	80	10	US-09-864-761-22206	Sequence 22206, A
c 37	11.6	58.0	85	10	US-09-864-761-22386	Sequence 22386, A
c 38	11.6	58.0	97	10	US-09-867-701-4678	Sequence 4678, Ap
c 39	11.4	57.0	20	10	US-09-749-728B-60	Sequence 60, Appl
c 40	11.4	57.0	31	10	US-09-801-274-238	Sequence 238, App
c 41	11.4	57.0	35	9	US-09-453-289-1	Sequence 1, Appl1
c 42	11.4	57.0	35	10	US-09-214-606-1	Sequence 16, Appl
c 43	11.4	57.0	35	12	US-10-036-507-16	Sequence 19, Appl
c 44	11.4	57.0	41	10	US-09-828-366-19	Sequence 53, Appl
c 45	11.4	57.0	89	10	US-09-861-893-53	

## ALIGNMENTS

RESULT 1  
US-09-864-761-19125  
Sequence 19125, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeomlca-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 19125
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007425.16
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EST HUMAN HIT: AML72350.1, EVALUATE 1.20e-02
; OTHER INFORMATION: NT HIT: X03638.1, EVALUATE 1.90e-01
US-09-864-761-19125
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Query Match 66.0%; Score 13.2; DB 10; Length 90;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
Oy 2 GACCCACAGACAGCC 19
    11 11 1111111111
Db 9 GAATCCACAGACAGCC 26
```

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RESULT 2
US-09-764-877-400/c
; Sequence 400, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 400
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-400
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Query Match 64.0%; Score 12.8; DB 10; Length 80;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Oy 5 CCCACAGACAGCC 20
    11111111 111 1
Db 51 CCCACAGACAGCC 36
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RESULT 3
US-10-079-623-80/c
; Sequence 80, Application US/10079623
; Patent No. US20020169302A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J.
```

```
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molesaar, Adrian J.
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: mammary gland and methods for their use.
; FILE REFERENCE: 11000.10443
; CURRENT APPLICATION NUMBER: US/10/079,623
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 82
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-623-80
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Query Match 64.0%; Score 12.8; DB 9; Length 82;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Oy 1 CGACCCACAGACAGC 16
    111111 1111 11
Db 18 CGACCCACAGACAGC 3
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```
RESULT 4
US-09-866-108-5565/c
; Sequence 5565, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Weisheng
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: AeoMica Sequence Listing Engine
```



SEQ ID NO 5565  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108-5565

Query Match 63.0%; Score 12.6; DB 10; Length 25;  
Best Local Similarity 78.9%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GACCCACAGACAGCCGCC 20  
Db 25 GACCCGCCAACAGCCGCC 7

RESULT 5  
US-09-866-108-5566/c  
Sequence 5566, Application US/09866108  
Patent No. US20020048800A1  
GENERAL INFORMATION:

APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharon G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AROMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
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PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
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PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 60/266,860  
PRIOR FILING DATE: 2001-02-05  
NUMBER OF SEQ ID NOS: 15752  
SOFTWARE: Aecmlca Sequence Listing Engine  
SEQ ID NO 5566  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108-5566

Query Match 63.0%; Score 12.6; DB 10; Length 25;  
Best Local Similarity 78.9%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GACCCACAGACAGCCGCC 20  
Db 24 GACCCGCCAACAGCCGCC 6

RESULT 6  
US-09-866-108-5567/c  
Sequence 5567, Application US/09866108  
Patent No. US20020048800A1  
GENERAL INFORMATION:

APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharon G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AROMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
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PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 60/266,860  
PRIOR FILING DATE: 2001-02-05  
NUMBER OF SEQ ID NOS: 15752  
SOFTWARE: Aecmlca Sequence Listing Engine  
SEQ ID NO 5567  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108-5567

Query Match 63.0%; Score 12.6; DB 10; Length 25;  
Best Local Similarity 78.9%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GACCCACAGACAGCCGCC 20  
Db 23 GACCCGCCAACAGCCGCC 5

RESULT 7  
US-09-866-108-5568/c  
Sequence 5568, Application US/09866108  
Patent No. US20020048800A1  
GENERAL INFORMATION:

```

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 5568
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-5568

Query Match      63.0%; Score 12.6; DB 10; Length 25;
Best Local Similarity 78.9%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 GACCCGACAGACGCCCC 20
DB      22 GACCCGCGCAACAGCCCGC 4

RESULT 8
; US-09-866-108-5569/c
; Sequence 5569, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 5568
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-5568
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; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 5569
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-5569

Query Match      63.0%; Score 12.6; DB 10; Length 25;
Best Local Similarity 78.9%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 GACCCGACAGACGCCCC 20
DB      21 GACCCGCGCAACAGCCCGC 3

RESULT 9
; US-09-866-108-5570/c
; Sequence 5570, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00662  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00661  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 60/234,687  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 60/266,860  
;; PRIOR FILING DATE: 2001-02-05  
;; NUMBER OF SEQ ID NOS: 15752  
;; SOFTWARE: Aecomica Sequence Listing Engine  
;; SEQ ID NO 5570  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-866-108-5570

Query Match 63.0%; Score 12.6; DB 10; Length 25;  
Best Local Similarity 78.9%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GACCCGACAGACGCCCC 20  
Db 20 GACCCGACAGACGCCCG 2

RESULT 10  
US-09-866-108-5571/c  
; Sequence 5571, Application US/09866108  
; Patent No. US2002004800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AECOMICA-7  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663

;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00662  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00661  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 60/234,687  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 60/266,860  
;; PRIOR FILING DATE: 2001-02-05  
;; NUMBER OF SEQ ID NOS: 15752  
;; SOFTWARE: Aecomica Sequence Listing Engine  
;; SEQ ID NO 5571  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-866-108-5571

Query Match 63.0%; Score 12.6; DB 10; Length 25;  
Best Local Similarity 78.9%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GACCCGACAGACGCCCC 20  
Db 19 GACCCGACAGACGCCCG 1

RESULT 11  
US-09-374-671-77/c  
; Sequence 77, Application US/09374671  
; Patent No. US20020012963A1  
; GENERAL INFORMATION:  
; APPLICANT: Morgenstern, Jay P.  
; APPLICANT: Kanieczny, Andriy  
; APPLICANT: Bizidaukas, Christine B.  
; APPLICANT: Brauer, Andrew W.  
; TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/374,671  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/491,861  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragoras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: IMI-026CP(IFC-048CP)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 742-4214  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA





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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:53:51 : Search time 21.55 Seconds  
(without alignments)  
284.619 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20  
Sequence: 1 cgacccacagacagaccccc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, NA:  
1: /cgn2\_6/ptodata/1/lna/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/lna/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/lna/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/lna/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/lna/PCITUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/lna/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	60	2	US-08-353-476-56
2	13.8	69.0	25	1	US-08-447-179-8
3	13.8	69.0	30	4	US-09-270-542-11
4	13.6	68.0	26	1	US-08-145-704-20
5	13.6	68.0	26	1	US-08-145-704-25
6	13.6	68.0	26	1	US-08-145-704-27
7	13.6	68.0	26	3	US-08-987-574-25
8	13.6	68.0	26	3	US-08-987-574-25
9	13.6	68.0	26	3	US-08-987-574-27
10	13.6	68.0	26	4	US-08-535-168-20
11	13.6	68.0	26	4	US-08-535-168-25
12	13.6	68.0	26	4	US-08-535-168-27
13	13.6	68.0	26	4	US-09-017-974-20
14	13.6	68.0	26	4	US-09-017-974-25
15	13.6	68.0	26	4	US-09-017-974-27
16	13.6	68.0	26	4	US-08-682-255A-20
17	13.6	68.0	26	4	US-08-682-255A-25
18	13.6	68.0	26	4	US-08-682-255A-27
19	13.6	68.0	26	4	US-09-429-130-20
20	13.6	68.0	26	4	US-09-429-130-25
21	13.6	68.0	26	4	US-09-429-130-27
22	13.6	68.0	26	5	PCR-US96-11786-20
23	13.6	68.0	26	5	PCR-US96-11786-25
24	13.6	68.0	26	5	PCR-US96-11786-27
25	13.6	68.0	45	1	US-08-145-704-21
26	13.6	68.0	45	1	US-08-145-704-22
27	13.6	68.0	45	3	US-08-987-574-21

c 28	13.6	68.0	45	3	US-08-987-574-22	Sequence 22, Appl
c 29	13.6	68.0	45	4	US-08-535-168-21	Sequence 21, Appl
c 30	13.6	68.0	45	4	US-08-535-168-22	Sequence 21, Appl
c 31	13.6	68.0	45	4	US-09-017-974-21	Sequence 22, Appl
c 32	13.6	68.0	45	4	US-09-017-974-22	Sequence 21, Appl
c 33	13.6	68.0	45	4	US-08-682-255A-21	Sequence 22, Appl
c 34	13.6	68.0	45	4	US-08-682-255A-22	Sequence 21, Appl
c 35	13.6	68.0	45	4	US-09-429-130-21	Sequence 21, Appl
c 36	13.6	68.0	45	4	US-09-429-130-22	Sequence 22, Appl
c 37	13.6	68.0	45	5	PCR-US96-11786-21	Sequence 21, Appl
c 38	13.6	68.0	45	5	PCR-US96-11786-22	Sequence 22, Appl
c 39	13.4	67.0	32	2	US-08-867-941-60	Sequence 60, Appl
c 40	13.4	67.0	32	4	US-09-074-658-60	Sequence 60, Appl
c 41	13.2	66.0	27	2	US-08-356-060A-45	Sequence 45, Appl
c 42	13.2	66.0	27	4	US-08-460-900C-45	Sequence 45, Appl
c 43	13.2	66.0	27	4	US-08-674-509B-45	Sequence 45, Appl
c 44	13.2	66.0	27	4	US-08-954-698-45	Sequence 45, Appl
c 45	13.2	66.0	27	4	US-08-957-874-45	Sequence 45, Appl

## ALIGNMENTS

RESULT 1  
US-08-353-476-56  
Sequence 56, Application US/08353476  
Patent No. 3871902  
GENERAL INFORMATION:  
APPLICANT: Weininger, Susan  
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st St., Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,476  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bengen, Gerard H.  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 60 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-353-476-56

Query Match 71.0% Score 14.2: DB 2: Length 60:  
Best Local Similarity 84.2% Pred. No. 4.6e+02;  
Matches 16: Conservative 0: Mismatches 3: Indels 0:  
Gy 2 GACCCACAGACAGCCCC 20  
|||||

Db 15 GACACCAGACAGCCGCC 33

RESULT 2

US-08-447-179-8/c

Sequence 8, Application US/08447179

Patent No. 5744303

GENERAL INFORMATION:

APPLICANT: Iggo, Richard

APPLICANT: Friend, Stephen H.

APPLICANT: Frebourg, Thierry

APPLICANT: Ishioka, Chikashi

TITLE OF INVENTION: FUNCTIONAL ASSAY FOR TUMOR

TITLE OF INVENTION: SUPPRESSOR GENES

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/447,179

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/046,033

FILING DATE: 12 APRIL 1993

APPLICATION NUMBER: 07/956,696

FILING DATE: 10 OCTOBER 1992

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/159002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 25

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-447-179-8

Query Match 69.0%; Score 13.8; DB 1; Length 25;

Best Local Similarity 88.2%; Pred. No. 6.7e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCCCACAGACAGCCGCC 20

Db 20 CCCCACTGACAGCCTCC 4

RESULT 3

US-09-270-542-11

Sequence 11, Application US/09270542

Patent No. 6322976

GENERAL INFORMATION:

APPLICANT: Altman, Timothy

APPLICANT: Scott, James

APPLICANT: Stanton, Lawrence

TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and

TITLE OF INVENTION: Therapy

FILE REFERENCE: 4198/78179

CURRENT APPLICATION NUMBER: US/09/270,542

CURRENT FILING DATE: 1999-03-17

EARLIER APPLICATION NUMBER: 09/221,222

EARLIER FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 207

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 11

LENGTH: 30

TYPE: DNA

ORGANISM: Rattus norvegicus

US-09-270-542-11

Query Match 69.0%; Score 13.8; DB 4; Length 30;

Best Local Similarity 88.2%; Pred. No. 6.7e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACCCACAGACAGCCGCC 18

Db 9 GACCCCAAGACAGCAC 25

RESULT 4

US-08-145-704-20/c

Sequence 20, Application US/08145704

Patent No. 5567604

GENERAL INFORMATION:

APPLICANT: Kando, Robert F.

APPLICANT: Fennemald, Susan

APPLICANT: Zendegeul, Joseph G.

APPLICANT: Joshua O. Ojwang

TITLE OF INVENTION: Anti-viral Guanoxine-rich

TITLE OF INVENTION: Oligonucleotides

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski

STREET: 1301 McKinney, Suite 5100

CITY: Houston

STATE: Texas

COUNTRY: U.S.A.

ZIP: 77010-3095

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/145,704

FILING DATE: 28-OCT-1993

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/053,027

FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Paul, Thomas D.

REGISTRATION NUMBER: 32,714

REFERENCE/DOCKET NUMBER: D-5574-CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713/651-5151

TELEFAX: 713/651-5246

TELEX: 762829

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 26

OTHER INFORMATION: /note= "Amlne molty attached to 3'

OTHER INFORMATION: end"

US-08-145-704-20



Query Match 68.0%; Score 13.6; DB 1; Length 26;  
Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20  
11111111111111111111  
Db 23 CCACCCACCAACACACCCCC 4

RESULT 5  
US-08-145-704-25/c

; Sequence 25, Application US/08145704  
; Patent No. 5567604  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Fennwald, Susan  
; APPLICANT: Zendegui, Joseph G.  
; APPLICANT: Joshua O. Ojwang  
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
; TITLE OF INVENTION: Oligonucleotides  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/145,704  
; FILING DATE: 28-OCT-1993  
; CLASSIFICATION: 514  
; TELEFAX: 713/651-5246  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,027  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul, Thomas D.  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5574-CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/651-5151  
; TELEFAX: 713/651-5246  
; TELEX: 762829  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 26  
; OTHER INFORMATION: /note="cholesterol molty attached"  
; OTHER INFORMATION: to 3' end"  
US-08-145-704-25

Query Match 68.0%; Score 13.6; DB 1; Length 26;  
Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20  
11111111111111111111  
Db 23 CCACCCACCAACACACCCCC 4

RESULT 6  
US-08-145-704-27/c

; Sequence 27, Application US/08145704  
; Patent No. 5567604  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Fennwald, Susan  
; APPLICANT: Zendegui, Joseph G.  
; APPLICANT: Joshua O. Ojwang  
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
; TITLE OF INVENTION: Oligonucleotides  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/145,704  
; FILING DATE: 28-OCT-1993  
; CLASSIFICATION: 514  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,027  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul, Thomas D.  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5574-CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/651-5151  
; TELEFAX: 713/651-5246  
; TELEX: 762829  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 26  
; OTHER INFORMATION: /note="phosphorothioate backbone"  
; OTHER INFORMATION: and amine molty attached to backbone"  
US-08-145-704-27

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Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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11111111111111111111  
Db 23 CCACCCACCAACACACCCCC 4

RESULT 7  
US-08-987-574-20/c

; Sequence 20, Application US/08987574  
; Patent No. 6150339  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Fennwald, Susan  
; APPLICANT: Zendegui, Joseph G.  
; APPLICANT: Ojwang, Joshua O.  
; APPLICANT: Hogan, Michael E.  
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
; TITLE OF INVENTION: Oligonucleotides  
; NUMBER OF SEQUENCES: 52

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fulbright & Jaworski  
;; STREET: 1301 McKinney, Suite 5100  
;; CITY: Houston  
;; STATE: Texas  
;; COUNTRY: U.S.A.  
;; ZIP: 77010-3095  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/987,574  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US94/04529  
;; FILING DATE: 28-OCT-1993  
;; APPLICATION NUMBER: US 08/053,027  
;; FILING DATE: 23-APR-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Paul, Thomas D.  
;; REGISTRATION NUMBER: 32,714  
;; REFERENCE/DOCKET NUMBER: D-5574-CIP  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 713/651-5151  
;; TELEFAX: 713/651-5246  
;; TELEX: 762829  
;;  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 26 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: misc-feature  
;; LOCATION: 26  
;; OTHER INFORMATION: /note="Amine molty  
;; OTHER INFORMATION: attached to 3' end"  
;;  
;; US-08-987-574-20  
;;  
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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QY 1 CGACCCACAGACGCCCC 20  
Db 23 CCACCCACACACACCCCC 4  
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RESULT 8  
US-08-987-574-25/C  
;; Sequence 25, Application US/08987574  
;; Patent No. 6150339  
;; GENERAL INFORMATION:  
;; APPLICANT: Rando, Robert F.  
;; APPLICANT: Fennewald, Susan  
;; APPLICANT: Zendegui, Joseph G.  
;; APPLICANT: Ojwang, Joshua O.  
;; APPLICANT: Hogan, Michael E.  
;; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
;; NUMBER OF SEQUENCES: 52  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fulbright & Jaworski  
;; STREET: 1301 McKinney, Suite 5100  
;; CITY: Houston  
;; STATE: Texas  
;; COUNTRY: U.S.A.  
;; ZIP: 77010-3095  
;;  
;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/987,574  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US94/04529  
;; FILING DATE: 28-OCT-1993  
;; APPLICATION NUMBER: US 08/053,027  
;; FILING DATE: 23-APR-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Paul, Thomas D.  
;; REGISTRATION NUMBER: 32,714  
;; REFERENCE/DOCKET NUMBER: D-5574-CIP  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 713/651-5151  
;; TELEFAX: 713/651-5246  
;; TELEX: 762829  
;;  
;; INFORMATION FOR SEQ ID NO: 25:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 26 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: misc-feature  
;; LOCATION: 26  
;; OTHER INFORMATION: /note="cholesterol molty  
;; OTHER INFORMATION: attached to 3' end"  
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;; US-08-987-574-25  
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Query Match 68.0%; Score 13.6; DB 3; Length 26;  
Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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QY 1 CGACCCACAGACGCCCC 20  
Db 23 CCACCCACACACACCCCC 4  
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RESULT 9  
US-08-987-574-27/C  
;; Sequence 27, Application US/08987574  
;; Patent No. 6150339  
;; GENERAL INFORMATION:  
;; APPLICANT: Rando, Robert F.  
;; APPLICANT: Fennewald, Susan  
;; APPLICANT: Zendegui, Joseph G.  
;; APPLICANT: Ojwang, Joshua O.  
;; APPLICANT: Hogan, Michael E.  
;; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
;; NUMBER OF SEQUENCES: 52  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fulbright & Jaworski  
;; STREET: 1301 McKinney, Suite 5100  
;; CITY: Houston  
;; STATE: Texas  
;; COUNTRY: U.S.A.  
;; ZIP: 77010-3095  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/987,574  
;; FILING DATE:  
;; CLASSIFICATION: 514

Prior Application Data:  
APPLICATION NUMBER: PCT/US94/04529  
FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: US 08/053,027  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5574-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 26  
OTHER INFORMATION: /note="phosphorothioate  
OTHER INFORMATION: backbone and amine moiety attached to  
OTHER INFORMATION: backbone"  
US-08-987-574-27

Query Match 68.0%; Score 13.6; DB 3; Length 26;  
Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CGACCCACAGACAGCCCCC 20  
11111111111111111111  
Db 23 CCACCCACAGACAGCCCCC 4

RESULT 10  
US-08-535-168-20/C  
Sequence 20, Application US/08535168  
Patent No. 6184369  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Zendegeul, Susan  
APPLICANT: Ojwang, Joseph G.  
APPLICANT: Hogan, Michael E.  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/535,168  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04529  
FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: US 08/053,027  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.

REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5574-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 26  
OTHER INFORMATION: /note="Amine moiety  
OTHER INFORMATION: attached to 3' end"  
US-08-535-168-20

Query Match 68.0%; Score 13.6; DB 4; Length 26;  
Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CGACCCACAGACAGCCCCC 20  
11111111111111111111  
Db 23 CCACCCACAGACAGCCCCC 4

RESULT 11  
US-08-535-168-25/C  
Sequence 25, Application US/08535168  
Patent No. 6184369  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Zendegeul, Susan  
APPLICANT: Ojwang, Joseph G.  
APPLICANT: Hogan, Michael E.  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/535,168  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04529  
FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: US 08/053,027  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5574-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:

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?      LENGTH: 26 base pairs
?      TYPE: nucleic acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      MOLECULE TYPE: DNA (genomic)
?      FEATURE:
?      NAME/KEY: misc_feature
?      LOCATION: 26
?      OTHER INFORMATION: /note="cholesterol" molty
?      OTHER INFORMATION: attached to 3' end"
?      OS-08-535-168-25

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Best Local Similarity	80.0%	Pred. No. 8.2e+02;		
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Db	23	CCACCCCAAGCAACGCCCC	4

RESULT 12  
US-08-535-168-27/c

; Sequence 27, Application US/08535168  
; Patent No. 6184369  
; CHURCH & DWIGHT

GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Fennewald, Susan  
APPLICANT: Zendegeul, Joseph G.  
APPLICANT: Ojwang, Joshua O.  
APPLICANT: Hogan, Michael E.  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:

OTHER INFORMATION: /note="phosphorothioate  
OTHER INFORMATION: backbone and amine moiety attached to  
OTHER INFORMATION: backbone"  
US-08-535-168-27

Query Match	68.0%;	Score 13.6;	DB 4;	length 26;
Best Local Similarity	80.0%;	Pred. No. 8.2e+02;		
Matches	16;	Conservative	0;	Mismatches 4;
			Indels	0;
			Gaps	0

QY	1	CGACCCCA	GAGACG	CCCCC	20
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RESULT 13  
US-09-017-974-20/c

; Sequence 20, Application US/09017974  
; Patent No. 6288042

GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Ojwang, Joshua O.  
APPLICANT: Hogan, Michael E.  
APPLICANT: Wallace, Thomas L.  
APPLICANT: Cossum, Paul A.  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
TITLE OF INVENTION: Tetrad Forming Oligonucleotides  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Conley, Rose & Tayon, P.C.  
STREET: 600 Travis, Suite 1800

```

:      OTHER INFORMATION: /note="Amine moiety
;      OTHER INFORMATION: attached to 3' end"
US-09-017-974-20

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MOLECULE TYPE:	DNA (genomic)	Query Match	68.0%	Score 13.6;	DB 4;	Length 26;
FEATURE:		Best Local Similarity	80.0%;	Pred. No. 8.2e+02;		
NAME/KEY:	misc_feature	Matches 16;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0
LOCATION:	26					



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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2002, 14:46:40 : Search time 302.2 Seconds

(Without alignments)  
1926.063 Million cell updates/sec

Title: US-09-296-264-13

Perfect score: 20

Sequence: 1 tctctgtccccaatcgaa 20

Scoring table: IDENTITY\_NUC

Gapop 10.0', Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: gb_ba:*
3: gb_hcg:*
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40: em_hcgo_mus:*
41: em_hcgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	14.2	71.0	84	6	I16749	I16749 Sequence 10
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5	13.8	69.0	45	6	AR009531	AR009531 Sequence
6	13.8	69.0	45	6	AR172143	AR172143 Sequence
7	13.8	69.0	45	6	I66205	I66205 Sequence 12
8	13.8	69.0	45	6	I66218	I66218 Sequence 12
9	13.8	69.0	51	6	AX157723	AX157723 Sequence
10	13.8	69.0	51	6	AX157724	AX157724 Sequence
11	13.8	69.0	51	6	AX157725	AX157725 Sequence
12	13.8	69.0	51	6	AX157726	AX157726 Sequence
13	13.6	68.0	30	6	AR118775	AR118775 Sequence
14	13.6	68.0	30	6	E51958	E51958 Diagnostic
15	13.6	68.0	52	6	AR145888	AR145888 Sequence
16	13.6	68.0	52	6	AX003018	AX003018 Sequence
17	13.2	66.0	20	6	AX462752	AX462752 Sequence
18	13.2	66.0	45	6	AX195434	AX195434 Sequence
19	13	65.0	16	6	AR021087	AR021087 Sequence
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21	13	65.0	16	6	AR062417	AR062417 Sequence
22	13	65.0	16	6	AR183876	AR183876 Sequence
23	13	65.0	17	6	AR190496	AR190496 Sequence
24	13	65.0	18	6	AR190778	AR190778 Sequence
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33	12.8	64.0	51	6	AX297652	AX297652 Sequence
34	12.8	64.0	51	6	AX297655	AX297655 Sequence
35	12.8	64.0	52	6	AX297658	AX297658 Sequence
36	12.8	64.0	53	6	AR172220	AR172220 Sequence
37	12.6	63.0	31	11	AL807511	AL807511 Arabidops
38	12.6	63.0	75	8	Y5CTGWA	Y5CTGWA
39	12.6	63.0	75	8	Y5CTGWA	Y5CTGWA
40	12.6	63.0	81	6	I40761	I40761 Sequence 92
41	12.6	63.0	89	17	H5EXTK35	H5EXTK35
42	12.4	62.0	20	6	AR086399	AR086399 Sequence
43	12.4	62.0	20	6	AR122386	AR122386 Sequence
44	12.4	62.0	20	6	AR144251	AR144251 Sequence
45	12.4	62.0	20	6	AR209933	AR209933 Sequence

#### ALIGNMENTS

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RESULT 1
PTU27511/c
LOCUS PTU27511 71 bp DNA linear INV 22-MAR-1996
DEFINITION Parametrium tetraurelia trichocyst matrix protein (T2c) gene,
ACCESSION U27511
VERSION U27511
KEYWORDS partial cds.
SOURCE U27511.1 GI:881411
ORGANISM Parametrium tetraurelia.
Parametrium tetraurelia
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
Parametrium.
1 (bases 1 to 71)
REFERENCE
Madeddu,L., Gautier,M.C., Le Caer,J.P., Garreau de Loubresse,N. and
Sperling,L.
```

```

TITLE      Protein processing and morphogenesis of secretory granules in
JOURNAL    Biochimie 76 (3-4), 329-335 (1994)
MEDLINE    95119139
PUBMED     7819344
REFERENCE  2 (bases 1 to 71)
AUTHORS    Madeddu,L., Gautier,M.C., Vaysse,L., Houari,A. and Sperling,L.
TITLE      A large multigene family codes for the polypeptides of the
           crystalline trichocyst matrix in Paramaecium
JOURNAL    Mol. Biol. Cell 6 (6), 649-659 (1995)
MEDLINE    96059477
PUBMED     7579685
REFERENCE  3 (bases 1 to 71)
AUTHORS    Madeddu,L., Gautier,M.C. and Sperling,L.
TITLE      Direct Submission
JOURNAL    Submitted (23-MAY-1995) Linda Sperling, Centre de Genetique
           Moleculaire, CNRS, Avenue de la Terrasse, Gif-sur-Yvette 91198,
           France

FEATURES
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              1..71
                /organism="Paramaecium tetraurelia"
                /strain="g4-2"
                /db_xref="taxon:5888"
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                /gene="T2c"
                /note="member of the Paramaecium trichocyst multigene
                family; Paramaecium secretory granule protein"
                /codon_start=1
                /transl_table=6
                /product="trichocyst matrix protein T2"
                /protein_id="AA92611.1"
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BASE COUNT  26 a      12 c      15 g      18 t

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Query Match 74.0%: Score 14.8; DB 3; Length 71;
Best Local Similarity 88.9%: Pred. No. 9.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCTGTCCTCCAAATGCG 18
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Db 50 TATCTGTCCTCCAAATGCG 33

RESULT 2
A26456 84 bp DNA linear PAT 22-SEP-1995
LOCUS A26456/c
DEFINITION Soya beta-1,3-glucanase C-terminal sequence.
ACCESSION A26456
VERSION A26456.1 GI:1247332
KEYWORDS
SOURCE
ORGANISM Glycine max.
           Glycine max.
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
           Glycine.
FEATURES
  source      Location/Qualifiers
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                /db_xref="taxon:3847"

BASE COUNT  25 a      12 c      23 g      24 t

ORIGIN
Query Match 71.0%: Score 14.2; DB 6; Length 84;
Best Local Similarity 84.2%: Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB	26	CTCTTTCCTCCAAACCGAA	8
RESULT 3			
LOCUS	116749		84 bp DNA linear PAT 03-APR-1996
DEFINITION	Sequence 10 from patent US 5477001.		
ACCESSION	U16749		
VERSION	U16749.1	GI:1251657	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 84)		
TITLE	Sass,C., Leguay,J.-J., Grison,R. and Toppan,A. Recombinant DNA coding for a novel protein having .beta.-1,3-glucanase activity; bacteria containing this DNA, transformed plant cells and plants Patent: US 5477001-A 10 19-DEC-1995;		
JOURNAL			
FEATURES	Location/Qualifiers		
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BASE COUNT	25 a 12 c 23 g 24 t		
ORIGIN	/organism="unknown"		
Query Match	71.0%; Score 14.2; DB 6; Length 84; Best Local Similarity 84.2%; Pred.No.2.4e+03;		
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
OY	2 CTCTGTCTCCTCCAATCGAA 20		
Db	26 CTCTTTCCTCCAAACCGAA 8		
RESULT 4			
S68158S1/c			
LOCUS	S68158S1	100 bp RNA linear VRL 23-SEP-1994	
DEFINITION	NS5 [5' and 3' conserved regions] [central european tick-borne encephalitis virus Kunlinge, Genomic RNA, 100 nt, segment 1 of 2].		
ACCESSION	S68158		
VERSION	S68158.1	GI:544621	
KEYWORDS			
SEGMENT	1 of 2		
SOURCE	Kunlinge virus.		
ORGANISM	Kunlinge virus.		
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; tick-borne encephalitis virus group.		
AUTHORS	1 (bases 1 to 100) Fujoip,L., Barrett,A.D., Philippotts,R., Martin,K., Leslie,D. and Titball,R.W.		
TITLE	Rapid identification of flaviviruses based on conserved NS5 gene sequences		
JOURNAL	J. Virol. Methods 44 (2-3), 179-188 (1993)		
MEDLINE	94086710		
PUBMED	8263114		
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gidsq 142831] from the original journal article. This sequence comes from Fig. 3a and 3b.		
FEATURES	Location/Qualifiers		
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BASE COUNT	26 a 26 c 29 g 19 t		
ORIGIN	/organism="Kunlinge virus" /db_xref="taxon:11092"		
Query Match	71.0%; Score 14.2; DB 14; Length 100; Best Local Similarity 84.2%; Pred.No.2.5e+03;		
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
OY	1 TCTCTGTCCTCCAATCGA 19		
Db	83 TCTCTGTCCTCCAACCGA 65		



RESULT 5	AR009531	45 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR009531				
DEFINITION	Sequence 12 from patent US 5756312.				
ACCESSION	AR009531				
VERSION	AR009531.1	GI:3968336			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 45)				
AUTHORS	Weiner,A.J. and Houghton,M.				
TITLE	Immunoreactive polypeptide compositions				
JOURNAL	Patent: US 5756312-A 12 26-MAY-1998;				
FEATURES	Location/Qualifiers				
source	1..45				
BASE COUNT	8 a 16 c 6 g 15 t				
ORIGIN	/organism="unknown"				
Query Match	69.0%; Score 13.8; DB 6;	length 45;			
Best Local Similarity	88.2%; Pred. No. 3.6e+03;				
Matches	15; Conservative 0; Mismatches 2;	Indels 0; Gaps 0;			
OY	1 TCTCTGTCCTCCAAATC 17				
Db	29 TCCTGTCCTCCAAAGTC 45				
RESULT 6	AR172143	45 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	AR172143				
DEFINITION	Sequence 12 from patent US 6303292.				
ACCESSION	AR172143				
VERSION	AR172143.1	GI:17911634			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 45)				
AUTHORS	Weiner,A.J. and Houghton,M.				
TITLE	Immunoreactive polypeptide compositions				
JOURNAL	Patent: US 6303292-A 12 16-OCT-2001;				
FEATURES	Location/Qualifiers				
source	1..45				
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ORIGIN	/organism="unknown"				
Query Match	69.0%; Score 13.8; DB 6;	length 45;			
Best Local Similarity	88.2%; Pred. No. 3.6e+03;				
Matches	15; Conservative 0; Mismatches 2;	Indels 0; Gaps 0;			
OY	1 TCTCTGTCCTCCAAATC 17				
Db	29 TCCTGTCCTCCAAAGTC 45				
RESULT 7	I66205	45 bp	DNA	linear	PAT 28-DEC-1997
LOCUS	I66205				
DEFINITION	Sequence 12 from patent US 5670152.				
ACCESSION	I66205				
VERSION	I66205.1	GI:2724182			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 45)				
AUTHORS	Weiner,A.J. and Houghton,M.				
TITLE	Immunoreactive polypeptide compositions				
JOURNAL	Patent: US 5670152-A 12 23-SEP-1997;				

FEATURES									
SOURCE		1. 45 location/Qualifiers							
BASE COUNT		8 a 16 c 6 g 15 t							
ORIGIN									
Query Match									
Best Local Similarity		69.0%; Score 13.8; DB 6; Length 45;							
Matches 15; Conservative		88.2%; Pred. No. 3.6e+03; Mismatches 2; Indels 0; Gaps 0;							
OY 1 TCTCTGTCCTCCAAATC 17									
Db 29 TCCTGTCCTCCAAAGTC 45									
RESULT 8									
LOCUS 166218		45 bp DNA Linear PAT 28-DEC-1997							
DEFINITION		Sequence 12 from patent US 5670153.							
ACCESSION		166218							
VERSION		166218.1 GI:2724195							
KEYWORDS		.							
SOURCE		Unknown.							
ORGANISM		Unknown.							
REFERENCE		1 (bases 1 to 45)							
AUTHORS		Weiner, A.J. and Houghton, M.							
TITLE		Immunoreactive polypeptide compositions							
JOURNAL		Patent: US 5670153-A 12 23-SEP-1997;							
FEATURES		location/Qualifiers							
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ORIGIN									
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Best Local Similarity		69.0%; Score 13.8; DB 6; Length 45;							
Matches 15; Conservative		88.2%; Pred. No. 3.6e+03; Mismatches 2; Indels 0; Gaps 0;							
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RESULT 9									
LOCUS AX157723		51 bp DNA Linear PAT 22-JUN-2001							
DEFINITION		Sequence 1051 from Patent W00140521.							
ACCESSION		AX157723							
VERSION		AX157723.1 GI:14539054							
KEYWORDS		.							
SOURCE		human.							
ORGANISM		Homo sapiens							
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
AUTHORS		1 (bases 1 to 51)							
TITLE		Shimkets, R.A. and Leach, M.							
JOURNAL		Nucleic acids containing single nucleotide polymorphisms and methods of use thereof							
PATENT		WO 0140521-A 1051 07-JUN-2001;							
CORPORATION (US)		Curagen							
LOCATION/Qualifiers		1..51							
FEATURES		/organism="Homo sapiens"							
SOURCE		/db_xref="taxon:9606"							
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Matches 15; Conservative		88.2%; Pred. No. 3.7e+03; Mismatches 2; Indels 0; Gaps 0;							
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 7 CTGTCCTCGAAGTCGAA 23

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DEFINITION Sequence 1052 from Patent WO0140521.  
ACCESSION AX157724  
VERSION AX157724.1 GI:14539055  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 51)  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 1052 07-JUN-2001;  
Curagen Corporation (US)

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Best Local Similarity 88.2%; Pred. No. 3.7e+03;  
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RESULT 11  
AX157725  
LOCUS AX157725 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 1053 from Patent WO0140521.  
ACCESSION AX157725  
VERSION AX157725.1 GI:14539056  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 51)  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 1053 07-JUN-2001;  
Curagen Corporation (US)

FEATURES  
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 CTGTCCTCGAAGTCGAA 17

RESULT 12  
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LOCUS AX157726 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 1054 from Patent WO0140521.  
ACCESSION AX157726  
VERSION AX157726.1 GI:14539057  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 51)  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 1054 07-JUN-2001;  
Curagen Corporation (US)

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LOCUS AR118775 30 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 205 from patent US 6150087.  
ACCESSION AR118775  
VERSION AR118775.1 GI:14100685  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Chien,D.Y.  
TITLE NANBV diagnostics and vaccines  
JOURNAL Patent: US 6150087-A 205 21-NOV-2000;  
Location/Qualifiers  
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BASE COUNT 9 a 5 c 12 g 4 t  
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 14  
E51958/c

Search completed: December 3, 2002, 18:13:24  
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LOCUS E51958 30 bp DNA linear PAT 18-JUN-2001  
DEFINITION Diagnostic for NANBV.  
ACCESSION E51958  
VERSION E51958.1 GI:13019285  
KEYWORDS JP 2000039434-A/1.  
SOURCE unidentified.  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Michael H., Oullim,C. and George,K.  
TITLE Diagnostic for NANBV.  
JOURNAL Patent: JP 2000039434-A 1 08-FEB-2000;  
CHIRON CORP  
COMMENT OS Unidentified  
PN JP 2000039434-A/1  
PD 08-FEB-2000  
PR 03-JUN-1989 JP 1999157192  
PR 17-MAR-1989 US 325,338,20-APR-1989 US 341,334, PR  
18-MAY-1989 US 355,002  
PI MICHAEL HOUGHTON,QUI-LIM CHOO,GEORGE KUO  
PC G01N33/569,C07K14/18,G01N33/576//C12M15/09,C12P21/02, PC  
(C12P21/02,C12R1:19),  
PC C12N15/00  
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 TCTCTGCTCTCCAAATCGAA 20  
Db 26 TCCCTGCTTCCAGATCGCA 7  
RESULT 15  
ARI45888  
LOCUS ARI45888 52 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 8 from patent US 6218139.  
ACCESSION ARI45888  
VERSION ARI45888.1 GI:15109077  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 52)  
AUTHORS Achsteiner,T., Cautel,G. and Degryse,E.  
TITLE Yeast strains possessing the interrupted ATF2 gene and their  
applications  
JOURNAL Patent: US 6218139-A 8 17-APR-2001;  
FEATURES location/Qualifiers  
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Db 2 TCTCTGCTGACAAATGCA 21

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QM nucleic - nucleic search, using sw model

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#### SUMMARIES

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5	12.4	62.0	26	10	US-09-909-320-381
6	12.4	62.0	25	10	US-09-909-088B-381
7	12.4	62.0	95	10	US-09-969-373-1290
8	12.4	62.0	97	10	US-09-969-373-838
9	12.2	61.0	30	9	US-09-733-042-2
10	12.2	61.0	30	12	US-10-041-400A-5
11	12.2	61.0	30	12	US-10-041-264A-5
12	12.2	61.0	30	12	US-10-042-091A-5
13	12.2	61.0	33	9	US-10-040-803-10
14	12.2	61.0	67	10	US-09-815-242-1629
15	12.2	61.0	96	10	US-09-828-538-17
16	12.2	61.0	96	10	US-09-878-574-3585
17	11.8	59.0	68	10	US-09-760-139-36
18	11.8	59.0	23	10	US-09-950-902-13
19	11.8	59.0	31	10	US-09-801-274-1171

c 20	11.8	59.0	86	10	US-09-864-761-31474	Sequence 31474, A
c 21	11.8	59.0	87	10	US-09-878-574-13597	Sequence 13597, A
c 22	11.8	59.0	100	10	US-09-864-761-18163	Sequence 18163, A
c 23	11.8	59.0	100	10	US-09-864-761-35290	Sequence 35290, A
c 24	11.6	58.0	31	8	US-08-834-666A-59	Sequence 59, A
c 25	11.6	58.0	48	10	US-09-565-233-7	Sequence 7, Appl1
c 26	11.6	58.0	52	10	US-09-962-628B-41	Sequence 41, Appl1
c 27	11.6	58.0	52	10	US-09-962-628B-42	Sequence 42, Appl1
c 28	11.6	58.0	98	10	US-09-878-574-14881	Sequence 14881, A
c 29	11.4	57.0	18	10	US-09-963-373-1572	Sequence 1572, Ap
c 30	11.4	57.0	19	10	US-09-832-424-10	Sequence 10, Appl1
c 31	11.4	57.0	31	10	US-09-801-274-259	Sequence 259, App
c 32	11.4	57.0	87	10	US-09-834-975-62	Sequence 62, Appl1
c 33	11.4	57.0	95	10	US-09-878-574-920	Sequence 920, App
c 34	11.4	57.0	100	10	US-09-963-373-1195	Sequence 1195, Ap
c 35	11.2	56.0	16	10	US-09-823-847-38	Sequence 38, Appl1
c 36	11.2	56.0	18	10	US-09-969-373-3820	Sequence 3820, Ap
c 37	11.2	56.0	20	10	US-09-735-995-62	Sequence 62, Appl1
c 38	11.2	56.0	21	10	US-09-844-493-16	Sequence 16, Appl1
c 39	11.2	56.0	21	10	US-09-844-501-16	Sequence 16, Appl1
c 40	11.2	56.0	21	10	US-09-844-265-16	Sequence 16, Appl1
c 41	11.2	56.0	23	10	US-09-753-667A-9	Sequence 9, Appl1
c 42	11.2	56.0	28	10	US-09-898-323-7	Sequence 7, Appl1
c 43	11.2	56.0	28	10	US-09-898-323-16	Sequence 16, Appl1
c 44	11.2	56.0	29	10	US-09-957-974-10	Sequence 10, Appl1
c 45	11.2	56.0	29	10	US-09-898-323-4	Sequence 4, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-933-797-384  
; Sequence 384, Application US/09933797  
; Patent No. US20020155119A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert A. Sikes et al.  
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital  
; FILE REFERENCE: 9901-007-999  
; CURRENT APPLICATION NUMBER: US/09/933, 797  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: US/09/482, 933  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: PCT/US99/10746  
; PRIOR FILING DATE: 1999-05/14  
; PRIOR APPLICATION NUMBER: 60/085, 383  
; NUMBER OF SEQ ID NOS: 811  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 384  
; LENGTH: 63  
; TYPE: DNA  
; ORGANISM: Murine  
; US-09-933-797-384  
  
Query Match 70.0%; Score 14; DB 9; Length 63;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 3 TCTGTCTCTCAAT 16  
Db 50 TCTGTCTCTCAAT 63  
  
RESULT 2  
US-09-797-239-8  
; Sequence 8, Application US/09797239  
; Patent No. US20010012630A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoechst Marion Roussel  
; TITLE OF INVENTION: Yeast strains possessing the interrupted ATF2 gene and  
; their applications.

```

FILE REFERENCE: 2482 PCT SEQUENCES IN ENGLISH
CURRENT APPLICATION NUMBER: US/09/797,239
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 8
LENGTH: 52
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: OLIGONUCLEOTIDE
US-09-797-239-8

Query Match          68.0%; Score 13.6; DB 10; Length 52;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      1 TCTGTGCTCCCAATCGAA 20
        ||||| | | ||| ||
Db      2 TCTGTGTGACAAATGCGA 21

RESULT 3
US-09-760-139-33/c
Sequence 33, Application US/09760139
Patent No. US20020058304A1
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie S.
APPLICANT: Bellini, Daniel A.
TITLE OF INVENTION: Methods for Producing A Polypeptide
FILE REFERENCE: 5966,200-US
CURRENT APPLICATION NUMBER: US/09/760,139
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/482,751
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 45
TYPE: DNA
ORGANISM: Aspergillus oryzae
US-09-760-139-33

Query Match          66.0%; Score 13.2; DB 10; Length 45;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 TCTGTGCTCCCAATCG 18
        | | ||||| ||| ||
Db      2 TTATGTCTCCCAAGTCG 11

RESULT 4
US-09-905-291A-381/c
Sequence 381, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.

```

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1  APPLICANT: Hillan, Kenneth, J.
2  APPLICANT: Kiljavin, Ivar J.
3  APPLICANT: Mather, Jennie P.
4  APPLICANT: Pan, James
5  APPLICANT: Paoni, Nicholas F.
6  APPLICANT: Roy, Margaret Ann
7  APPLICANT: Stewart, Timothy A.
8  APPLICANT: Tumas, Daniel
9  APPLICANT: Williams, P. Mickey
10 APPLICANT: Wood, William, I.
11 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
12 FILE REFERENCE: 10466-14
13 CURRENT APPLICATION NUMBER: US/09/905,291A
14 CURRENT FILING DATE: 2001-07-12
15 PRIOR APPLICATION NUMBER: PCT/US00/04414
16 PRIOR FILING DATE: 2000-02-22
17 PRIOR APPLICATION NUMBER: US 60/143,048
18 PRIOR FILING DATE: 1999-07-07
19 PRIOR APPLICATION NUMBER: US 60/145,698
20 PRIOR FILING DATE: 1999-07-26
21 PRIOR APPLICATION NUMBER: US 60/146,222
22 PRIOR FILING DATE: 1999-07-28
23 PRIOR APPLICATION NUMBER: PCT/US99/20594
24 PRIOR FILING DATE: 1999-09-08
25 PRIOR APPLICATION NUMBER: PCT/US99/20944
26 PRIOR FILING DATE: 1999-09-13
27 PRIOR APPLICATION NUMBER: PCT/US99/21090
28 PRIOR FILING DATE: 1999-09-15
29 PRIOR APPLICATION NUMBER: PCT/US99/21547
30 PRIOR FILING DATE: 1999-09-15
31 PRIOR APPLICATION NUMBER: PCT/US99/23089
32 PRIOR FILING DATE: 1999-10-05
33 PRIOR APPLICATION NUMBER: PCT/US99/28214
34 PRIOR FILING DATE: 1999-11-29
35 PRIOR APPLICATION NUMBER: PCT/US99/28313
36 PRIOR FILING DATE: 1999-11-30
37 PRIOR APPLICATION NUMBER: PCT/US99/28564
38 PRIOR FILING DATE: 1999-12-02
39 PRIOR APPLICATION NUMBER: PCT/US99/28565
40 PRIOR FILING DATE: 1999-12-02
41 PRIOR APPLICATION NUMBER: PCT/US99/30095
42 PRIOR FILING DATE: 1999-12-16
43 PRIOR APPLICATION NUMBER: PCT/US99/30911
44 PRIOR FILING DATE: 1999-12-20
45 PRIOR APPLICATION NUMBER: PCT/US99/30999
46 PRIOR FILING DATE: 1999-12-20
47 PRIOR APPLICATION NUMBER: PCT/US00/00219
48 PRIOR FILING DATE: 2000-01-05
49 NUMBER OF SEQ ID NOS: 423
50 SEQ ID NO 381
51 LENGTH: 26
52 TYPE: DNA
53 ORGANISM: Artificial Sequence
54 FEATURE:
55 OTHER INFORMATION: Synthetic oligonucleotide probe
56 US-09-905-291A-381
57
58 Query Match 62.0%; Score 12.4; DB 9; Length 26;
59 Best Local Similarity 92.9%; Pred. No. 1.9e+03;
60 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
61
62 Oy 4 CTGCTCCCAATC 17
63 | | | | | | | | | |
64 Db 17 CTGCTCCCAATC 4
65
66 RESULT 5
67 US-09-909-320-381/C
68 ; Sequence 381, Application US/09909320
69 ; Patent No. US20020132240A1
70 ; GENERAL INFORMATION:
71 ; APPLICANT: Genentech, Inc.

```

APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/909,320  
CURRENT FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 381  
LENGTH: 26  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide probe  
US-09-909-320-381  
Query Match 62.0%; Score 12.4; DB 10; Length 26;

Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 CTGTCCTCAATC 17  
|||||||  
Db 17 CTGTCCTCAATC 4  
RESULT 6  
US-09-909-088B-381/c  
Sequence 381, Application US/09909088B  
Patent No. US20020146709A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/909,088B  
CURRENT FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20

;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
;; PRIOR FILING DATE: 2000-01-05  
;; NUMBER OF SEQ ID NOS: 423  
;; SEQ ID NO 381  
;; LENGTH: 26  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-09-909-0888-381

Query Match 62.0%; Score 12.4; DB 10; Length 26;  
Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGCTCCTCAATC 17  
DB 17 CTGCTCCTCAATC 4

RESULT 7  
US-09-969-373-1290/C  
; Sequence 1290 Application US/09969373  
; Patent No. US20020133852A1  
; GENERAL INFORMATION:  
; APPLICANT: Efferetz, Roger J.  
; APPLICANT: Hauge, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 1290  
; LENGTH: 95  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-1290

Query Match 62.0%; Score 12.4; DB 10; Length 95;  
Best Local Similarity 92.9%; Pred. No. 2.3e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TCCTCCAAATCGAA 20  
DB 73 TGCTCCAAATCGAA 60

RESULT 8  
US-09-969-373-838/C  
; Sequence 838 Application US/09969373  
; Patent No. US20020133852A1  
; GENERAL INFORMATION:  
; APPLICANT: Efferetz, Roger J.  
; APPLICANT: Hauge, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
US-09-969-373-838

;; SEQ ID NO 838  
;; LENGTH: 97  
;; TYPE: DNA  
;; ORGANISM: Glycine max  
US-09-969-373-838

Query Match 62.0%; Score 12.4; DB 10; Length 97;  
Best Local Similarity 92.9%; Pred. No. 2.3e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCTCCTCCTCAATC 14  
DB 67 TCCTCCTCCTCAATC 54

RESULT 9  
US-09-733-042-2  
; Sequence 2 Application US/09733042  
; Patent No. US20020168709A1  
; GENERAL INFORMATION:  
; APPLICANT: Hennecke, Frank  
; APPLICANT: Renner, Wolfgang A.  
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes  
; FILE REFERENCE: 1700.0100001  
; CURRENT APPLICATION NUMBER: US/09/733,042  
; CURRENT FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 60/169,988  
; PRIOR FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Enh-FOR  
US-09-733-042-2

Query Match 61.0%; Score 12.2; DB 9; Length 30;  
Best Local Similarity 82.4%; Pred. No. 2.5e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCTCCTCCTCAATC 17  
DB 5 TCCTCCTCCTCAATC 21

RESULT 10  
US-10-041-400A-5/C  
; Sequence 5 Application US/10041400A  
; Patent No. US20020110895A1  
; GENERAL INFORMATION:  
; APPLICANT: Darlow, Andrew  
; APPLICANT: Andrade-Gordon, Patricia  
; APPLICANT: Qi, Jensen  
; TITLE OF INVENTION: DNA Encoding the Human Serine  
; FILE REFERENCE: ORT-1031  
; CURRENT APPLICATION NUMBER: US/10/041,400A  
; CURRENT FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: US/09/387,375  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
US-10-041-400A-5

Query Match 61.0%; Score 12.2; DB 12; Length 30;  
Best Local Similarity 82.4%; Pred. No. 2.5e+03;



Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 TCTCTGTCCTCCAATC 17  
Db 19 TCTCGTCTCTAGATC 3

RESULT 11  
US-10-041-264A-5/c  
; Sequence 5, Application US/10041264A  
; Patent No. US20020142446A1  
; GENERAL INFORMATION:  
; APPLICANT: Darrow, Andrew  
; APPLICANT: Andrade-Gordon, Patricia  
; APPLICANT: Qi, Jensen  
; TITLE OF INVENTION: DNA Encoding the Human Serine  
; FILE REFERENCE: CRT-1031  
; CURRENT APPLICATION NUMBER: US/10/041,264A  
; CURRENT FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: US/09/387,375  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: oligonucleotide  
US-10-041-264A-5

Query Match 61.0%; Score 12.2; DB 12; Length 30;  
Best Local Similarity 82.4%; Pred. No. 2.5e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TCTCTGTCCTCCAATC 17  
Db 19 TCTCGTCTCTAGATC 3

RESULT 12  
US-10-042-091A-5/c  
; Sequence 5, Application US/10042091A  
; Patent No. US20020142447A1  
; GENERAL INFORMATION:  
; APPLICANT: Darrow, Andrew  
; APPLICANT: Andrade-Gordon, Patricia  
; APPLICANT: Qi, Jensen  
; TITLE OF INVENTION: DNA Encoding the Human Serine  
; FILE REFERENCE: CRT-1031  
; CURRENT APPLICATION NUMBER: US/10/042,091A  
; CURRENT FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: US/09/387,375  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: oligonucleotide  
US-10-042-091A-5

Query Match 61.0%; Score 12.2; DB 12; Length 30;  
Best Local Similarity 82.4%; Pred. No. 2.5e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 TCTCTGTCCTCCAATC 17

Db 19 TCTCGTCTCTAGATC 3

RESULT 13  
US-10-040-803-10/c  
; Sequence 10, Application US/10040803  
; Patent No. US20020164767A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrade-Gordon, Patricia  
; APPLICANT: Darrow, Andrew L.  
; APPLICANT: Qi, Jensen  
; TITLE OF INVENTION: DNA encoding human serine protease C-E  
; FILE REFERENCE: CRT-1030  
; CURRENT APPLICATION NUMBER: US/10/040,803  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-040-803-10

Query Match 61.0%; Score 12.2; DB 9; Length 33;  
Best Local Similarity 82.4%; Pred. No. 2.5e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TCTCTGTCCTCCAATC 17  
Db 19 TCTCGTCTCTAGATC 3

RESULT 14  
US-09-815-242-1629  
; Sequence 1629, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1629  
; LENGTH: 67  
; TYPE: DNA

; ORGANISM: Staphylococcus aureus  
US-09-815-242-1629

Query Match 61.0%; Score 12.2; DB 10; Length 67;  
Best Local Similarity 82.4%; Pred. No. 2.8e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCTGTCCTCCAATC 17  
|||||  
Db 3 TCCTGTCCTCCAATC 19

RESULT 15

US-09-828-538-17  
; Sequence 17, Application US/09828538  
; Patent No. US20010025031A1  
; GENERAL INFORMATION:  
; APPLICANT: Ellis, Catherine E.  
; APPLICANT: Kwok, Chenl  
; APPLICANT: Bodsworth, Nicola J.  
; APPLICANT: Halsey, Wendy  
; APPLICANT: Van Horn, Stephanie  
; TITLE OF INVENTION: HEGAN72 Receptor Genomic DNA and Methods  
; FILE REFERENCE: GH-50038-C1  
; CURRENT APPLICATION NUMBER: US/09/828,538  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/088,624  
; PRIOR FILING DATE: 1998-06-08  
; PRIOR APPLICATION NUMBER: 60/093,726  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: 09/328,014  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 96  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-828-538-17

Query Match 61.0%; Score 12.2; DB 10; Length 96;  
Best Local Similarity 82.4%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTCGTGCTCCAATCG 18  
|||||  
Db 22 CTCGTGCTCCAATCG 38

Search completed: November 23, 2002, 06:42:10  
Job time : 18.25 secs

Db 26 GCCGAACGAGGAGCCAGCA 9  
||||| |||||||  
RESULT 6  
LOCUS ARI27237 33 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 41 from patent US 6180391.  
ACCESSION ARI27237  
VERSION ARI27237.1 GI:14113830  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Brown,W.C.  
TITLE Highly efficient controlled expression of exogenous genes in e. coli  
JOURNAL Patent: US 6180391-A 41 30-JAN-2001;  
FEATURES  
source Location/Qualifiers  
1..33  
/organism="unknown"  
BASE COUNT 4 a 11 c 11 g 7 t  
ORIGIN  
Query Match 66.0%; Score 13.2; DB 6; Length 33;  
Best Local Similarity 83.3%; Pred. No. 3.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2 TCCGACGTGGAGCCAG 19  
||||| |||||||  
Db 12 TCCCTACGTGGCTCTAG 29  
||||| |||||||  
RESULT 7  
LOCUS ARI27238 33 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 42 from patent US 6180391.  
ACCESSION ARI27238  
VERSION ARI27238.1 GI:14113831  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Brown,W.C.  
TITLE Highly efficient controlled expression of exogenous genes in e. coli  
JOURNAL Patent: US 6180391-A 42 30-JAN-2001;  
FEATURES  
source Location/Qualifiers  
1..33  
/organism="unknown"  
BASE COUNT 8 a 10 c 10 g 5 t  
ORIGIN  
Query Match 66.0%; Score 13.2; DB 6; Length 33;  
Best Local Similarity 83.3%; Pred. No. 3.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2 TCCGACGTGGAGCCAG 19  
||||| |||||||  
Db 26 TCCCTACGTGGCTCTAG 9  
||||| |||||||  
RESULT 8  
LOCUS AX358674 35 bp DNA linear PAT 13-FEB-2002  
DEFINITION Sequence 52 from Patent W00190419.  
ACCESSION AX358674  
VERSION AX358674.1 GI:18675208  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.

artificial sequences.  
REFERENCE 1  
AUTHORS Stanton,V.P.  
TITLE Methods for genetic analysis of dna to detect sequence variances  
JOURNAL Patent: WO 0190419-A 52 29-NOV-2001;  
VARIAGENICS, Inc. (US) ; Stanton, Vincent P., Jr. (US)  
FEATURES  
source Location/Qualifiers  
1..35  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Exemplary motif"  
BASE COUNT 9 a 11 c 6 g 8 t 1 others  
ORIGIN  
Query Match 66.0%; Score 13.2; DB 6; Length 35;  
Best Local Similarity 83.3%; Pred. No. 3.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 3 GCCGACGTGGAGCCAGCA 20  
||||| |||||||  
Db 29 GCCGAGTGGAGACRCAGCA 12  
||||| |||||||  
RESULT 9  
LOCUS AX358675 35 bp DNA linear PAT 13-FEB-2002  
DEFINITION Sequence 53 from Patent W00190419.  
ACCESSION AX358675  
VERSION AX358675.1 GI:18675209  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Stanton,V.P.  
TITLE Methods for genetic analysis of dna to detect sequence variances  
JOURNAL Patent: WO 0190419-A 53 29-NOV-2001;  
VARIAGENICS, Inc. (US) ; Stanton, Vincent P., Jr. (US)  
FEATURES  
source Location/Qualifiers  
1..35  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Exemplary motif"  
BASE COUNT 8 a 6 c 11 g 9 t 1 others  
ORIGIN  
Query Match 66.0%; Score 13.2; DB 6; Length 35;  
Best Local Similarity 83.3%; Pred. No. 3.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 3 GCCGACGTGGAGCCAGCA 20  
||||| |||||||  
Db 7 GCCGAGTGGAGACRCAGCA 24  
||||| |||||||  
RESULT 10  
LOCUS ARI43578 44 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 34 from patent US 6204371.  
ACCESSION ARI43578  
VERSION ARI43578.1 GI:15104864  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 44)  
AUTHORS Levinson,D.Adam.  
TITLE Compositions and methods for the treatment and diagnosis of immune disorders  
JOURNAL Patent: US 6204371-A 34 20-MAR-2001;  
FEATURES  
source Location/Qualifiers  
1..44  
/organism="unknown"

BASE COUNT 9 a 15 c 10 g 10 t  
ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 44;  
Best Local Similarity 83.3%; Pred. No. 3.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCA 18  
|||||  
Db 33 GTGCAGACTTGGATCCA 16

RESULT 11  
LOCUS ARI168947 44 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 34 from patent US 6288218.  
ACCESSION ARI168947  
VERSION ARI168947.1 GI:17905145  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 44)  
AUTHORS Levinson,D.Adam.  
TITLE Compositions and methods for the treatment and diagnosis of immune disorders

JOURNAL Patent: US 6288218-A 34 11-SEP-2001;  
FEATURES Location/Qualifiers  
source 1..44  
/organism="unknown"  
BASE COUNT 9 a 15 c 10 g 10 t  
ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 44;  
Best Local Similarity 83.3%; Pred. No. 3.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCA 18  
|||||  
Db 33 GTGCAGACTTGGATCCA 16

RESULT 12  
LOCUS HSEXR2 90 bp DNA linear PRI 15-APR-1997  
DEFINITION H.sapiens exon trapped from 6q27, 4J4VSex100c4.  
ACCESSION X99574  
VERSION X99574.1 GI:1490304  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 90)  
Barna,U., Rouseaux,S. and Edwards,Y.H.  
TITLE Identification of exons in a region of human chromosome 6q known to contain tumour suppressor genes  
JOURNAL DNA Seq. 7 (1), 13-19 (1996)  
MEDLINE 97217669  
PUBMED 9063630

REFERENCE 2 (bases 1 to 90)  
AUTHORS Edwards,Y.H.  
TITLE Direct Submision  
JOURNAL Submitted (25-JUL-1996) Y.H. Edwards, Molfson House, MRC Human Biochemical Genetics Unit, UCL, 4 Stephenson Way, London, NW1 2HE, UK

FEATURES Location/Qualifiers  
source 1..90  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="6"  
/map="q27"  
/clone\_lib="IFGT 4J4"

gene 1..90  
/gene="4J4VSex11c4"  
exon 1..90  
BASE COUNT 26 a 23 c 18 g 23 t  
ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 90;  
Best Local Similarity 83.3%; Pred. No. 3.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCCGACGTGGACCCAG 19  
|||||  
Db 68 TGCCGACGTGGACACAG 85

RESULT 13  
LOCUS E11187 22 bp DNA linear PAT 29-SEP-1997  
DEFINITION Probe.  
ACCESSION E11187  
VERSION E11187.1 GI:22024828  
KEYWORDS JP 1996089300-A/2.  
SOURCE unidentified.  
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Tokuda,C., Fukuda,T. and Saito,I.  
TITLE METHOD FOR DETECTING NUCLEIC ACID  
JOURNAL Patent: JP 1996089300-A 2 09-APR-1996;  
MITSUI TOATSU CHEM INC, MITSUI PHARMACEUT INC  
OS None  
OC Artificial sequences.  
PM JP 1996089300-A/2  
PD 09-APR-1996  
PF 28-SEP-1994 JP 1994232637  
PI TOKUDA CHIKASHI, FUKUDA TAMOTSU, SATO IZUMI  
PC C1201/68.G01N33/58//C12M15/09,C1201/70;  
CC strandedness: Single;  
CC topology: Linear;  
FH key Location/Qualifiers  
FT source 1..22  
/organism="Artificial sequences".

FEATURES Location/Qualifiers  
source 1..22  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 7 a 6 c 7 g 2 t  
ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 22;  
Best Local Similarity 87.5%; Pred. No. 5.6e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGACGTGGACCCAG 19  
|||||  
Db 1 CCGAATGGGACCCAG 16

RESULT 14  
LOCUS AX019309 24 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 9 from Patent W09940221.  
ACCESSION AX019309  
VERSION AX019309.1 GI:10043296  
KEYWORDS  
SOURCE human.  
ORGANISM human  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 24)  
Dahn,M.W., Phelps,R.C. and Brockmeyer,C.

## TITLE

Method for quantitatively analyzing tumor cells in a body fluid and test kits suited therefor

## JOURNAL

Patent: WO 9840221-A 9 12-AUG-1999;

DAHM MICHAEL W (DE); PHELPS ROBERT C (DE); BROCKMEYER CARSTEN (DE)

## FEATURES

Location/Qualifiers

1. .24

/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 3 a 9 c 6 g 6 t

## ORIGIN

## Query Match

64.0%; Score 12.8; DB 6; Length 24;

Best Local Similarity 87.5%; Pred. No. 5.6e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 CGACGTGGAGCCAGA 20

Db 19 CGTCGTGGAGCCAGA 4

## RESULT 15

## LOCUS

AR065111 25 bp DNA linear PAT 29-SEP-1999

## DEFINITION

Sequence 1 from patent US 5849487.

## ACCESSION

AR065111

## VERSION

AR065111.1 GI:5995327

## KEYWORDS

Unknown.

## SOURCE

Unknown.

## ORGANISM

Unknown.

## REFERENCE

1 (bases 1 to 25)

## AUTHORS

Base,T. and Masubuchi,H.

## TITLE

Nucleic acid detection by repetitive synthesis and degradation of a

nucleotide on a nuclease resistant oligonucleotide

Patent: US 5849487-A 1 15-DEC-1998;

Location/Qualifiers

1. .25

/organism="unknown"

BASE COUNT 7 a 8 c 7 g 3 t

ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 25;

Best Local Similarity 87.5%; Pred. No. 5.6e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCGACGTGGAGCCAG 19

Db 3 CCGAATGGAGCCAG 18

Search completed: December 3, 2002, 18:13:03

Job time : 309.2 secs

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C	10	13.6	68.0	65	24	ABN29817	Rat spliced transcrit
C	11	13.4	67.0	50	22	AAL34194	Human SNP oligonuc
C	12	13.2	66.0	27	20	AAK03341	PCR primer used to
C	13	13.2	66.0	33	20	AAK89941	Sequence of primer
C	14	13.2	66.0	33	20	AAH89942	Sequence of primer
C	15	13.2	66.0	35	24	ABL32002	Dihydropyrimidine
C	16	13.2	66.0	44	17	AAT338282	Murine I03 gene 3'
C	17	13.2	66.0	44	21	AAA51915	Reverse primer to
C	18	13.2	66.0	44	22	AAI70278	Murine I03 gene rev
C	19	13.2	66.0	44	22	AAD03383	3' primer, to ampli
C	20	13.2	66.0	44	22	AAF82626	Murine TH2-enriched
C	21	13.2	66.0	44	22	AAE29152	Murine TH2 gene PCR
C	22	13.2	66.0	44	22	AAF23475	3' oligonucleotide
C	23	13.2	66.0	65	24	ABN31280	Rat spliced transcr
C	24	13.2	66.0	83	21	AACT1161	Human secreted prote
C	25	12.8	64.0	22	17	AAT36509	Synthetic probe A
C	26	12.8	64.0	24	20	AAZ00723	Human telomerase c
C	27	12.8	64.0	25	16	ABO92893	Nuclease resistant
C	28	12.8	64.0	35	24	ABL51942	Ankyrin repeat mod
C	29	12.8	64.0	36	21	AAA35872	Permutated linker e
C	30	12.8	64.0	36	21	AAA35873	Permutated linker e
C	31	12.8	64.0	51	22	AAI28412	Human SNP oligonuc
C	32	12.8	64.0	53	17	AAT36510	Synthetic probe B
C	33	12.8	64.0	62	18	AAT47610	Primer p651 for h
C	34	12.8	64.0	70	13	AAO32146	Probe specific to
C	35	12.8	64.0	70	13	AAO32144	Probe specific to
C	36	12.6	63.0	20	18	AAT85719	Placental growth h
C	37	12.6	63.0	20	24	ABK46991	COX-2 antisense ol
C	38	12.6	63.0	27	16	AAO75152	GIT-II NEO casette
C	39	12.6	63.0	27	21	AAZ92601	Neomycin resistanc
C	40	12.6	63.0	30	22	AAK08319	Human CLASP-1, PCP
C	41	12.6	63.0	30	22	AAK07399	CLASP-1 PCR prim
C	42	12.6	63.0	30	22	AAH41906	Human CLASP-1 PCR
C	43	12.6	63.0	30	24	ABK84952	Cadherin-like asym
C	44	12.6	63.0	30	24	ABK84953	Cadherin-like asym
C	45	12.6	63.0	30	24	AAK18922	Human CLASP-1 anti

ALIGNMENTS

RESULT 1						
ID	AAZ31440	standard;	DNA;	20 BP.		
XX	AAZ31440:					
DT	07-FEB-2000	(first entry)				
XX						
DE	Human neuropilin mRNA specific antisense oligo GTT3610.					
XX						
KW	Neuropilin: human; growth; metastasis; tumor; neovascularisation;					
KW	cancer; papilloma; diabetic retinopathy; antisense; ss.					
OS	Synthetic.					
OS	Homo sapiens.					
XX						
PN	WO955855-A2.					
XX						
PD	04-NOV-1999.					
XX						
PF	23-APR-1999;	99MO-CA00324.				
XX						
PR	23-APR-1998;	98US-0082791.				
XX						
PA	(GENE-) GENENSENSE TECHNOLOGIES INC.					
XX						
PI	Wright JA, Young AH, Lee YS;					
XX						
DR	WPI; 2000-023357/02.					
XX						
PT	Antisense oligonucleotides that inhibit neuropilin expression, useful for treating cancer -					

```

XX Claim 4; Page 16; 57pp; English.
PS
XX Sequences AA231431-460 represent antisense oligonucleotides which
CC inhibit human neutrophil expression. The antisense oligonucleotides can
CC be used to inhibit the growth or metastasis of a mammalian tumor and
CC inhibit neovascularisation. The oligonucleotides may be used to treat
CC various forms of cancers or tumors, such as sarcomas, melanomas,
CC adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell
CC carcinomas of the mouth, throat, larynx and lung, genitourinary cancers
CC such as cervical and bladder cancer, hematopoietic cancers, colon cancer,
CC breast cancer, pancreatic cancer, renal cancer, brain cancer, skin
CC cancer, liver cancer, head and neck cancers, and nervous system cancers,
CC as well as benign lesions such as papillomas. The methods may be used to
CC treat neovascularisation disorders such as diabetic retinopathy, and
CC retinopathy of prematurity and age related macular degeneration.
XX
SQ Sequence 20 BP; 4 A; 6 C; 8 G; 2 T; 0 other;

Query Match      100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCAGA 20
   ||||||||||||||||
Db 1 GTGCCGACGTGGACCCAGA 20

RESULT 2
AAF97678/C
ID AAF97678 standard; DNA; 21 BP.
XX
AC AAF97678;
XX
DF 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #2439.
XX
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KM polymorphism; vascular disease; coronary artery disease; forensics;
KM myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KM pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,A)
FT /tag a
FT /standard_name= "single nucleotide polymorphism"
PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
XX 07-SEP-2000; 2000WO-US24503.
XX
XX 10-SEP-1999; 99US-0153357.
XX 26-JUL-2000; 2000US-0220947.
XX 16-AUG-2000; 2000US-0225724.
XX
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JT,
PI WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis -
XX
PS Examples; Page 213; 242pp; English.

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XX The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism
CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification.
XX
SQ Sequence 21 BP; 3 A; 8 C; 6 G; 4 T; 0 other;

Query Match      90.0%; Score 18; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCA 18
   ||||||||||||||||
Db 18 GTGCCGACGTGGACCCA 1

RESULT 3
AAS07631
ID AAS07631 standard; DNA; 27 BP.
XX
AC AAS07631;
XX
DT 23-OCT-2001 (first entry)
XX
DE Streptococcus coelicolor mmyTOG promoter PCR primer CR344.
XX
XX SCp1: ss: methylenomycin cluster; mmc: MmyR; MmfP; MmfI; mmyTOG;
KM MmfU; MmfR; MmyT; MmyG; MmyG; MmyU; Mmr; heterologous gene expression;
KM PCR primer; CR344.
XX
OS Streptococcus coelicolor.
XX
XX WO200148228-A1.
XX
PN 05-JUL-2001.
XX
PD 20-DEC-2000; 2000WO-GB04972.
XX
XX 23-DEC-1999; 99GB-0030477.
XX
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Chater KF, Bruton CJ, O'Rourke SJ, Wietzorrek AW;
XX
XX WPI; 2001-425675/45.
XX
XX Novel expression cassette for expressing a nucleic acid of interest,
PT derived from the regulatory region of methylenomycin gene cluster of
PT SCp1 plasmid of Streptomyces coelicolor A3(2) -
XX
XX Example 11; Page 75; 142pp; English.
XX
XX The sequence represents a PCR primer used to amplify the promoter mmyTOG
CC from an expression cassette SCp1 (the regulatory region of the
CC methylenomycin cluster (mmc) from Streptomyces coelicolor A3(2), which
CC encodes the MmyR, MmfP, MmfH, MmfI, MmfR, MmyT, MmyG, MmyU and
CC partial Mmr polypeptides) for use as a strong promoter for heterologous
CC gene expression. The expression cassette is useful for expressing a
CC nucleic acid of interest, substantially only when the host cell culture
CC reaches high cell density at or close to the stationary phase of host
CC cell culture. In particular the system is useful in regulating
CC methylenomycin production. Reduced or no expression of the nucleic acid
CC of interest is observed earlier in growth, avoiding toxic effects of some
CC gene products on growth and the system does not require addition of a
CC exogenous inducer. The methylenomycin cluster naturally present on a

```



CC highly transmissible plasmid permits properly regulated expression in  
CC diverse streptomyces host and the expression is driven by a strong  
CC promoter, leading to high yield of the desired end product.

XX  
XX  
SQ Sequence 27 BP; 3 A; 12 C; 9 G; 3 T; 0 other;

Query Match 69.0%; Score 13.8; DB 22; Length 27;

Best Local Similarity 88.2%; Pred. No. 2.6e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GCCGACGTGGGACCCAG 19

DB 3 GCCGACGTGGGACCCAG 19

RESULT 4  
AAK83785/C

ID AAK83785 standard; DNA; 28 BP.

XX  
XX  
AC AAK83785;

DT 06-SEP-1999 (first entry)

XX  
XX  
DE PmeI restriction endonuclease PCR primer PmeI-IP1.

XX  
XX  
KW PmeI restriction endonuclease; modification methylase;

KM recombinant DNA technique; molecular cloning; gene characterization;

KM Pseudomonas mendocina; PCR primer; ss.

OS Synthetic.

OS Pseudomonas mendocina.

PN EP931835-A2.

PD 28-JUL-1999.

PF 24-NOV-1998; 98BP-0309629.

PR 24-NOV-1997; 97US-0976703.

XX  
XX  
PA (NEW) NEW ENGLAND BIOLABS INC.

PI Chang Z, Morgan RD;

DR WPI: 1999-397163/34.

XX  
XX  
PT New restriction endonuclease useful in recombinant DNA techniques

PS Example 1; Page 9; 28pp; English.

CC The present sequence represents a PCR primer for the 27 kD

CC Pseudomonas mendocina PmeI restriction endonuclease protein. The PmeI

CC restriction endonuclease is used to cut DNA in the middle of the site

CC GTTAAAC between the third T and the first A, to produce blunt ends.

CC The PmeI restriction endonuclease is therefore useful in recombinant

CC DNA techniques such as molecular cloning and gene characterization.

XX  
XX  
SQ Sequence 28 BP; 5 A; 7 C; 10 G; 6 T; 0 other;

OY 2 TCCGACGTGGGACCCA 18

DB 19 TCCGACGTGGGATCCA 3

RESULT 5

AAK34511/C

ID AAK34511 standard; DNA; 50 BP.

XX  
XX  
AC AAK34511;

XX  
XX  
DT 24-JAN-2002 (first entry)

XX  
XX  
DE Human SNP oligonucleotide #7719.

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;

KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;

KW amyloid protein; angiotensin; apoptosis related protein; cadherin;

KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

KW complement related protein; cytochrome; kinesin; cytokine; interferon;

KW interleukin; G-protein coupled receptor; thioesterase; inflammation;

KW multifactorial disease; autoimmune disease; infection;

XX  
XX  
OS Homo sapiens.

XX  
XX  
PN WO200147944-A2.

XX  
XX  
PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

XX  
XX  
PA (CURA-) CURAGEN CORP.

XX  
XX  
PI Shinkets RA, Leach M;

DR WPI: 2001-465210/50.

XX  
XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,

PT oncogenes and histones, useful for diagnosing and treating, e.g.

PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 3620; 4143pp; English.

CC The present invention relates to oligonucleotides encoding polymorphic

CC variants of proteins related to amylases, amyloid proteins, angiotensin,

CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,

CC histones, kinases, colony stimulating factors, complement related

CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,

CC G-protein coupled receptors and thioesterases. The present sequence is

CC one such oligonucleotide. The oligonucleotides and the peptides encoded

CC by them may be used in the prevention, diagnosis and treatment of

CC diseases associated with inappropriate expression of the proteins listed

CC above. Disorders that may be prevented, diagnosed and/or treated include

CC multifactorial diseases with a genetic component, such as autoimmune

CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,

CC systemic lupus erythematosus and Grave's disease), inflammation, cancer

CC (e.g. cancers of the bladder, brain, breast, colon and kidney,

CC leukaemia), diseases of the nervous system and an infection of pathogenic

XX  
XX  
SQ Sequence 50 BP; 7 A; 15 C; 17 G; 11 T; 0 other;

OY 3 GCCGACGTGGGACCCAG 19

DB 26 GCCCAAGTGGGACCCAG 10

RESULT 6

ABN29579

ID ABN29579 standard; DNA; 65 BP.

XX  
XX  
AC ABN29579;

DT 15-JUL-2002 (first entry)

```

DE Rat spliced transcript detection oligonucleotide SEQ ID NO:2327.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KM splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Rattus norvegicus.
XX
PN MO200210449-A2.
XX
PD 07-FEB-2002.
XX
PE 20-JUL-2001; 2001MO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
PA Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI WPI; 2002-257383/30.
DR
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
XX Example 1; SEQ ID 2327; 47bp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 65 BP; 14 A; 14 C; 18 G; 19 T; 0 other;
XX
XX Query Match 69.0%; Score 13.8; DB 24; Length 65;
XX Best Local Similarity 88.2%; Pred. No. 2.6e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 3 GCCGACGTGGAGCCAG 19
XX 11 111111111 1111
DB 23 GCAGACGCTGGAGCCAG 39
XX
RESULT 7
AAI79205
ID AAI79205 standard; DNA; 27 BP.
XX
XX AAI79205;
XX
XX 11-JUN-1999 (first entry)
XX
XX

```

```

DE H. vulgare cysteine protease PCR primer GSP1.
XX
XX Cysteine protease; barley; transgenic plant; disease resistance;
KM prevention; treatment; infection; stress; temperature; drought; salt;
KM wound; root-specific expression; antimicrobial; antistress;
KM anti-wounding; PCR primer; ss.
XX
XX Synthetic.
OS Hordeum vulgare.
XX
XX MO9910500-A1.
XX
XX 04-MAR-1999.
XX
XX 21-AUG-1998; 98MO-EP05339.
XX
XX 22-JAN-1998; 98DE-1002384.
PR 26-AUG-1997; 97DE-1037118.
XX
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA Antoniw J, Schlichter U, Steinbiss H;
PI WPI; 1999-204668/17.
DR
XX Nucleic acid encoding plant cysteine protease - that increases
PT resistance to injury and infection
XX
XX Example 5; Page 71; 81bp; German.
XX
XX This invention describes a novel Hordeum vulgare cysteine protease
CC which is used to produce transgenic plants with (a) increased
CC or reduced expression of protease or (b) increased resistance to disease
CC (particularly prevention or treatment of infection) or other stress
CC factors such as extreme temperatures, drought, salt or wounding. The
CC invention also describes a regulatory region which is used to provide
CC root-specific expression of heterologous DNA following infection/injury
CC of roots. The products of the invention have antimicrobial, antistress
CC and anti-wounding activity in plants.
XX
XX
SQ Sequence 27 BP; 6 A; 6 C; 11 G; 4 T; 0 other;
XX
XX Query Match 68.0%; Score 13.6; DB 20; Length 27;
XX Best Local Similarity 80.0%; Pred. No. 3.2e+03;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 GTGCCGACGTGGAGCCAGA 20
XX 111 111 11 11111111
DB 6 GTGTGACCTGCGACCCAGA 25
XX
RESULT 8
AAI79205/C
ID AAI79205 standard; DNA; 51 BP.
XX
XX AAI79205;
XX
XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:6146.
DE
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000MO-US32758.
XX
XX

```

PR 30-NOV-1999; 99US-0168138.  
XX 29-NOV-2000; 2000US-0726173.  
XX (CURA-) CURAGEN CORP.  
XX Shimkets RA, Leach M;  
XX WPI; 2001-356160/37.  
XX  
PT Polymorphic nucleic acid sequences, useful in genetic testing and  
XX therapy -  
XX  
PS Claim 1; Page 2390; 2653pp; English.  
XX  
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).  
CC AA53114 to AA53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (1) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides.  
CC For example, (1) may be used to treat disorders by rectifying mutations  
CC or deletions in a patient's genome that affect the activity of  
CC polypeptides by expressing inactive proteins or to supplement the  
CC patients own production of polypeptide. Additionally, (1) and its  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays to detect and quantitate the presence of similar nucleic acids  
CC in samples, and therefore which patients may be in need of restorative  
CC therapy. The polypeptides encoded by (1) may be used as antigens in the  
CC production of antibodies specific for polymorphic polypeptides. The  
CC antibodies may also be used to down regulate expression and activity.  
CC The antibodies may also be used as diagnostic agents for detecting the  
CC presence of polymorphic polypeptides in samples.  
XX  
SQ Sequence 51 BP; 14 A; 18 C; 12 G; 7 T; 0 other;  
XX  
Query Match 68.0%; Score 13.6; DB 22; Length 51;  
Best Local Similarity 80.0%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
XX  
QY 1 GTGCCGACGTGGACCCAGA 20  
XX ||| ||||| |||||  
DB 45 GTTCACAGCGTGGCGCAGA 26  
XX  
RESULT 9  
ABN29322  
ID ABN29322 standard; DNA: 65 BP.  
XX  
AC ABN29322;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Rat spliced transcript detection oligonucleotide SEQ ID NO:2070.  
XX  
KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Rattus norvegicus.  
XX  
PN WO200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB01903.  
XX  
PR 28-JUL-2000; 2000US-221607P.  
PR 02-MAY-2001; 2001US-287724P.  
XX  
XX (COMP-) COMPUGEN INC.  
XX  
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX

DR WPI; 2002-257383/30.  
XX  
XX  
PT New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of  
PT a genome, useful for detecting "tissue", "pathology", and  
PT developmental-specific genes -  
XX  
PS Example 1; SEQ ID 2070; 47pp; English.  
XX  
XX The present invention describes oligonucleotide libraries for detecting  
XX messenger RNAs that populate a (sub-)transcriptome, where the  
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
XX transcription units that populate a genome. The library comprises  
XX several oligonucleotides, each capable of hybridizing selectively to a  
XX set of messenger RNAs transcribed from a given transcription unit of  
XX the genome, which encodes one or more messenger RNA splice variants.  
XX The oligonucleotide libraries are useful for detecting mRNAs from a  
XX biological sample, in expression profiling studies, in qualitatively or  
XX quantitatively characterizing the corresponding transcriptome, and in  
XX detecting RNA transcripts and splice variants of human or animal  
XX transcriptomes. The libraries may also be used as specialised mini  
XX libraries to detect transcripts of a sub-transcriptome under a  
XX particular biological or pathological state, and so allowing the  
XX detection of tissue- and pathology-specific genes such as those genes  
XX only expressed in specific tissue under a specific pathological  
XX condition; to detect developmental specific genes; and to detect RNA  
XX transcripts and splice variants of a transcriptome of a patient suffering  
XX from a particular disorder. ABN27253 to ABN55589 represent  
XX oligonucleotide sequences from rats, humans and mice, which are used in  
XX the exemplification of the present invention.  
XX N.B. The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 65 BP; 19 A; 16 C; 18 G; 12 T; 0 other;  
XX  
Query Match 68.0%; Score 13.6; DB 24; Length 65;  
Best Local Similarity 80.0%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
XX  
QY 1 GTGCCGACGTGGACCCAGA 20  
XX ||| ||||| |||||  
DB 5 GTTCACAGCGTGGACCCAGA 24  
XX  
RESULT 10  
ABN29817/c  
ID ABN29817 standard; DNA: 65 BP.  
XX  
AC ABN29817;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Rat spliced transcript detection oligonucleotide SEQ ID NO:2565.  
XX  
KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Rattus norvegicus.  
XX  
PN WO200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB01903.  
XX  
PR 28-JUL-2000; 2000US-221607P.  
PR 02-MAY-2001; 2001US-287724P.  
XX  
XX (COMP-) COMPUGEN INC.  
XX  
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX

DR WPI; 2002-257383/30.  
XX  
XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of  
PT a genome, useful for detecting tissue-, pathology-, and  
PT developmental-specific genes -  
XX  
XX Example 1; SEQ ID 2565; 47pp; English.  
XX  
XX The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the  
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises  
CC several oligonucleotides, each capable of hybridizing selectively to a  
CC set of messenger RNAs transcribed from a given transcription unit of  
CC the genome, which encodes one or more messenger RNA splice variants.  
CC The oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterizing the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a  
CC particular biological or pathological state, and so allowing the  
CC detection of tissue- and pathology-specific genes such as those genes  
CC only expressed in specific tissue under a specific pathological  
CC condition; to detect developmental specific genes; and to detect RNA  
CC transcripts and splice variants of a transcriptome of a patient suffering  
CC from a particular disorder. ABN27253 to ABN59589 represent  
CC oligonucleotide sequences from rats, humans and mice, which are used in  
CC the exemplification of the present invention.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 65 BP; 16 A; 23 C; 14 G; 12 T; 0 other;  
OY Query Match 68.0%; Score 13.6; DB 24; Length 65;  
Best Local Similarity 80.0%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
DB 1 GTGCGACGTGGAGCCAGA 20  
20 GTGCCGATGTGGCACTGCA 1

RESULT 11  
AAL34194/C  
ID AAL34194 standard; DNA; 50 BP.  
XX  
AC AAL34194;  
XX  
XX 24-JAN-2002 (first entry)  
DE Human SNP oligonucleotide #7402.  
XX  
XX  
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200147944-A2.  
PN  
XX  
XX 05-JUL-2001.  
PD  
XX  
XX 28-DEC-2000; 2000WO-US35498.  
PF  
XX  
XX 28-DEC-1999; 99US-0173419.  
PR

PR 27-DEC-2000; 2000US-0173419.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX  
XX Shinkets RA, Leach M;  
PI  
XX  
XX WPI; 2001-465210/50.  
DR  
XX  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -  
XX  
XX Claim 1; Page 3517; 4143pp; English.  
PS  
XX  
XX The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.  
XX  
SQ Sequence 50 BP; 4 A; 26 C; 13 G; 7 T; 0 other;  
OY Query Match 67.0%; Score 13.4; DB 22; Length 50;  
Best Local Similarity 93.3%; Pred. No. 4e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
DB 1 GTGCCGACGTGGAGC 15  
29 GTGCCGACGTGGGCGC 15

RESULT 12  
AA03341/C  
ID AA03341 standard; DNA; 27 BP.  
XX  
AC AA03341;  
XX  
XX 26-MAR-1999 (first entry)  
DT  
XX  
XX PCR primer used to delete nucleotides 654-671 of HIV-1.  
DE  
XX  
XX Primer binding site; PBS; HIV-1; megaprimer; mutant; attenuated virus;  
KW DNA polymerization; ML84V mutated HIV-1 reverse transcriptase;  
KW vaccine; acquired immunodeficiency syndrome; AIDS; PCR primer; ss.  
XX  
XX Synthetic.  
OS  
XX Human immunodeficiency virus type 1.  
PN  
XX  
XX WO9900490-A2.  
PD  
XX  
XX 07-JAN-1999.  
PF  
XX  
XX 26-JUN-1998; 98WO-CA00617.  
PR  
XX  
XX 26-JUN-1997; 97CA-2208946.  
PA (DAVI-) DAVIS-JEWISH GEN HOSPITAL MORTIMER B.  
PI  
XX  
XX Wainberg MA;  
XX  
XX WPI; 1999-095736/08.  
DR

PT New nucleic acid encoding an attenuated human immunodeficiency virus  
PT - containing a deletion downstream of the primer binding site and  
PT is useful as a vaccine against acquired immune deficiency syndrome  
XX  
PS Example 1; Page 16; 41pp; English.  
XX  
CC The present PCR primer is used (with primer AAX03301) to delete  
CC nucleotides 654-671 in sequences surrounding the primer binding site  
CC (PBS) of Human Immunodeficiency virus type 1 (HIV-1). The amplification  
CC reactions produce nucleotide deleted mutant HIV-1 sequences. The  
CC specification describes deletion mutant viruses, where the deletion is  
CC located immediately downstream of PBS, and permits attenuation of the  
CC virus, as expressed by the PBS. More specifically, the deletion is within  
CC or includes either the 54 nucleotide segment immediately downstream of  
CC the PBS, or 16 nucleotide segment at the 3' end of the 54 nucleotide  
CC segment. The molecule also preferably includes the known M184V  
CC substitution. The deletion in the 54-nucleotide segment reduces the  
CC fidelity of the RNA- and DNA-dependent DNA polymerization of M184V  
CC mutated HIV-1 reverse transcriptase. The 54 nucleotide segment is needed  
CC for efficient reverse transcription of the viral DNA product, and  
CC efficient generation of viral RNA, which affects subsequent viral  
CC protein synthesis and infectivity. The attenuated HIV (preferably HIV-1)  
CC forms a vaccine for immunizing a mammal (preferably a human) against  
CC HIV, which prevents acquired immunodeficiency syndrome (AIDS).  
XX  
SQ Sequence 27 BP; 3 A; 7 C; 11 G; 6 T; 0 other;  
XX  
Query Match 66.0%; Score 13.2; DB 20; Length 27;  
Best Local Similarity 83.3%; Pred. No. 5e+03; 3; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 GCCGACGTGGAGCCAGA 20  
Db 26 GCCGACGAGGAGCCAGA 9  
|||||  
AAX89941  
ID AAX89941 standard; DNA; 33 BP.  
XX  
AC AAX89941;  
XX  
DT 18-OCT-1999 (first entry)  
XX  
DE Sequence of primer 1553-73.  
XX  
KW Translational repression system; translational repressor; coat protein;  
KW constitutive promoter; heterologous gene; bacteriophage MS2; toxic gene;  
KW transcriptional control protein; mola; asla; bacteriophage T4;  
KW PCR primer; protease gene; ss.  
XX  
XX  
OS Synthetic.  
OS Bacteriophage sp.  
XX  
PN MO9938985-A2.  
XX  
PD 05-AUG-1999.  
XX  
PF 27-JAN-1999; 99WO-US01725.  
XX  
PR 26-JAN-1999; 99US-0237712.  
PR 28-JAN-1998; 98US-0072794.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI BROWN WC;  
XX  
DR WPI; 1999-494095/41.  
XX  
PT A bacteriophage MS2 translational repression system for use in  
PT cloning or expressing specific heterologous genes, especially toxic  
PT genes  
XX

PS Examples; Page 63; 133pp; English.  
XX  
CC The invention relates to a translational repression system comprising a  
CC translational repressor operably linked to a constitutive promoter for  
CC use in cloning or expressing a specific heterologous gene. The improved  
CC translational repressor is bacteriophage MS2 coat protein. The improved  
CC expression vector systems are capable of expressing exogenous genes,  
CC including toxic genes, in Escherichia coli and other host cells. The  
CC bacteriophage MS2-based system can be used to stably clone and express  
CC certain toxic genes. The MS2-based T4 cassette is useful for the cloning  
CC of accessory proteins that are useful in the production of a target  
CC protein. The vector systems overcome the problem of promoter leakiness  
CC which leads to inappropriate transcription and expression of a gene  
CC cloned under the control of the promoter. This can be a problem when  
CC cloning toxic genes. The transcriptional control proteins, e.g. mola and  
CC asla of bacteriophage T4, regulate transcription and provide a staged  
CC inducible promoter system which is much less complicated and more  
CC versatile than prior art non-staged systems. T4 middle promoters direct  
CC transcription from specific promoters while inhibiting transcription  
CC from E. coli promoters, which therefore minimises competition for  
CC translational apparatus and inhibits the cell from responding to target  
CC protein production by inducing transcription of protease genes.  
CC Sequences AAX89905-998 represent PCR primers used in the course of the  
CC invention.  
XX  
SQ Sequence 33 BP; 4 A; 11 C; 11 G; 7 T; 0 other;  
XX  
Query Match 66.0%; Score 13.2; DB 20; Length 33;  
Best Local Similarity 83.3%; Pred. No. 5e+03; 3; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TGCCGACGTGGAGCCAG 19  
Db 12 TGCCACTGCTGCTCTAC 29  
|||||  
AAX89942/C  
ID AAX89942 standard; DNA; 33 BP.  
XX  
AC AAX89942;  
XX  
DT 18-OCT-1999 (first entry)  
XX  
DE Sequence of primer 1553-74.  
XX  
KW Translational repression system; translational repressor; coat protein;  
KW constitutive promoter; heterologous gene; bacteriophage MS2; toxic gene;  
KW transcriptional control protein; mola; asla; bacteriophage T4;  
KW PCR primer; protease gene; ss.  
XX  
XX  
OS Synthetic.  
OS Bacteriophage sp.  
XX  
PN MO9938985-A2.  
XX  
PD 05-AUG-1999.  
XX  
PF 27-JAN-1999; 99WO-US01725.  
XX  
PR 26-JAN-1999; 99US-0237712.  
PR 28-JAN-1998; 98US-0072794.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI BROWN WC;  
XX  
DR WPI; 1999-494095/41.  
XX  
PT A bacteriophage MS2 translational repression system for use in  
PT cloning or expressing specific heterologous genes, especially toxic  
PT genes  
XX

PS Examples: Page 63; 133pp; English.  
XX  
CC The invention relates to a translational repression system comprising a  
CC translational repressor operably linked to a constitutive promoter for  
CC use in cloning or expressing a specific heterologous gene. The  
CC translational repressor is bacteriophage MS2 coat protein. The improved  
CC expression vector systems are capable of expressing exogenous genes,  
CC including toxic genes, in *Escherichia coli* and other host cells. The  
CC bacteriophage MS2-based system can be used to stably clone and express  
CC certain toxic genes. The MS2-based T4 cassette is useful for the cloning  
CC of accessory proteins that are useful in the production of a target  
CC protein. The vector systems overcome the problem of promoter leakiness  
CC which leads to inappropriate transcription and expression of a gene  
CC cloned under the control of the promoter. This can be a problem when  
CC cloning toxic genes. The transcriptional control proteins, e.g. *motA* and  
CC *asfA* of bacteriophage T4, regulate transcription and provide a staged  
CC inducible promoter system which is much less complicated and more  
CC versatile than prior art non-staged systems. T4 middle promoters direct  
CC transcription from specific promoters while inhibiting transcription  
CC from E. coli promoters, which therefore minimizes competition for  
CC translational apparatus and inhibits the cell from responding to target  
CC protein production by inducing transcription of protease genes.  
CC Sequences AAX89905-998 represent PCR primers used in the course of the  
CC invention.  
XX  
SQ Sequence 33 BP; 8 A; 10 C; 10 G; 5 T; 0 other;  
XX  
Query Match 66.0%; Score 13.2; DB 20; Length 33;  
Best Local Similarity 83.3%; Pred. No. 5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2 TGCGGACGTGGACCCAG 19  
||| ||||| |||  
Db 26 TGCGTACGTGGCTCTAG 9  
||| ||||| |||  
RESULT 15  
ABL32002/c  
ID ABL32002 standard; DNA; 35 BP.  
XX  
AC ABL32002;  
XX  
DT 22-MAR-2002 (first entry)  
XX  
DE Dihydropyrimidine dehydrogenase (DPD) DNA fragment #1.  
XX  
KM Genetic analysis: sequence variant detection; genotype: ApoE: SNP;  
KM single nucleotide polymorphism; polymorphic site; atherosclerosis;  
KM dementia; Parkinson's disease; Huntington's disease; PCR primer;  
KM neurodegenerative disease; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200190419-A2.  
PD 29-NOV-2001.  
XX  
PF 23-MAY-2001; 2001WO-US16577.  
XX  
PR 23-MAY-2000; 2000US-206613P.  
PR 25-OCT-2000; 2000US-069698.  
PR 25-OCT-2000; 2000US-0697013.  
XX  
PA (VAR-) VARIAGENTS INC.  
PA (STAN/) STANTON V P.  
XX  
PI Stanton VP.  
XX  
WPI: 2002-097670/13.  
DR  
XX  
PT Determining the haplotype of at least one allele of a selected gene at  
PT two or more polymorphic sites, for assessing disease risk, comprises

PT allele-specific enrichment, optical mapping, or atomic force microscopy  
PT  
XX  
PS Example 1; Fig 22; 166pp; English.  
XX  
CC The present invention describes a method for determining the haplotype  
CC of an allele of a selected gene at two or more polymorphic sites  
CC comprising allele-specific enrichment, optical mapping, or atomic force  
CC microscopy. The method is useful for genetic analysis when the DNA  
CC segment being haplotyped consists of polymorphisms that are in some  
CC degree of linkage disequilibrium with each other, that is they do not  
CC assort randomly in the population being studied. The method allows early  
CC implementation of preventive measures in patients at risk of diseases  
CC such as atherosclerosis, dementia, Parkinson's disease, Huntington's  
CC disease or other organic or vascular neurodegenerative diseases. Genotype  
CC and haplotype information can be used to make diagnostic tests useful for  
CC disease risk assessment, for prognostic prediction of the course or  
CC outcome of a disease, to diagnose a disease or condition, or to select  
CC an optimal therapy for a disease or condition. ABL31915 to ABL32035  
CC represent nucleotide sequence used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 35 BP; 9 A; 11 C; 6 G; 8 T; 1 other;  
XX  
Query Match 66.0%; Score 13.2; DB 24; Length 35;  
Best Local Similarity 83.3%; Pred. No. 5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 3 GCCGACGTGGACCCAGA 20  
||| ||||| ||||| |||  
Db 29 GCCGAAGTGGACRCAGA 12  
||| ||||| ||||| |||  
Search completed: November 23, 2002, 06:28:59  
Job time : 102.6 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:53:51 : Search time 21.55 seconds  
(without alignments)  
284.619 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20  
Sequence: 1 gtgcgcagctggagaccaga 20

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 44162 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCITUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.8	69.0	28	2	US-08-976-703-10
2	13.2	66.0	33	4	US-09-237-712-41
3	13.2	66.0	33	4	US-09-237-712-41
4	13.2	66.0	44	3	US-08-829-525-34
5	13.2	66.0	44	4	US-08-609-583A-34
6	13.2	66.0	44	4	US-08-937-399-34
7	13.2	66.0	44	4	US-09-560-639-27
8	13.2	66.0	44	4	US-09-310-367-34
9	13.2	66.0	44	4	US-09-032-337-34
10	12.8	64.0	25	2	US-08-590-674-11
11	12.8	64.0	62	2	US-08-658-665-153
12	12.8	64.0	62	4	US-08-796-101-129
13	12.8	64.0	62	4	US-09-085-273-153
14	12.6	63.0	20	3	US-08-777-708C-14
15	12.6	63.0	20	4	US-09-397-168-92
16	12.6	63.0	21	2	US-08-480-473B-61
17	12.6	63.0	21	3	US-08-915-213-61
18	12.6	63.0	21	4	US-09-235-211-61
19	12.6	63.0	45	4	US-09-199-737-46
20	12.6	63.0	45	4	US-09-058-333A-46
21	12.2	61.0	20	4	US-09-561-497-65
22	12.2	61.0	20	4	US-09-561-497-66
23	12.2	61.0	23	4	US-08-852-001-29
24	12.2	61.0	34	2	US-08-852-806-11
25	12.2	61.0	34	3	US-09-163-669-11
26	12.2	61.0	57	2	US-08-149-097D-25
27	12.2	61.0	92	3	US-08-973-965-4

28	12.2	61.0	93	3	US-08-973-965-5	Sequence 5, Appl1
29	12.2	61.0	93	3	US-08-973-965-38	Sequence 38, Appl
30	12.2	61.0	97	3	US-08-973-965-40	Sequence 40, Appl
31	12.2	61.0	24	2	US-08-784-386-5	Sequence 5, Appl1
32	12.2	60.0	25	2	US-08-784-386-10	Sequence 10, Appl
33	12.2	60.0	33	6	5520913-35	Patent No. 5520913
34	12.2	60.0	44	1	US-08-344-695-5	Sequence 5, Appl1
35	12.2	60.0	50	4	US-09-298-886-19	Sequence 19, Appl
36	12.2	60.0	50	4	US-09-298-886-25	Sequence 25, Appl
37	12.2	60.0	50	4	US-09-298-886-28	Sequence 28, Appl
38	12.2	60.0	54	1	US-08-311-486C-1026	Sequence 1026, Ap
39	12.2	60.0	56	5	PCR-US95-02917-5	Sequence 5, Appl1
40	12.2	60.0	59	2	US-08-371-377-7	Sequence 7, Appl1
41	12.2	60.0	67	4	US-09-025-769B-83	Sequence 83, Appl
42	12.2	60.0	90	6	5175255-6	Patent No. 5175255
43	11.8	59.0	20	4	US-09-011-197-10	Sequence 10, Appl
44	11.8	59.0	25	2	US-08-933-749-2	Sequence 2, Appl1
45	11.8	59.0	25	3	US-09-235-583-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-08-976-703-10/c

Sequence 10, Application US/08976703  
Patent No. 5945288

GENERAL INFORMATION:

APPLICANT: CHANG, ZHIYU

APPLICANT: MORGAN, RICHARD D.

TITLE OF INVENTION: METHOD FOR CLONING AND  
PRODUCING THE PHEI RESTRICTION ENDONUCLEASE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:  
ADDRESSEE: New England Biolabs, Inc.

STREET: 32 Tozer Road

CITY: Beverly

STATE: MA

COUNTRY: US

ZIP: 01915

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/976,703

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Williams, Gregory D

REGISTRATION NUMBER: 30901

REFERENCE/DOCKET NUMBER: NEB-132

TELECOMMUNICATION INFORMATION:

TELEPHONE: 978-927-5054

TELEFAX: 978-927-1705

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

US-08-976-703-10

Query Match 69.0%; Score 13.8; DB 2; length 28;  
Best Local Similarity 88.2%; Pred. No. 3.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 TGCCGACGTGGACCCA 18  
Db 19 TGCCGACGTGGATCCA 3

## RESULT 2

US-09-237-712-41  
; Sequence 41, Application US/09237712  
; Patent No. 6180391  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, WILLIAM C.  
; TITLE OF INVENTION: HIGHLY EFFICIENT CONTROLLED EXPRESSION OF EXOGENOUS  
; FILE REFERENCE: A-518  
; CURRENT APPLICATION NUMBER: US/09/237,712  
; CURRENT FILING DATE: 1999-01-26  
; EARLIER APPLICATION NUMBER: 60/072,794  
; EARLIER FILING DATE: 1998-01-28  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 41  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: oligonucleotide  
US-09-237-712-41

Query Match 66.0%; Score 13.2; DB 4; Length 33;  
Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TGCCGACGTGGACCCA 19  
Db 12 TGCCGACGTGGCTCTAG 29

## RESULT 3

US-09-237-712-42/C  
; Sequence 42, Application US/09237712  
; Patent No. 6180391  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, WILLIAM C.  
; TITLE OF INVENTION: HIGHLY EFFICIENT CONTROLLED EXPRESSION OF EXOGENOUS  
; FILE REFERENCE: A-518  
; CURRENT APPLICATION NUMBER: US/09/237,712  
; CURRENT FILING DATE: 1999-01-26  
; EARLIER APPLICATION NUMBER: 60/072,794  
; EARLIER FILING DATE: 1998-01-28  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: oligonucleotide  
US-09-237-712-42

Query Match 66.0%; Score 13.2; DB 4; Length 33;  
Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TGCCGACGTGGACCCA 19  
Db 26 TGCCGACGTGGCTCTAG 9

## RESULT 4

US-08-829-525-34/C  
; Sequence 34, Application US/08829525  
; Patent No. 6084083  
; GENERAL INFORMATION:  
; APPLICANT: Levinson, Douglas A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS

NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA

ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/829,525  
FILING DATE: 28-MAR-1997  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/609,583  
FILING DATE: 01-MAR-1996  
APPLICATION NUMBER: US 08/487,748  
FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/398,633  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-081

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-829-525-34

Query Match 66.0%; Score 13.2; DB 3; Length 44;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTCCGACGTGGACCCA 18  
Db 33 GTCCGACGTGGATCCA 16

## RESULT 5

US-08-609-583A-34/C  
; Sequence 34, Application US/08609583A  
; Patent No. 6204371  
; GENERAL INFORMATION:  
; APPLICANT: Levinson, Douglas A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA

ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/609,583A



FILED DATE: 01-MAR-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,748  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/398,633  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-048  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-609-583A-34

Query Match  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGCCGACGTGGACCA 18  
|||||  
DB 33 GTCCGACCTTGATCA 16

RESULT 6  
US-08-937-399-34/C  
Sequence 34, Application US/08937399  
Patent No. 6288218  
GENERAL INFORMATION:  
APPLICANT: Levinson, Douglas A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,399  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/609,583  
FILING DATE: 01-MAR-1996  
APPLICATION NUMBER: US 08/487,748  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/398,633  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-048  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-937-399-34

Query Match  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGCCGACGTGGACCA 18  
|||||  
DB 33 GTCCGACCTTGATCA 16

RESULT 7  
US-09-560-639-27/C  
Sequence 27, Application US/09560639  
Patent No. 632334  
GENERAL INFORMATION:  
APPLICANT: Kingsbury, G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TREATMENT OF IMMUNE DISORDERS  
FILE REFERENCE: 7853-158  
CURRENT APPLICATION NUMBER: US/09/560,639  
CURRENT FILING DATE: 2000-04-28  
EARLIER APPLICATION NUMBER: 60/155,862  
EARLIER FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 27  
LENGTH: 44  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: 3' oligonucleotide  
US-09-560-639-27

Query Match  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGCCGACGTGGACCA 18  
|||||  
DB 33 GTCCGACCTTGATCA 16

RESULT 8  
US-09-310-367-34/C  
Sequence 34, Application US/09310367  
Patent No. 641417  
GENERAL INFORMATION:  
APPLICANT: Levinson, Douglas A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/310,367  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/829,525  
FILING DATE: 28-MAR-1997  
APPLICATION NUMBER: US 08/609,583  
FILING DATE: 01-MAR-1996  
APPLICATION NUMBER: US 08/487,748  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/398,633  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-081  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-310-367-34

Query Match 66.0%; Score 13.2; DB 4; Length 44;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAGCCCA 18  
DB 33 GTGCAGACTTGGATGCA 16

RESULT 9  
US-09-032-337-34/C  
Sequence 34, Application US/09032337  
Patent No. 6455685  
GENERAL INFORMATION:  
APPLICANT: Levinson, Douglas A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TITILE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEO Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,337  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/609,583  
FILING DATE: 01-MAR-1996  
APPLICATION NUMBER: US 08/487,748  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/398,633  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-016  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-032-337-34

Query Match 66.0%; Score 13.2; DB 4; Length 44;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAGCCCA 18  
DB 33 GTGCAGACTTGGATGCA 16

RESULT 10  
US-08-590-674-1  
Sequence 1, Application US/08590674  
Patent No. 5849487  
GENERAL INFORMATION:

APPLICANT: Hase, Tetsu  
APPLICANT: Masubuchi, Harumi  
TITLE OF INVENTION: METHOD OF DETECTING A SPECIFIC  
TITILE OF INVENTION: POLYNUCLEOTIDE  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto  
STREET: 277 Park Avenue  
CITY: New York  
STATE: NY

COUNTRY: United States  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,674  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/356137  
FILING DATE: 15-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Woliman, Penina  
REGISTRATION NUMBER: 30816  
REFERENCE/DOCKET NUMBER: 1241.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-2400  
TELEFAX: 212-758-2982  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
ORIGINAL SOURCE:  
ORGANISM: cytomegalovirus (CMV)  
US-08-590-674-1

Query Match 64.0%; Score 12.8; DB 2; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.1e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGAGCTGGGACCCAG 19  
||||| |||||||||  
Db 3 CCGAATGGGACCCAG 18

RESULT 11  
US-08-658-665-153/c  
Sequence 153, Application US/08658665  
Patent No. 5997878

GENERAL INFORMATION:  
APPLICANT: Paoletti, Enzo  
APPLICANT: Pincus, Steven E.  
APPLICANT: Cox, William I.  
TITLE OF INVENTION: Recombinant Poxvirus - Cytomegalovirus,  
TITLE OF INVENTION: Compositions and Uses  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,665  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer Esq., William S.  
REGISTRATION NUMBER: 25,506  
TELECOMMUNICATION INFORMATION:  
REFERENCE/DOCKET NUMBER: 454310-2720.1  
TELEPHONE: (212)840-3333  
TELEFAX: (212)840-0712  
INFORMATION FOR SEQ ID NO: 153:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 62 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-08-658-665-153

Query Match 64.0%; Score 12.8; DB 2; Length 62;  
Best Local Similarity 87.5%; Pred. No. 1.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGAGCTGGGACCCAG 19  
||||| |||||||||  
Db 61 CCGAATGGGACCCAG 46

RESULT 12  
US-08-796-101-129/c  
Sequence 129, Application US/08796101  
Patent No. 6183752

GENERAL INFORMATION:  
APPLICANT: EPSTEIN, STEPHEN E.  
APPLICANT: FINKEL, TOREN  
APPLICANT: SPEIR, EDITH  
APPLICANT: ZHOU, YI FU  
APPLICANT: ZHU, JIANHUI  
APPLICANT: ERDLE, LORNE  
APPLICANT: PINCUS, STEVEN  
TITLE OF INVENTION: RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,

TITLE OF INVENTION: PROPHYLAXIS AND THERAPY  
NUMBER OF SEQUENCES: 184  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.  
STREET: 530 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NY  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/796,101  
FILING DATE: 05-FEB-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: KOWALSKI, THOMAS J.  
REGISTRATION NUMBER: 32,147  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 764-5574  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 62 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-08-796-101-129

Query Match 64.0%; Score 12.8; DB 4; Length 62;  
Best Local Similarity 87.5%; Pred. No. 1.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGAGCTGGGACCCAG 19  
||||| |||||||||  
Db 61 CCGAATGGGACCCAG 46

RESULT 13  
US-09-085-273-153/c  
Sequence 153, Application US/09085273  
Patent No. 6267965

GENERAL INFORMATION:  
APPLICANT: Paoletti, Enzo  
APPLICANT: Pincus, Steven E.  
APPLICANT: Cox, William I.  
TITLE OF INVENTION: RECOMBINANT POXVIRUS - CYTOMEGALOVIRUS,  
TITLE OF INVENTION: COMPOSITIONS AND USES  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/085,273  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,014  
FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Frommer Esq., William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 153:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 62 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-085-273-153

Query Match 64.0%; Score 12.6; DB 4; Length 62;  
Best Local Similarity 87.5%; Pred. No. 1.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCGACGTGGAGCCAG 19  
||| |||||  
Db 61 CCGAATGGAGCCAG 46

RESULT 14  
US-08-777-708C-14/C  
Sequence 14, Application US/08777708C  
Patent No. 6159934  
GENERAL INFORMATION:  
APPLICANT: Pescovitz, Ora H.  
TITLE OF INVENTION: USE OF GRH-RP TO STIMULATE STEM CELL FACTOR PRODUCTION  
FILE REFERENCE: 7037-175/TU-62  
CURRENT APPLICATION NUMBER: US/08/777,708C  
CURRENT FILING DATE: 1996-12-20  
PRIOR APPLICATION NUMBER: US 60/008,933  
PRIOR FILING DATE: 1995-12-20  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 14  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-08-777-708C-14

Query Match 63.0%; Score 12.6; DB 3; Length 20;  
Best Local Similarity 78.9%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GTGCCGACGTGGAGCCAG 19  
||| | |||||  
Db 19 GTGCAGTTGTGGATCCAG 1

RESULT 15  
US-09-397-168-92/C  
Sequence 92, Application US/09397168  
Patent No. 6344323  
GENERAL INFORMATION:  
APPLICANT: Seifert, Wilfried  
TITLE OF INVENTION: INHIBITION OF COX-2 EXPRESSION BY ANTISENSE OLIGONUCLEOTIDES  
FILE REFERENCE: 11151/002001  
CURRENT APPLICATION NUMBER: US/09/397,168  
CURRENT FILING DATE: 1999-09-16  
EARLIER APPLICATION NUMBER: US 60/100,550  
EARLIER FILING DATE: 1998-09-16  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 92  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Synthetically generated antisense oligonucleotides  
US-09-397-168-92

Query Match 63.0%; Score 12.6; DB 4; Length 20;  
Best Local Similarity 78.9%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 TGCCGACGTGGAGCCAGA 20  
||| ||| ||| |||  
Db 20 TGCAGACCTGTACTCAGA 2

Search completed: November 23, 2002, 06:36:11  
Job time: 23.55 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:54:41 ; Search time 17.25 Seconds  
(without alignments)  
439.108 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20

Sequence: 1 gtccgcagctggagaccaga 20

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 335578 seqs, 18936513 residues

Total number of hits satisfying chosen parameters: 195614

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.2	66.0	35	10	US-09-967-013-60
2	13.2	66.0	35	10	US-09-967-013-61
3	13.2	66.0	44	10	US-09-899-980A-27
4	13.2	66.0	83	10	US-09-923-876-3414
5	12.6	63.0	30	10	US-09-736-969A-150
6	12.6	63.0	30	10	US-09-736-960-130
7	12.4	62.0	50	10	US-09-880-732-15
8	12.4	62.0	51	10	US-09-880-732-14
9	12.2	61.0	34	9	US-09-879-813-33
10	12.2	61.0	91	10	US-09-833-381-1832
11	12.2	61.0	100	10	US-09-728-445-277
12	12.2	61.0	25	10	US-09-866-108-3704
13	12.2	61.0	25	10	US-09-866-108-3705
14	12.2	60.0	25	10	US-09-866-108-3706
15	12.2	60.0	25	10	US-09-866-108-3707
16	12.2	60.0	25	10	US-09-866-108-3708
17	12.2	60.0	25	10	US-09-866-108-3709
18	12.2	60.0	50	10	US-09-999-672-19
19	12.2	60.0	50	10	US-09-999-672-25

20	12	60.0	50	10	US-09-999-672-28	Sequence 28, Appl
21	12	60.0	50	12	US-10-040-863-19	Sequence 19, Appl
22	12	60.0	50	12	US-10-040-863-25	Sequence 25, Appl
23	12	60.0	50	12	US-10-040-863-28	Sequence 28, Appl
24	11.8	59.0	31	10	US-09-801-274-16	Sequence 16, Appl
25	11.8	59.0	96	10	US-09-864-761-32538	Sequence 32538, A
26	11.6	58.0	22	10	US-09-999-672-1	Sequence 1, Appl
27	11.6	58.0	22	12	US-10-040-863-1	Sequence 1, Appl
28	11.6	58.0	25	10	US-09-866-108-3710	Sequence 3710, Ap
29	11.6	58.0	25	10	US-09-866-108-3711	Sequence 3711, Ap
30	11.6	58.0	42	10	US-09-811-094-28	Sequence 28, Appl
31	11.6	58.0	42	10	US-09-810-644-18	Sequence 18, Appl
32	11.6	58.0	50	10	US-09-999-672-16	Sequence 16, Appl
33	11.6	58.0	50	10	US-09-999-672-22	Sequence 22, Appl
34	11.6	58.0	50	12	US-10-040-863-16	Sequence 16, Appl
35	11.6	58.0	50	12	US-10-040-863-22	Sequence 22, Appl
36	11.6	58.0	66	9	US-10-013-033-5	Sequence 5, Appl
37	11.6	58.0	78	10	US-09-972-809-6	Sequence 6, Appl
38	11.6	58.0	92	10	US-09-953-342-6	Sequence 6, Appl
39	11.6	58.0	93	10	US-09-864-761-31595	Sequence 5301, Ap
40	11.4	57.0	90	10	US-09-878-574-5301	Sequence 5301, Ap
41	11.2	56.0	18	9	US-09-842-111-4	Sequence 4, Appl
42	11.2	56.0	18	10	US-09-796-807-4	Sequence 4, Appl
43	11.2	56.0	27	10	US-09-371-307-29	Sequence 29, Appl
44	11.2	56.0	67	10	US-09-847-637B-5	Sequence 5, Appl
45	11	55.0	19	10	US-09-965-373-4348	Sequence 4348, Ap

#### ALIGNMENTS

RESULT 1  
US-09-967-013-60/c  
; Sequence 60, Application US/09967013  
; Patent No. US20020045840A1  
; GENERAL INFORMATION:  
; APPLICANT: Stanton, Jr. Vincent P.  
; TITLE OF INVENTION: METHOD FOR GENETIC ANALYSIS OF APOE DNA  
; FILE REFERENCE: 11926-022001  
; CURRENT APPLICATION NUMBER: US/09/967,013  
; CURRENT FILING DATE: 2000-10-25  
; PRIOR APPLICATION NUMBER: 60/206,613  
; PRIOR FILING DATE: 2000-05-23  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 60  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: exemplary motif  
US-09-967-013-60

Query Match 66.0%; Score 13.2; DB 10; Length 35;  
Best Local Similarity 83.3%; Pred. No. 3.9e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 29 GCCGAGCTGGAGCCAGCA 20  
||||| ||||| |||||  
GCCGAGCTGGAGCCAGCA 12

RESULT 2  
US-09-967-013-61  
; Sequence 61, Application US/09967013  
; Patent No. US20020045840A1  
; GENERAL INFORMATION:  
; APPLICANT: Stanton, Jr. Vincent P.  
; TITLE OF INVENTION: METHOD FOR GENETIC ANALYSIS OF APOE DNA  
; FILE REFERENCE: 11926-022001  
; CURRENT APPLICATION NUMBER: US/09/967,013

;; CURRENT FILING DATE: 2000-10-25  
;; PRIOR APPLICATION NUMBER: 60/206,613  
;; PRIOR FILING DATE: 2000-05-23  
;; NUMBER OF SEQ ID NOS: 91  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 61  
;; LENGTH: 35  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: exemplary motif  
US-09-967-013-61

Query Match 66.0%; Score 13.2; DB 10; Length 35;  
Best Local Similarity 83.3%; Pred. No. 5.9e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 GCCGACGTGGAGCCAGA 20  
DB 7 GCCGAGTGGACRCAGA 24

## RESULT 3

US-09-899-980A-27/C  
;; Sequence 27, Application US/09899980A  
;; Patent No. US2002005800A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Kingsbury, G.  
;; APPLICANT: Leiby, K.  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
;; TREATMENT OF IMMUNE DISORDERS  
;; FILE REFERENCE: 7853-158  
;; CURRENT APPLICATION NUMBER: US/09/899,980A  
;; PRIOR FILING DATE: 2001-07-06  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/560,639  
;; PRIOR FILING DATE: EARLIER FILING DATE: 2000-04-28  
;; NUMBER OF SEQ ID NOS: 33  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 27  
;; LENGTH: 44  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: 3' oligonucleotide  
US-09-899-980A-27

Query Match 66.0%; Score 13.2; DB 10; Length 44;  
Best Local Similarity 83.3%; Pred. No. 6e+02; 3; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGCCAGCTGGAGCCCA 18  
DB 33 GTGCAGACTTGGATCA 16

## RESULT 4

US-09-923-876-3414/C  
;; Sequence 3414, Application US/09923876  
;; Patent No. US20020013958A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Laligudi, Raghunath V.  
;; APPLICANT: Kamigaki, Laura Y. (lto)  
;; APPLICANT: Sherman, Bradley K.  
;; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING  
;; FILE REFERENCE: PL-0012-1 CON  
;; CURRENT APPLICATION NUMBER: US/09/923,876  
;; CURRENT FILING DATE: 2001-08-06  
;; PRIOR APPLICATION NUMBER: 09/298,329  
;; PRIOR FILING DATE: 1999-04-21  
;; PRIOR APPLICATION NUMBER: 60/085,331  
;; PRIOR FILING DATE: 1998-05-05  
;; NUMBER OF SEQ ID NOS: 6332  
;; SOFTWARE: PERL Program

;; SEQ ID NO 3414  
;; LENGTH: 83  
;; TYPE: DNA  
;; ORGANISM: zea mays  
;; FEATURE:  
;; NAME/KEY: misc-feature  
;; OTHER INFORMATION: Incyte ID No. US20020013958A1 700162221H1  
;; NAME/KEY: unsure  
;; LOCATION: 2, 28, 49, 63, 76, 79-80  
;; OTHER INFORMATION: a, t, c, g, or other  
US-09-923-876-3414

Query Match 66.0%; Score 13.2; DB 10; Length 83;  
Best Local Similarity 78.9%; Pred. No. 6e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GTGCCAGCTGGAGCCAG 19  
DB 50 GNGCGACGTGGAGCCAG 32

## RESULT 5

US-09-736-969A-150/C  
;; Sequence 150, Application US/09736969A  
;; Patent No. US20020068302A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Lu, Peter  
;; APPLICANT: Garman, Jonathan David  
;; APPLICANT: Candia, Irit, Albert Frederick  
;; TITLE OF INVENTION: CLASP-4 Transmembrane Protein  
;; FILE REFERENCE: 020054-00041US  
;; CURRENT APPLICATION NUMBER: US/09/736,969A  
;; PRIOR FILING DATE: 2000-12-13  
;; PRIOR APPLICATION NUMBER: US 60/160,860  
;; PRIOR FILING DATE: 1999-10-21  
;; PRIOR APPLICATION NUMBER: US 60/162,498  
;; PRIOR FILING DATE: 1999-10-29  
;; PRIOR APPLICATION NUMBER: US 60/170,453  
;; PRIOR FILING DATE: 1999-12-13  
;; PRIOR APPLICATION NUMBER: US 60/176,195  
;; PRIOR FILING DATE: 2000-01-14  
;; PRIOR APPLICATION NUMBER: US 60/182,296  
;; PRIOR FILING DATE: 2000-02-14  
;; PRIOR APPLICATION NUMBER: US 09/547,276  
;; PRIOR FILING DATE: 2000-04-11  
;; PRIOR APPLICATION NUMBER: US 60/196,267  
;; PRIOR FILING DATE: 2000-04-11  
;; PRIOR APPLICATION NUMBER: US 60/196,460  
;; PRIOR FILING DATE: 2000-04-11  
;; PRIOR APPLICATION NUMBER: US 60/196,527  
;; PRIOR FILING DATE: 2000-04-11  
;; PRIOR APPLICATION NUMBER: US 60/196,528  
;; PRIOR FILING DATE: 2000-04-11  
;; PRIOR APPLICATION NUMBER: US 09/687,837  
;; PRIOR FILING DATE: 2000-10-13  
;; PRIOR APPLICATION NUMBER: US 60/240,503  
;; PRIOR FILING DATE: 2000-10-13  
;; PRIOR APPLICATION NUMBER: US 60/240,508  
;; PRIOR FILING DATE: 2000-10-13  
;; PRIOR APPLICATION NUMBER: US 60/240,539  
;; PRIOR FILING DATE: 2000-10-13  
;; PRIOR APPLICATION NUMBER: US 60/240,543  
;; PRIOR FILING DATE: 2000-10-13  
;; NUMBER OF SEQ ID NOS: 153  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 150  
;; LENGTH: 30  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: antisense  
;; OTHER INFORMATION: primer HCLAS3' kpn

US-09-736-969A-150

Query Match	63.0%	Score 12.6;	DB 10;	length 30;
Best Local Similarity	78.9%	Pred. No. 1.2e+03;		
Matches 15; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

Qy 1 GTGCCGACGTGGGACCAG 19  
||| | | | | | |  
Db 19 GTGCTGAAGTGTTACCAAG 1

RESULT 6  
US-09-73

```

US-09-736-960-130/c
: Sequence 130. Application us/09736960
: Patent No. US2002010287A1
: GENERAL INFORMATION:
: APPLICANT: Lu, Peter
: APPLICANT: Garman, Jonathan David
: APPLICANT: Candia III, Albert Frederick
: APPLICANT: Arbor Vita Corporation
: TITLE OF INVENTION: CLASP-5 Transmembrane Protein
: FILE REFERENCE: 020054-000511US
: CURRENT APPLICATION NUMBER: US/09/736,960
: CURRENT FILING DATE: 2001-09-20
: PRIOR APPLICATION NUMBER: US 60/160,860
: PRIOR FILING DATE: 1999-10-21
: PRIOR APPLICATION NUMBER: US 60/162,498
: PRIOR FILING DATE: 1999-10-29
: PRIOR APPLICATION NUMBER: US 60/170,453
: PRIOR FILING DATE: 1999-12-13
: PRIOR APPLICATION NUMBER: US 60/176,195
: PRIOR FILING DATE: 2000-01-14
: PRIOR APPLICATION NUMBER: US 60/182,296
: PRIOR FILING DATE: 2000-02-14
: PRIOR APPLICATION NUMBER: US 09/547,276
: PRIOR FILING DATE: 2000-04-11
: PRIOR APPLICATION NUMBER: US 60/196,267
: PRIOR FILING DATE: 2000-04-11
: PRIOR APPLICATION NUMBER: US 60/196,460
: PRIOR FILING DATE: 2000-04-11
: PRIOR APPLICATION NUMBER: US 60/196,527
: PRIOR FILING DATE: 2000-04-11
: PRIOR APPLICATION NUMBER: US 60/196,528
: PRIOR FILING DATE: 2000-04-11
: PRIOR APPLICATION NUMBER: US 09/687,837
: PRIOR FILING DATE: 2000-10-13
: PRIOR APPLICATION NUMBER: US 60/240,503
: PRIOR FILING DATE: 2000-10-13
: PRIOR APPLICATION NUMBER: US 60/240,508
: PRIOR FILING DATE: 2000-10-13
: PRIOR APPLICATION NUMBER: US 60/240,539
: PRIOR FILING DATE: 2000-10-13
: PRIOR APPLICATION NUMBER: US 60/240,543
: PRIOR FILING DATE: 2000-10-13
: NUMBER OF SEQ ID NOS: 134
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 130
: LENGTH: 30
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:antisense
: US-09-736-960-130

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Query Match	63.0%	Score 12.6;	DB 10;	Length 30;
Best Local Similarity	78.9%	Pred. No. 1.2e+03;		
Matches 15; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

Qy 1 GTGCCGACGTGGACCAG 19  
 ||| | | | | | | |  
 Db 19 GTGCTGAAGTGGTACCAAG 1

## RESULT 7

US-09-880-732-15  
; Sequence 15, Application US/09880732  
; Patent No. US20020127561A1

```

: APPLICANT: GENICON SCIENCES CORPORATION
:
: APPLICANT: BEE, Gary
:
: APPLICANT: KOHNE, David E.
:
: APPLICANT: KORB, Linda
:
: APPLICANT: PETERSON, Todd
:
: APPLICANT: YGUERABIDE, Juan
:
: TITLE OF INVENTION: ASSAY FOR GENETIC POLYMORPHISMS USING SCATTERED LIGHT DETECTAB
:
: FILE REFERENCE: 089498/0403
:
: CURRENT APPLICATION NUMBER: US/09/880,732
:
: CURRENT FILING DATE: 2001-09-17
:
: PRIOR APPLICATION NUMBER: US 60/210,988
:
: PRIOR FILING DATE: 2000-06-12
:
: NUMBER OF SEQ ID NOS: 64
:
: SOFTWARE: PatentIn version 3.0

```

Query Match	62.0%	Score 12.4	DB 10	Length 50
Best Local Similarity	92.9%	Pred. No. 1.5e+03		
Matches 13, Conservative	0	Mismatches 1	Indels 0	Gaps 0

```

Qy      6 GACGTGGGACCCAG 19
          ||| |||||
Db     30 GACCTGGGACCCAG 43

```

RESULT  
US-09-88

```

: Sequence 14 Application US/09880732
: Patent No. US20020127561A1
:
: GENERAL INFORMATION:
: APPLICANT: GENICON SCIENCES CORPORATION
: APPLICANT: BEE, Gary
: APPLICANT: KOHNE, David E.
: APPLICANT: KORB, Linda
: APPLICANT: PETERSON, Todd
: APPLICANT: YGERABIDE, Juan
: TITLE OF INVENTION: ASSAY FOR GENETIC POLYMORPHISMS USING SCATTERED LIGHT DETECTAB
: FILE REFERENCE: 089498/0403
: CURRENT APPLICATION NUMBER: US/09/880,732
: CURRENT FILING DATE: 2001-09-17
: PRIOR APPLICATION NUMBER: US 60/210,988
: PRIOR FILING DATE: 2000-06-12
: NUMBER OF SEQ ID NOS: 64
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 14
:
: LENGTH: 51
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Exemplary probe for CYP2D6 allele detection
: US-09-880-732-14

```

Query Match	62.0%	Score 12.4	DB 10	Length 51
Best Local Similarity	92.9%	Pred. No. 1.5e+03		
Matches 13, Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY	6	GACGTGGACCCAG	19
Db	31	GACCTGGGACCCAG	44

```
RESULT 9
US-09-879-813-33/C
; Sequence 33, Application US/09879813
; Patent No. US20020155453A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005
; CURRENT APPLICATION NUMBER: US/09/879,813
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 3.1
; SEQ ID NO 33
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(29)
; OTHER INFORMATION: U318
; OTHER INFORMATION: The sequence 'ACGTCGTGGCGCCA' is inserted and duplicates sequence
; US-09-879-813-33
```

```
Query Match 61.0%; Score 12.2; DB 9; Length 34;
Best Local Similarity 82.4%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 4 CCGAGCTGGACCCAGA 20
| | | | | | | | | | |
DB 22 CAGAGCTGGCCCGAGA 6
```

```
RESULT 10
US-09-833-381-1832
; Sequence 1832, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1832
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(91)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1832
```

```
Query Match 61.0%; Score 12.2; DB 10; Length 91;
Best Local Similarity 82.4%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 4 CCGAGCTGGACCCAGA 20
| | | | | | | | | | |
DB 74 CAGAGCTGGCCCGAGA 90
```

```
RESULT 11
US-09-728-445-277
; Sequence 277, Application US/09728445
; Patent No. US20020102543A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020102543A1el Mutated Mammalian Cells and
; TITLE OF INVENTION: Animals
; FILE REFERENCE: LEX-0102-USA
; CURRENT APPLICATION NUMBER: US/09/728,445
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 277
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(100)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-445-277
```

```
Query Match 61.0%; Score 12.2; DB 10; Length 100;
Best Local Similarity 82.4%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 TCCGACGTGGACCCA 18
| | | | | | | | | | |
DB 65 TCCGTAACGTGCACCCA 81
```

```
RESULT 12
US-09-866-108-3704/C
; Sequence 3704, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
```



```

; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO: 3704
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-3704

Query Match          60.0%; Score 12; DB 10; Length 25;
Best Local Similarity 75.0%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCCGACGTGGGACCACA 20
Db 25 GTGCTGGCCTGGGACCACA 6

RESULT 13
US-09-866-108-3705/c
; Sequence 3705, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
```

```

; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO: 3705
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-3705

Query Match          60.0%; Score 12; DB 10; Length 25;
Best Local Similarity 75.0%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCCGACGTGGGACCACA 20
Db 24 GTGCTGGCCTGGGACCACA 5

RESULT 14
US-09-866-108-3706/c
; Sequence 3706, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO: 3706
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-3706

Query Match          60.0%; Score 12; DB 10; Length 25;
Best Local Similarity 75.0%; Pred. No. 2.3e+03;
```

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCAGA 20  
|||||  
DB 23 GTGCTGGCCTGGGAGCCACA 4

## RESULT 15

US-09-866-108-3707/c  
; Sequence 3707, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263,6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
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; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 3707  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-3707

Query Match 60.0%; Score 12; DB 10; Length 25;  
Best Local Similarity 75.0%; Pred. No. 2.3e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCAGA 20  
|||||  
DB 22 GTGCTGGCCTGGGAGCCACA 3

Search completed: November 23, 2002, 06:42:08  
Job time : 18.25 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 25, 2002, 09:10:06 : Search time 755.55 Seconds  
(without alignments)  
428.707 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20  
Sequence: 1 gtccgacgtgagaccaga 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_estlm:\*  
3: em\_estln:\*  
4: em\_estlm:\*  
5: em\_estlm:\*  
6: em\_estlm:\*  
7: em\_estlm:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estlm:\*  
16: em\_estlm:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	74	17	BH215436 1006027A1
2	13.8	69.0	91	9	AA837667 cd73h03.s
3	13.6	66.0	91	9	AA930982 vY79f05.r
4	13.4	67.0	60	17	AZ776503 2M0010J11
5	13.2	66.0	50	9	AU103727 AU103727
6	13.2	66.0	51	17	AZ438521 1M0228f12

Result No.	Score	Query Match	Length	DB ID	Description
7	13.2	66.0	88	14	BQ756506
8	13.2	66.0	95	17	AZ653293 1M0526G21
9	12.8	64.0	67	12	BG327801
10	12.8	64.0	88	9	AU077180
11	12.8	64.0	89	9	AA094815
12	12.6	63.0	50	9	AU106651
13	12.6	63.0	50	9	AU106652
14	12.6	63.0	50	9	AU106653
15	12.6	63.0	50	9	AU106654
16	12.6	63.0	50	9	AU106655
17	12.6	63.0	50	9	AU106656
18	12.6	63.0	50	9	AU106657
19	12.6	63.0	50	9	AU106658
20	12.6	63.0	50	9	AU106659
21	12.6	63.0	50	9	AU106660
22	12.6	63.0	50	9	AU106661
23	12.6	63.0	50	9	AU106662
24	12.6	63.0	50	9	AU106663
25	12.6	63.0	50	9	AU106664
26	12.6	63.0	50	9	AU106665
27	12.6	63.0	50	9	AU106666
28	12.6	63.0	50	9	AU106667
29	12.6	63.0	50	9	AU106668
30	12.6	63.0	50	9	AU106669
31	12.6	63.0	50	9	AU106670
32	12.6	63.0	50	9	AU106671
33	12.6	63.0	50	9	AU106672
34	12.6	63.0	50	9	AU106673
35	12.6	63.0	50	9	AU106674
36	12.6	63.0	50	9	AU106675
37	12.6	63.0	50	9	AU106676
38	12.6	63.0	50	9	AU106677
39	12.6	63.0	50	9	AU106678
40	12.6	63.0	50	9	AU106679
41	12.6	63.0	50	9	AU106680
42	12.6	63.0	50	9	AU106681
43	12.6	63.0	50	9	AU106682
44	12.6	63.0	50	9	AU106683
45	12.6	63.0	50	9	AU106684

# ALIGNMENTS

RESULT 1  
BH215436 74 bp DNA linear GSS 08-NOV-2001  
LOCUS 1006027A1.2EL\_y2 1006 - Rescuemu Grid G Zea mays genomic, DNA  
DEFINITION  
sequence.  
ACCESSION BH215436  
VERSION BH215436.1 GI:16806094  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays.  
Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
Clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
1 (bases 1 to 74)  
Waldot.V.  
Maize genomic sequences found using engineered Rescuemu transposon  
JOURNAL  
TITLE  
Unpublished (2001)  
COMMENT  
Contact: Waldot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: waldot@stanford.edu  
Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1006027 row: 42  
Class: transposon-tagged.  
Location/Qualifiers

# FEATURES

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source
1..74
/organism="Zea mays"
/cultivar="mixed background W23/A189/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT      15 a       24 c       25 g       10 t
ORIGIN

Query Match
Best Local Similarity   84.2%;   Pred. No. 1.3e+04;
Matches    16:   Conservative     0;   Mismatches    3;   Indels        0;   Gaps        0;

QY      1  GTGCCGACGTGGGACCAG 19
          | ||||| ||||| || ||
Db       41  GCGCCGACGTGGCACCAG 59

RESULT 2
LOCUS      AA837667
DEFINITION odt3hd3.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1373621 similar to gp:M30938 LUPUS KU AUTOANTIGEN PROTEIN P66 (HUMAN))., mRNA sequence.
VERSION    AA837667
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 91)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT    Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapps@email.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Michael R. Emmer-Buck, M.D., Ph.D.
            CDNA Library Preparation: David B. Kitzman, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: www-bio.llnl.gov/bdrp/image/image.html
            Insert length: 258 Std Error: 0.00
            Seq primer: ~40ml3 fwd. ET from Amersham High quality sequence stop: 1.
FEATURES             source
Location/Qualifiers
1..91
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1373621"
/clone_lib="NCI_CGAP_Ov2"
/sex="female"
/tissue_type="ovary"
/lab_host="DH10B"
/note="Vector: PAMPI0; mRNA made from invasive ovarian

```

	tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
BASE COUNT	21 a 27 c 29 g 14 t
ORIGIN	
Query Match	69.0%; Score 13.8; DB 9; Length 91;
Best Local Similarity	88.2%; Pred. No.2e+04;
Matches 15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Oy	3 GCCGACGTGGAGCCAG 19 1
Db	30 GACCGCGCTGGAGCCAG 46
RESULT 3	
AA930982	91 bp mRNA linear EST 23-APR-1998
LOCUS	VY79F05.r1 StrataGene mouse macrophage (#937306) Mus musculus CDNA
DEFINITION	clone IMAGE:131249 5' similar to gb:X52839 60S RIBOSOMAL PROTEIN L17 (HUMAN); mRNA sequence.
ACCESSION	AA930982
VERSION	AA930982.1 GI:3079415
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 91) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE	The WashU-HIMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project WashU-HIMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LINT ; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information. MGI:682745 Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 20. Location/Qualifiers 1..91 /organism="Mus musculus" /db_xref="taxon:10090" /clone_image="IMAGE:131249" /clone_lib="Stratagene mouse macrophage (#937306)" /tissue_type="macrophage" /dev_stage="WEHI-3 cell line" /lab_host="SOLR (kanamycin resistant)" /note="Organ: blood; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb, UniZAP XR Vector;- 5' adaptor sequence: 5' GAATTCGGCAGCAG 3' ~3' adaptor sequence: 5' CTCGACGTTTTTTTTTTTTTTTT 3'
FEATURES	
SOURCE	
BASE COUNT	25 a 19 c 25 g 22 t
ORIGIN	
Query Match	68.0%; Score 13.6; DB 9; Length 91;
Best Local Similarity	80.0%; Pred. No.2.5e+04;
Matches 16; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
Oy	1 GTGCAGACTGTGGACCAGA 20 
Db	21 GTGCAGACTTGTGCCACGA 40

RESULT 4  
A2776503/c 60 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0010J1F Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
DEFINITION clone UGCG2M0010J1 F, DNA sequence.  
ACCESSION A2776503  
VERSION A2776503.1 GI:12904143  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 60)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
Plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0010 row: J column: 11  
Seq primer: CTTGTAAACGACGCGCAT  
Class: plasmid ends  
High quality sequence stop: 60.  
Location/Qualifiers  
1..60  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_lib="UGCG2M0010J1"  
/clone\_lib="Mouse 10kb plasmid UGCGIM library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-gold, T1-resistant, F-"  
/note="Vector: PMD42ny; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g1147321419b/AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 10 a 18 c 20 g 12 t  
ORIGIN  
Query Match 67.0%; Score 13.4; DB 17; Length 60;  
Best Local Similarity 93.3%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGCGACGTGGACG 16  
|||||  
Db 39 TGGCTACGTGGACG 25

RESULT 5  
AU103727/c 50 bp mRNA linear EST 30-AUG-2001  
LOCUS AU103727 Sugano Homo sapiens cDNA library Homo sapiens clone  
DEFINITION HEP6017, mRNA sequence.  
ACCESSION AU103727  
VERSION AU103727.1 GI:13553248  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata  
H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
21270072  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8638, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
S., Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="HEP6017"  
/clone\_lib="Sugano Homo sapiens cDNA library"  
/note="Differential display comparison of untreated and  
dimethylformate treated U937 cells"  
Location/Qualifiers

BASE COUNT 12 a 14 c 16 g 8 t  
ORIGIN  
Query Match 66.0%; Score 13.2; DB 9; Length 50;  
Best Local Similarity 83.3%; Pred. No. 3.2e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCCGACGTGGACCGA 20  
|||||  
Db 30 GCCACGTGGACTGCA 13

RESULT 6  
A2438521/c 51 bp DNA linear GSS 03-OCT-2000  
LOCUS A2438521 1M0228112R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
DEFINITION clone UGCG1M0228112 R, DNA sequence.  
ACCESSION A2438521  
VERSION A2438521.1 GI:10562534  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 51)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
Plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center



DB	74	GCAGACATGTGGACACAGA	57
Query Match	Best Local Similarity	83.3%	Pred. No. 3.9e+04
Matches	15	Conservative	0; Mismatches 3; Indels 0; Gaps 0;
BASE COUNT	16 a	32 c	17 g 30 t
ORIGIN			
RESULT 9			
LOCUS	BG327801/c	67 bp	mRNA linear EST 27-FEB-2001
DEFINITION	602426812p1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4564659 5',		
ACCESSION	BG327801		
VERSION	BG327801.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 67)		
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strusberg, Ph.D. Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a> Tissue Procurement: DCTD/DBP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: L1CML1280 row: h column: 04 High quality sequence stop: 67.		
FEATURES	Location/Qualifiers		
Source	1..67		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:4564659"		
	/clone_11b="NIH MGC 14"		
	/tissue_type="renal cell adenocarcinoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: kidney; Vector: pOT7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(C). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of		

BASE COUNT	21 a	21 c	13 g	12 t	California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN					
Query Match	64.0%	Score 12.8;	DB 9;	Length 88;	
Best Local Similarity	87.5%;	Pred. No. 5.3e+04;			
Matches	14;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps	0;				
OY	2	TGCCGACGTGGGACCC	17		
DB	64	TGCACACTGGGACCC	49		
RESULT 10					
AV0077180/c					
LOCUS					
DEFINITION	AV0077180	88 bp	mRNA	linear	EST 04-MAY-2000
	AV0077180	Sugano cDNA library Homo sapiens cDNA clone zrv61563			
		similar to 5'-end region of B.taurus mRNA for coatmer, mRNA			
		sequence.			
ACCESSION	AV0077180				
VERSION	AV0077180.1	GI:7439794			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS.	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	1 (bases 1 to 88)				
	Suzuki,Y., Ishihara,D., Sasaki,M., Nakagawa,H., Hata,H., Tsunoda,T.				
	, Matenabe,M., Komatsu,T., Ota,T., Isogai,T., Suyama,A. and Sugano				
	,S.				
	Statistical analysis of the 5' untranslated region of human mRNA				
	using 'Oligo-Capped' cDNA libraries				
	Genomics 64 (3), 286-297 (2000)				
JOURNAL	20221373				
MEDLINE	Contact: Yutaka Suzuki				
COMMENT	Department of Virology				
	Institute of Medical Science, University of Tokyo				
	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan				
	Email: yusuzuki@ims.u-tokyo.ac.jp				
	Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano				
	,S. Construction and characterization of a full length-enriched and				
	a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997)				
	This clone was obtained from a '5'-end-enriched' cDNA library				
	constructed by 'Oligo-Capping' method. The coding region starts				
	from the 50 bp upstream to the 3'-end.				
FEATURES	Location/Qualifiers				
source	1..88				
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	/db_xref="taxon:9606"				
	/clone="zrv61563"				
	/clone_11b="Sugano cDNA library"				
	/note="The cDNA was prepared using the anchor primer,				
	H-T11g, from Genhunter"				
BASE COUNT	16 a	26 c	24 g	22 t	
ORIGIN					
Query Match	64.0%	Score 12.8;	DB 9;	Length 88;	
Best Local Similarity	87.5%;	Pred. No. 5.8e+04;			
Matches	14;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps	0;				
OY	1	GTGCCGACGTGGGACCC	16		
DB	23	GTGCCGACGTGGGACCC	8		
RESULT 11					
AA0094815					
LOCUS					
DEFINITION	AA0094815	89 bp	mRNA	linear	EST 25-OCT-1996
	cp1650.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens				
	cDNA 5', mRNA sequence.				
ACCESSION	AA0094815				
VERSION	AA0094815.1	GI:1640408			

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 89)
TITLE	Liew,C.C.
JOURNAL	CDNAS from fetal heart (1996)
COMMENT	unpublished (1996) Contact: Liew CC Brigham and Women's Hospital Harvard Medical School 75 Francis St. Boston, MA 02115, USA Tel: 6177328915 Fax: 6179750995 Email: cliew@rics.bwh.harvard.edu
FEATURES	PCR Primers FORWARD: 5' GCCAAGCTCGAATTACCCCTCAGCTAAGG 3' BACKWARD: 5' CCAGTGAATTGATATAGCTCACTATAGGCG 3' Seq primer: 5' GAATTACCCCTCAGCTAAGG 3'. Location/Qualifiers 1. 89 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Human fetal heart, lambda ZAP Express" /lab_host="E. coli XL1-Blue" /note="Vector: lambda ZAP Express; Site:1: EcoRI; Site:2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predesigned lambda ZAP Express."
BASE COUNT	19 a 27 c 22 g 21 t
ORIGIN	
Query Match	64.0%; Score 12.8; DB 9; Length 89;
Best Local Similarity	87.5%; Pred. No.5.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
0Y 3 GCCGACGTGGACCA 18 11111111111111111111	
Db 40 GCTGACGTGGACCA 55	
RESULT 12	
LOCUS	AU106651/c 50 bp mRNA linear EST 30-AUG-2001
DEFINITION	AU106651 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION	CAS03704, mRNA sequence.
VERSION	AU106651
KEYWORDS	AU106651.1 GI:13556172
SOURCE	EST.
ORGANISM	human. Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
1 (bases 1 to 50)	
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hatake ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)	
21270072	
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano ,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers
FEATURES	

source	1. 50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CAS03704" /clone_lib="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"
BASE COUNT	7 a 19 c 14 g 10 t
ORIGIN	
Query Match	63.0%; Score 12.6; DB 9; Length 50;
Best Local Similarity	78.9%; Pred. No. 6e+04;
Matches 15; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
OY 2	TCGCACCGTGGACCCAGA 20       11 11
Db 31	TCGCACGCTGCCTCCGA 13
RESULT 13	
AUT06652/c	50 bp mRNA linear EST 30-AUG-2001
LOCUS	AUT06652 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION	CAS03727, mRNA sequence.
ACCESSION	AUT06652
VERSION	AUT06652.1 GI:13556173
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 50) Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hatake ,H., Oka,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)
TITLE	Contact: Yutaka Suzuki
JOURNAL	Department of Medical Science, University of Tokyo
MEDLINE	Institute of Medical Science, Minatoku, Tokyo 108-8639, Japan
COMMENT	Email: yusuzuki@ms.u-tokyo.ac.jp Suzuki,Y., Yoshimoto-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. ,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers 1. 50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CAS03727" /clone_lib="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"
BASE COUNT	8 a 19 c 15 g 8 t
ORIGIN	
Query Match	63.0%; Score 12.6; DB 9; Length 50;
Best Local Similarity	78.9%; Pred. No. 6e+04;
Matches 15; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
OY 2	TCGCACCGTGGACCCAGA 20       11 11
Db 28	TCGCACGCTGCCTCCGA 10
RESULT 14	
AUT06653/c	50 bp mRNA linear EST 30-AUG-2001
LOCUS	AUT06653 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION	CAS04264, mRNA sequence.
ACCESSION	AUT06653



VERSION AU106653.1 GI:13556174  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata  
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
JOURNAL Contact: Yutaka Suzuki  
MEDLINE Department of Virology  
COMMENT Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
,S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers  
1. 50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="CAS04264"  
/note="Differential display comparison of untreated and  
dimethylfluminate treated U937 cells"

BASE COUNT 6 a 19 c 14 g 11 t  
ORIGIN

Query Match 63.08; Score 12.6; DB 9; Length 50;  
Best Local Similarity 78.9%; Pred. No. 6e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 TGCCGACGTGGACCCAGA 20  
||||| 1 1 1 1 1  
Db 31 TGCCGACGTGGCTCCGGA 13

RESULT 15  
AU106654/c 50 bp mRNA linear EST 30-AUG-2001  
LOCUS AU106654 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION CAS04474, mRNA sequence.  
ACCESSION AU106654  
VERSION AU106654.1 GI:13556175  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata  
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
JOURNAL Contact: Yutaka Suzuki  
MEDLINE Department of Virology  
COMMENT Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
,S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers  
1. 50  
/organism="Homo sapiens"

FEATURES  
source

/db\_xref="taxon:9606"  
/clone\_lib="CAS04474"  
/note="Differential display comparison of untreated and  
dimethylfluminate treated U937 cells"

BASE COUNT 7 a 19 c 14 g 10 t  
ORIGIN

Query Match 63.08; Score 12.6; DB 9; Length 50;  
Best Local Similarity 78.9%; Pred. No. 6e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 TGCCGACGTGGACCCAGA 20  
||||| 1 1 1 1 1  
Db 31 TGCCGACGTGGCTCCGGA 13

Search completed: November 26, 2002, 04:07:51  
Job time : 758.8 secs

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2002, 14:46:40 : Search time 302.2 Seconds  
(without alignments)  
1926.063 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20

Sequence: 1 gacccacagcgacatcatg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Maximum Match 0%

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	17.6	78.0	21	6	AX153915
2	15.2	76.0	44	6	108796
3	13.6	68.0	59	6	AR073712
4	13.6	68.0	61	6	AX085810
5	13.6	68.0	93	6	E29108
6	13.4	67.0	78	6	AX404028
7	13.2	66.0	24	6	AR104159
8	13.2	66.0	51	6	AX117457
9	13.2	66.0	51	6	AX158478
10	13.2	66.0	51	9	AB013762
11	13.2	66.0	51	9	AB013763
12	13.2	66.0	51	9	AB013764
13	13.2	66.0	67	9	S75425504
14	13.2	66.0	75	6	AR182824
15	12.8	64.0	18	6	AR138054
16	12.8	64.0	60	9	HUMHPABA
17	12.8	64.0	66	6	E03396
18	12.8	64.0	69	6	I66412
19	12.8	64.0	87	6	AX135351
20	12.8	64.0	99	10	AF357349
21	12.6	63.0	20	6	AX100702
22	12.6	63.0	21	6	AX096010
23	12.6	63.0	24	6	AX291553
24	12.6	63.0	28	6	AR182413
25	12.6	63.0	28	6	AR182415
26	12.6	63.0	29	6	AR199662
27	12.6	63.0	30	6	AR068885
28	12.6	63.0	40	6	AR033896
29	12.6	63.0	40	6	AR175029
30	12.6	63.0	40	6	AX032461
31	12.6	63.0	45	6	AR033949
32	12.6	63.0	45	6	AR175082
33	12.6	63.0	45	6	AX032526
34	12.6	63.0	51	6	AX162480
35	12.6	63.0	51	6	AX190058
36	12.6	63.0	74	9	HUM13COL22
37	12.6	63.0	76	9	AF040224
38	12.6	63.0	76	9	S75383518
39	12.4	62.0	18	6	I25834
40	12.4	62.0	21	6	I05985
41	12.4	62.0	21	6	I08790
42	12.4	62.0	24	6	AR091297
43	12.4	62.0	24	6	AR137679
44	12.4	62.0	37	6	AR171242
45	12.4	62.0	38	6	AR058104

#### ALIGNMENTS

RESULT 1  
AX153915/c  
LOCUS AX153915  
DEFINITION Sequence 13 from Patent WO0138576.  
ACCESSION AX153915  
VERSION AX153915.1 GI:14535529  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.  
TITLE Human single nucleotide polymorphisms  
JOURNAL Patent: WO 0138576-A 13 31-MAY-2001;

Pred. No. is the number of results predicted by chance to have a

# WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

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Location/Qualifiers  
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Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 21 CCCCCGAGGCACTCATGG 4

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LOCUS 108796 44 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 18 from Patent WO 8804690.  
ACCESSION 108796  
VERSION 108796.1 GI:588501  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 44)  
AUTHORS Bollen,A.J., Cheyssen,D., Jacobs,P., Pierard,L. and Collen,D.J.  
JOURNAL Patent: WO 8804690-A 18 30-JUN-1988;  
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source  
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Best Local Similarity 85.0%; Pred. No. 9.1e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GACCCCGAGGCACTCATGG 20  
Db 42 GACCCCGAGGCACTCATGG 23

RESULT 3  
LOCUS AR073712 59 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 5 from patent US 5952190.  
ACCESSION AR073712  
VERSION AR073712.1 GI:10000472  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 59)  
AUTHORS Joenje,H. and Jo Ten Hoe,J.R.  
JOURNAL Patent: US 5952190-A 5 14-SEP-1999;  
FEATURES  
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GACCCCGAGGCACTCATGG 20  
Db 27 GACCCCGAGGCACTCATGG 46

RESULT 4  
LOCUS AX085810 61 bp DNA linear PAT 09-MAR-2001  
DEFINITION Sequence 72 from Patent WO0112858.  
ACCESSION AX085810  
VERSION AX085810.1 GI:13275760  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 61)  
AUTHORS He,T.C., Kinzler,K.W. and Vogelstein,B.  
JOURNAL par.g(d) links apc to chemopreventive drugs  
Patent: WO 0112858-A 72 22-FEB-2001;  
The Johns Hopkins University (US)  
FEATURES  
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 28 GACCCCGAGGCACTCATGG 47

RESULT 5  
LOCUS E29108 93 bp DNA linear PAT 18-JUN-2001  
DEFINITION Expression regulatory region of stress protein HSP47 and  
utilization thereof.  
ACCESSION E29108  
VERSION E29108.1 GI:13020964  
KEYWORDS JP 1999243968-A/1.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 93)  
AUTHORS Kazuhiro,N.  
TITLE Expression regulatory region of stress protein HSP47 and  
utilization thereof  
JOURNAL Patent: JP 1999243968-A 1 14-SEP-1999;  
COMMENT SCIENCE & TECH AGENCY  
OS Unidentified  
PN JP 1999243968-A/1  
PD 14-SEP-1999  
PE 05-MAR-1998 JP 1998071489  
PR  
PI KAZUHIRO NAGATA  
PC C12N15/09,A61K31/70,A61K48/00//C12N15/09,C12R1.91,C12N15/00,  
PC (C12N15/00,C12R1.91)  
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CC Topology: Linear;  
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCGACTCATGG 20  
Db 6 GGCATCCAGGCGACGCTGG 25

RESULT 6  
AX404028  
LOCUS AX404028 78 bp DNA linear PAT 14-JUN-2002  
DEFINITION Sequence 25 from Patent EP1195161.  
ACCESSION AX404028  
VERSION AX404028.1 GI:21437354  
KEYWORDS  
SOURCE dog.  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE  
AUTHORS Morsey, M.A., Sheppard, M.G. and Wheeler, D.W.  
TITLE Anti-lige vaccines  
JOURNAL Patent: EP 1195161-A 25 10-APR-2002;  
Pflizer Products Inc. (US)  
FEATURES  
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Best Local Similarity 93.3%; Pred. No. 6.5e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCCAGGCGACTCATG 19  
Db 25 CCCAGGCGCTCATG 39

RESULT 7  
AR104159/c  
LOCUS AR104159 24 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 8 from patent US 6093542.  
ACCESSION AR104159  
VERSION AR104159.1 GI:12816867  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE  
AUTHORS Romano, J., Pal, R. and Shurtliff, R.  
TITLE Isothermal transcription based amplification assay for the  
JOURNAL detection and quantitation of macrophage derived chemokine RNA  
FEATURES  
source 1..24  
/organism="unknown"  
BASE COUNT 4 a 8 c 8 g 4 t  
ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 24;  
Best Local Similarity 83.3%; Pred. No. 9.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCCCCAGGCGACTCATG 20  
Db 23 CACCCAGGCGACTCTGG 6

RESULT 8  
AX117457  
LOCUS AX117457 51 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 2580 from Patent WO0129262.  
ACCESSION AX117457

VERSION AX117457.1 GI:14034408  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Picoult-Newburg, L. and Pohl, M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 0129262-A 2580 26-APR-2001;  
Orchid Biosciences, Inc. (US)  
FEATURES  
source 1..51  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 18 a 14 c 10 g 9 t  
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Best Local Similarity 83.3%; Pred. No. 8.6e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACCCCGAGGCGACTCATG 19  
Db 14 ACCCCGAGGCGACTCATG 31

RESULT 9  
AX158478  
LOCUS AX158478 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 1806 from Patent WO0140521.  
ACCESSION AX158478  
VERSION AX158478.1 GI:14539809  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
JOURNAL methods of use thereof  
Patent: WO 0140521-A 1806 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES  
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCGACTCAT 18  
Db 25 GACCCCGAGGCTACTCCT 42

RESULT 10  
AB013762  
LOCUS AB013762 51 bp DNA linear PRI 29-JUN-2002  
DEFINITION Macaca assamensis gene for immunoglobulin alpha heavy chain,  
partial cds, isolate:UTS400.  
ACCESSION AB013762  
VERSION AB013762.1 GI:6681477  
KEYWORDS  
SOURCE Macaca assamensis (isolate:UTS400) DNA.  
ORGANISM Macaca assamensis

REFERENCE  
AUTHORS Sumiyama, K., Saitou, N. and Ueda, S.  
TITLE Adaptive evolution of the IGA hinge region in primates  
JOURNAL Mol. Biol. Evol. 19 (7), 1093-1099 (2002)  
MEDLINE 22077633  
PUBMED 12082128  
REFERENCE 2 (bases 1 to 51)  
AUTHORS Sumiyama, K., Ueda, S. and Saitou, N.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAY-1998) Kenta Sumiyama, National Institute of Genetics, Evolutionary Genetics Division, Yata 1111, Mishima, Shizuoka 411-8540, Japan (E-mail: ksumiyam@lab.nig.ac.jp, Tel:+81-559-81-6790, Fax:+81-559-81-6794)  
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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Db 22 ACCCCATGTCCCTCATG 39  
RESULT 11 51 bp DNA linear PRI 29-JUN-2002  
AB013763  
LOCUS Macaca assamensis gene for immunoglobulin alpha heavy chain,  
DEFINITION partial cds, isolate:UTS398B.  
ACCESSION AB013763  
VERSION AB013763.1 GI:6681479  
KEYWORDS IGA.  
SOURCE Macaca assamensis (isolate:UTS398B) DNA.  
ORGANISM  
REFERENCE  
AUTHORS Sumiyama, K., Saitou, N. and Ueda, S.  
TITLE Adaptive evolution of the IGA hinge region in primates  
JOURNAL Mol. Biol. Evol. 19 (7), 1093-1099 (2002)  
MEDLINE 22077633  
PUBMED 12082128  
REFERENCE 2 (bases 1 to 51)  
AUTHORS Sumiyama, K., Ueda, S. and Saitou, N.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAY-1998) Kenta Sumiyama, National Institute of Genetics, Evolutionary Genetics Division, Yata 1111, Mishima, Shizuoka 411-8540, Japan (E-mail: ksumiyam@lab.nig.ac.jp, Tel:+81-559-81-6790, Fax:+81-559-81-6794)  
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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||||||| | | | | | | |  
Db 22 ACCCCATGTCCCTCATG 39  
RESULT 12 51 bp DNA linear PRI 29-JUN-2002  
AB013764  
LOCUS Macaca fascicularis gene for immunoglobulin alpha heavy chain,  
DEFINITION partial cds, isolate:UTS362B.  
ACCESSION AB013764  
VERSION AB013764.1 GI:6681481  
KEYWORDS IGA.  
SOURCE Macaca fascicularis (isolate:UTS362B) DNA.  
ORGANISM  
REFERENCE  
AUTHORS Sumiyama, K., Saitou, N. and Ueda, S.  
TITLE Adaptive evolution of the IGA hinge region in primates  
JOURNAL Mol. Biol. Evol. 19 (7), 1093-1099 (2002)  
MEDLINE 22077633  
PUBMED 12082128  
REFERENCE 2 (bases 1 to 51)  
AUTHORS Sumiyama, K., Ueda, S. and Saitou, N.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAY-1998) Kenta Sumiyama, National Institute of Genetics, Evolutionary Genetics Division, Yata 1111, Mishima, Shizuoka 411-8540, Japan (E-mail: ksumiyam@lab.nig.ac.jp, Tel:+81-559-81-6790, Fax:+81-559-81-6794)  
FEATURES  
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:52:31 : Search time 98.55 Seconds  
(without alignments)  
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Title: US-09-296-264-11

Perfect score: 20

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Scoring table: IDENTITY\_NUC

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Searched: 2185239 seqs, 112599159 residues 2390332

Total number of hits satisfying chosen parameters:

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Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	21	AAZ31441
2	16.4	82.0	21	21	AAH62112
3	16	80.0	20	21	AAZ31450
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5	15.2	76.0	60	24	ABN34554
6	14.4	72.0	39	24	ABR88692
7	14.4	72.0	39	24	ABR13410
8	14.2	71.0	51	22	AAZ27305
9	14.2	71.0	51	22	AAZ27307

C	10	14.2	71.0	60	24	ABN59176	Human spliced tran
C	11	13.8	69.0	51	22	AAZ27308	Human SNP oligonuc
C	12	13.6	68.0	51	22	AAZ28078	Human SNP oligonuc
C	13	13.6	68.0	59	19	AAV18190	Primer for Fancon1
C	14	13.6	68.0	60	24	ABN39793	Human spliced tran
C	15	13.6	68.0	61	22	AAZ75272	Human pPARgamma PC
C	16	13.6	68.0	93	20	AAZ27697	Intron from HSP47
C	17	13.2	66.0	24	20	AAZ90284	Macrophage derived
C	18	13.2	66.0	31	20	AAZ07235	PCR primer ZC15.33
C	19	13.2	66.0	38	21	AAZ82076	p53 PCR primer FPS
C	20	13.2	66.0	50	22	AAZ28077	Human SNP oligonuc
C	21	13.2	66.0	51	22	AAZ74865	Human silent SNP c
C	22	13.2	66.0	51	22	AAZ39784	Human SNP flankin
C	23	13.2	66.0	60	24	ABN46919	Human spliced tran
C	24	13.2	66.0	75	21	ABZ62647	Mycobacterium tude
C	25	13.2	66.0	80	22	AAZ83397	Primer luc12. syn
C	26	13.2	66.0	82	22	AAZ83396	Primer luc11. syn
C	27	13	65.0	18	14	AAZ40337	p58 nested primer
C	28	13	65.0	20	24	ABZ61256	Human aquaporin 5
C	29	13	65.0	21	19	AAZ26653	Human polymorphic
C	30	13	65.0	21	22	AAZ96423	Human gene single
C	31	13	65.0	50	22	AAZ30652	Human SNP oligonuc
C	32	12.8	64.0	18	20	AAZ40915	Human CD40 phospho
C	33	12.8	64.0	18	21	AAZ47748	Human CD40 antisen
C	34	12.8	64.0	20	21	AAZ86393	Primer BMV R. syn
C	35	12.8	64.0	20	22	AAZ91199	BMV-F primer. syn
C	36	12.8	64.0	20	22	AAZ23596	Primer BMV R. unl
C	37	12.8	64.0	20	24	AAZ20531	Purified viral RNA
C	38	12.8	64.0	25	21	AAZ45010	UDP-glucuronosyltr
C	39	12.8	64.0	25	22	AAZ43234	Human Oestrogen re
C	40	12.8	64.0	27	19	AAV19570	Human LDL receptor
C	41	12.8	64.0	31	16	AAZ85848	MHC class I allele
C	42	12.8	64.0	31	16	AAZ85778	MHC CW3 amplifica
C	43	12.8	64.0	31	16	AAZ85742	MHC CW3 CDNA nts 1
C	44	12.8	64.0	33	24	ABZ42117	Primer #3 for huma
C	45	12.8	64.0	47	21	AAZ65851	Human map-related

## ALIGNMENTS

RESULT 1	AAZ31441	AAZ31441 standard; DNA: 20 BP.
ID	AAZ31441	
XX	AAZ31441	
AC	AAZ31441	
XX	07-FEB-2000	(first entry).
DT	07-FEB-2000	
XX	Human neuropilin mRNA specific antisense oligo GTT3611.	
DE	Human neuropilin mRNA specific antisense oligo GTT3611.	
XX	Neuropilin; human; growth; metastasis; tumor; neovascularisation;	
KW	Neuropilin; human; growth; metastasis; tumor; neovascularisation;	
KW	cancer; papilloma; diabetic retinopathy; antisense; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
PN	WO955855-A2.	
XX		
PD	04-NOV-1999.	
XX		
PF	23-APR-1999;	99WO-CA00324.
XX		
PR	23-APR-1999;	98US-0082791.
XX		
PA	(GENE-) GENESENSE TECHNOLOGIES INC.	
XX		
PI	Wright JA, Young AH, Lee YS;	
XX		
DR	WPI: 2000-023357/02.	
XX		
PT	Antisense oligonucleotides that inhibit neuropilin expression, useful for treating cancer -	

XX Claim 4; Page 16; 57pp; English.  
PS Sequences AA231431-460 represent antisense oligonucleotides which  
CC inhibit human neuropilin expression. The antisense oligonucleotides can  
CC be used to inhibit the growth or metastasis of a mammalian tumor and  
CC inhibit neovascularisation. The oligonucleotides may be used to treat  
CC various forms of cancers or tumors, such as sarcomas, melanomas,  
CC adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell  
CC carcinomas of the mouth, throat, larynx and lung, genitourinary cancers  
CC such as cervical and bladder cancer, hematopoietic cancers, colon cancer,  
CC breast cancer, pancreatic cancer, renal cancer, brain cancer, skin  
CC cancer, liver cancer, head and neck cancers, and nervous system cancers,  
CC as well as benign lesions such as papillomas. The methods may be used to  
CC treat neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration.  
XX  
SQ Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 other;  
Query Match 100.0%; Score 20; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GACCCCGAGGCGACTCATGG 20  
DB 1 GACCCCGAGGCGACTCATGG 20  
RESULT 2  
AAH62112/C  
ID AAH62112 standard; DNA; 21 BP.  
XX  
AC AAH62112;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Neuropilin 1 (NRP1) polymorphism containing DNA fragment #13.  
XX  
KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;  
KW heart disease; paternity testing; forensic science; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Variation replace(11,T)  
FT /tag= a  
FT /standard\_name= "single nucleotide polymorphism"  
XX  
PN WO200138576-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 17-NOV-2000; 2000WO-US31639.  
XX  
PR 24-NOV-1999; 99US-0167334.  
XX  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
XX  
PI Cargill M, Ireland JS, Lander ES.  
XX  
DR WPI: 2001-367705/38.  
XX  
XX New nucleic acid segments of the human genome, particularly from genes  
PT including polymorphic sites; for phenotype correlation, forensics,  
PT paternity testing, medicine and genetic analysis -  
XX  
PS Claim 1; Page 29; 80pp; English.  
XX  
CC DNA sequences AAH62100 - AAH62688 represent segments of human genes which  
CC contain single nucleotide polymorphisms (SNPs). A method is included in  
CC the invention for analysing a nucleic acid sample, which consists of  
CC determining the base occupying any one of the polymorphic sites given in  
CC the SNP containing sequences. The nucleotide sequences can be used in the

CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart  
CC diseases, diseases of the cardiovascular system, and infection by  
CC microorganisms. The oligonucleotides are also useful in the manufacture  
CC of a medicament for the treatment or prophylaxis of the diseases, and as  
CC a pharmaceutical. SNP containing oligonucleotides are useful in  
CC applications such as phenotype correlation, forensics, paternity testing,  
CC medicine and genetic analysis.  
XX  
SQ Sequence 21 BP; 3 A; 6 C; 9 G; 3 T; 0 other;  
Query Match 82.0%; Score 16.4; DB 22; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 3 CCCCCAGGCGACTCATGG 20  
DB 21 CCCCCAGGCGCTCATGG 4  
RESULT 3  
AAZ31450  
ID AAZ31450 standard; DNA; 20 BP.  
XX  
AC AAZ31450;  
XX  
DT 07-FEB-2000 (first entry)  
XX  
DE Human neuropilin mRNA specific antisense oligo GT13621.  
XX  
KW Neuropilin: human; growth; metastasis; tumor; neovascularisation;  
KW cancer; papilloma; diabetic retinopathy; antisense; ss.  
XX  
OS Synthetic.  
XX  
OS Homo sapiens.  
XX  
PN WO955855-A2.  
XX  
PD 04-NOV-1999.  
XX  
PF 23-APR-1999; 99WO-CA00324.  
XX  
PR 23-APR-1998; 98US-0082791.  
XX  
PA (GENE-) GENESENSE TECHNOLOGIES INC.  
XX  
PI Wright JA, Young AH, Lee YS;  
XX  
DR WPI: 2000-023357/02.  
XX  
PT Antisense oligonucleotides that inhibit neuropilin expression, useful  
PT for treating cancer -  
XX  
PS Claim 4; Page 16; 57pp; English.  
XX  
XX Sequences AA231431-460 represent antisense oligonucleotides which  
CC inhibit human neuropilin expression. The antisense oligonucleotides can  
CC be used to inhibit the growth or metastasis of a mammalian tumor and  
CC inhibit neovascularisation. The oligonucleotides may be used to treat  
CC various forms of cancers or tumors, such as sarcomas, melanomas,  
CC adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell  
CC carcinomas of the mouth, throat, larynx and lung, genitourinary cancers  
CC such as cervical and bladder cancer, hematopoietic cancers, colon cancer,  
CC breast cancer, pancreatic cancer, renal cancer, brain cancer, skin  
CC cancer, liver cancer, head and neck cancers, and nervous system cancers,  
CC as well as benign lesions such as papillomas. The methods may be used to  
CC treat neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration.  
XX  
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 other;  
Query Match 80.0%; Score 16; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 5 CCCAGGCACTCATGG 20  
| | | | | | | | | | | | | | | |  
DB 1 CCCAGGCACTCATGG 16

RESULT 4  
AAL27306  
ID AAL27306 standard; DNA; 51 BP.  
XX  
AC AAL27306;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #514.  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-US35498.  
XX  
PR 28-DEC-1999; 99US-0173419.  
XX  
PR 27-DEC-2000; 2000US-0173419.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shinkets RA, Leach M;  
XX  
DR WPI; 2001-465210/50.  
XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -  
XX  
PS Claim 1; Page 1536; 4143pp; English.  
XX  
CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoposis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.  
XX  
SQ Sequence 51 BP; 10 A; 18 C; 11 G; 12 T; 0 other;

Query Match 76.0%; Score 15.2; DB 22; Length 51;  
Best Local Similarity 85.0%; Pred. No. 7.9e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

0Y 1 GACCCGAGGCACTCATGG 20  
| | | | | | | | | | | | | | | |

DB 26 GAGCCTCAGGCACTCATGG 45

RESULT 5  
ABN34554/C  
ID ABN34554 standard; DNA; 60 BP.  
XX  
AC ABN34554;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO.7302.  
XX  
KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB01903.  
XX  
PR 28-JUL-2000; 2000US-221607P.  
XX  
PR 02-MAY-2001; 2001US-287724P.  
XX  
PA (COMP-) COMPUGEN INC.  
XX  
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Falgler S;  
XX  
DR WPI; 2002-257383/30.  
XX  
PT New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of  
PT a genome, useful for detecting tissue-, pathology-, and  
PT developmental-specific genes -  
XX  
PS Example 1; SEQ ID 7302; 47pp; English.  
XX  
CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the  
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises  
CC several oligonucleotides, each capable of hybridizing selectively to a  
CC set of messenger RNAs transcribed from a given transcription unit of  
CC the genome, which encodes one or more messenger RNA splice variants.  
CC The oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterizing the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a  
CC particular biological or pathological state, and so allowing the  
CC detection of tissue- and pathology-specific genes such as those genes  
CC only expressed in specific tissue under a specific pathological  
CC condition; to detect developmental specific genes; and to detect RNA  
CC transcripts and splice variants of a transcriptome of a patient suffering  
CC from a particular disorder. ABN27253 to ABN59589 represent  
CC oligonucleotide sequences from rats, humans and mice, which are used in  
CC the exemplification of the present invention.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
XX  
SQ Sequence 60 BP; 17 A; 14 C; 19 G; 10 T; 0 other;

Query Match 76.0%; Score 15.2; DB 24; Length 60;  
Best Local Similarity 85.0%; Pred. No. 7.9e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

0Y 1 GACCCGAGGCACTCATGG 20  
| | | | | | | | | | | | | | | |

DB 46 GAGCCTCAGGCGACTCATGG 27

RESULT 6  
ABK8692/C  
ID ABK8692 standard; DNA; 39 BP.

XX  
AC ABK8692;  
XX  
DT 07-OCT-2002 (first entry)  
XX

Human transmembrane activator and CAML-interactor (TACI), PCR primer #2.

XX  
KW Human; tumour necrosis factor; TNF delta; pulmonary system disorder;  
KW immunoglobulin production; B-cell proliferation; immune system disorder;  
KW autoimmune disease; cancer; lymphoproliferative disorder; pain;  
KW microbial infection; parasitic infection; bone disease; atherosclerosis;  
KW cardiovascular disorder; neurodegenerative disease; wound healing;  
KW graft versus host disease; haematopoietic cell disorder; nephritis;  
KW transmembrane activator and CAML-interactor; TACI; TNF epsilon; PCR;  
KW primer; ss.  
XX  
XX  
OS Homo sapiens.  
XX  
PN US2002064829-A1.  
XX  
PD 30-MAY-2002.  
XX  
PF 14-JUN-2001; 2001US-0879919.  
XX  
PR 14-MAR-1996; 96US-016812P.  
PR 15-JUN-2000; 2000US-211537P.  
PR 23-OCT-2000; 2000US-241952P.  
PR 13-DEC-2000; 2000US-254875P.  
PR 16-MAR-2001; 2001US-276248P.  
PR 23-MAR-2001; 2001US-277978P.  
PR 25-MAY-2001; 2001US-293499P.  
PR 12-MAR-1997; 97US-0815783.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Yu G, Ni J, Gentz RL, Dillon PJ;  
XX  
DR WPI; 2002-556722/59.  
XX  
PT Novel human multimeric tumour necrosis factor delta or epsilon protein  
PT useful for treating disease or disorder of immune system such as  
PT autoimmune disease, immunodeficiency, or cancer of immune system -  
XX  
XX  
PS Example 29; Page 115; 143pp; English.

The present invention relates to the isolation of human tumour necrosis factor (TNF) delta and TNF epsilon proteins, and the polynucleotide sequences encoding them. The proteins are useful for modulating immunoglobulin production or for modulating proliferation of B-cells. The sequences of the invention are useful for treating diseases or disorders of the immune system. Such disorders include autoimmune diseases (e.g. systemic lupus erythematosus (SLE), acquired immunodeficiency syndrome (AIDS)), cancers of the immune system (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma, non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative disorders, microbial infections (e.g. viral, bacterial), parasitic infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis, pain, cardiovascular disorders (e.g. myocardial infarction, stroke), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), graft versus host disease, wound healing, haematopoietic cell disorders (e.g. anaemia), inflammatory disorders (e.g. asthma), diseases or disorders associated with various mucous membranes of the body (e.g. mucositis), and disorders of the pulmonary system. The proteins are also useful as a vaccine adjuvant that enhances immune responsiveness to specific antigens. The present sequence represents a PCR primer used to amplify human transmembrane activator and CAML-interactor (TACI) cDNA in the examples of the present invention.

XX  
SQ Sequence 39 BP; 8 A; 11 C; 13 G; 7 T; 0 other;  
XX  
Query Match 72.0%; Score 14.4; DB 24; Length 39;  
Best Local Similarity 93.8%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCCAGGCGACTCATGG 20  
DB 32 CCCAGGCGACTCATGG 17

RESULT 7  
ABK13410/C  
ID ABK13410 standard; DNA; 39 BP.

XX  
AC ABK13410;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Tumour necrosis factor (TNF) receptor TACI, 5' PCR primer #2.  
XX  
KW Tumour necrosis factor; TNF; cytostatic; arteriosclerosis;  
KW analgesic; cerebroprotective; nocotropic; neuroprotective; hepatotropic;  
KW immunoglobulin production; B cell proliferation; immunosuppressive;  
KW HIV; human immunodeficiency virus; autoimmune disease; immunodeficiency;  
KW Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;  
KW common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS;  
KW acquired immunodeficiency virus; cancer; multiple myeloma; CLL;  
KW chronic lymphocytic leukaemia; lymphoproliferative disorder;  
KW bacterial infection; viral infection; osteoporosis; atherosclerosis;  
KW pain; cardiovascular disorder; stroke; allergy; Alzheimer's disease;  
KW neurodegenerative disease; inflammation; liver disease; cirrhosis;  
KW cardiomyopathy; diabetes; psoriasis; glomerulonephritis;  
KW ulcerative colitis; angiogenesis; septic shock; wound healing;  
KW PCR; primer; ss; tumour necrosis factor receptor; TACI.  
XX  
XX  
OS Homo sapiens.  
XX  
PN WO200196528-A2.  
XX  
PD 20-DEC-2001.  
XX  
PF 14-JUN-2001; 2001WO-US19026.  
XX  
PR 15-JUN-2000; 2000US-211537P.  
PR 23-OCT-2000; 2000US-241952P.  
PR 13-DEC-2000; 2000US-254875P.  
PR 16-MAR-2001; 2001US-276248P.  
PR 23-MAR-2001; 2001US-277978P.  
PR 25-MAY-2001; 2001US-293499P.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;  
XX  
DR WPI; 2002-130727/17.  
XX  
PT Novel multimeric human tumour necrosis factor delta or epsilon protein  
PT useful for treating cancer, immune system disorders, infection,  
PT cardiovascular disorders, liver disease, cardiomyopathy, diabetes and  
PT psoriasis -  
XX  
XX  
PS Example 29; Page 295; 344pp; English.

The invention describes a multimeric human tumour necrosis factor (TNF) delta or epsilon protein (I). (I) or a composition containing them (II) are useful for modulating immunoglobulin production or proliferation of B cells. (I) or (II) is useful for treating a disease or disorder of the immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome, systemic lupus erythematosus or common variable immunodeficiency (CVID)); an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS)); cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's

CC lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL); in  
CC the diagnosis and treatment or prevention of cancer, lymphoproliferative  
CC disorder, bacterial and viral infections, osteoporosis, atherosclerosis,  
CC pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,  
CC neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.  
CC cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,  
CC glomerulonephritis, ulcerative colitis, arteriosclerosis; for promoting  
CC angiogenesis and wound healing; as a diagnostic research reagent; as an  
CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon  
CC receptor; in apoptosis of transformed cell lines; mediation of cell  
CC activation and proliferation; and as an immunogen to produce (II). (II)  
CC is useful to purify, detect and target (I), for measuring levels of (I)  
CC in biological samples, for immunophenotyping samples, and to treat.  
CC inhibit or prevent diseases and disorders associated with aberrant  
CC expression and/or activity of (I). This sequence represents a 5' PCR  
CC primer used to isolate the TNF receptor superfamily member TNFRI, required  
CC in an assay to establish if tumour necrosis factor epsilon (TNF-epsilon)  
CC binds the receptor described in the method of the invention.

XX Sequence 39 BP; 8 A; 11 C; 13 G; 7 T; 0 other;

SO Query Match

Best Local Similarity 72.0%; Score 14.4; DB 24; Length 39;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 CCCAGGCGCCTCATGG 20

Db 32 CCCAGGCGCCTCATGG 17

RESULT 8

AAI27305 standard; DNA: 51 BP.

AC AAI27305;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #513.

XX Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;  
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;  
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
XX complement related protein; cytochrome; kinesin; cytokine; interferon;  
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;  
XX multifactorial disease; autoimmune disease; infection;  
XX nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI: 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
XX oncogenes and histones, useful for diagnosing and treating, e.g.  
XX cancer, autoimmune diseases and infections -

PS Claim 1; Page 1536; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic

CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interleukins, interleukin,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.

XX Sequence 51 BP; 12 A; 16 C; 11 G; 12 T; 0 other;

SO Query Match

Best Local Similarity 71.0%; Score 14.2; DB 22; Length 51;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ACCCCAGGCGCCTCATGG 20

Db 30 ACCCTCAGGCGCCTCATGG 48

RESULT 9

AAI27307 standard; DNA: 51 BP.

AC AAI27307;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #515.

XX Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;  
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;  
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
XX complement related protein; cytochrome; kinesin; cytokine; interferon;  
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;  
XX multifactorial disease; autoimmune disease; infection;  
XX nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI: 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
XX oncogenes and histones, useful for diagnosing and treating, e.g.  
XX cancer, autoimmune diseases and infections -

PS Claim 1; Page 1537; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
XX variants of proteins related to amylases, amyloid proteins, angiotensin,  
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
XX histones, kinases, colony stimulating factors, complement related

CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
 CC G-protein coupled receptors and thioesterases. The present sequence is  
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
 CC by them may be used in the prevention, diagnosis and treatment of  
 CC diseases associated with inappropriate expression of the proteins listed  
 CC above. Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer  
 CC leukaemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms.

XX SQ Sequence 51 BP; 12 A; 16 C; 11 G; 12 T; 0 other;

Query Match 71.0%; Score 14.2; DB 22; Length 51;  
 Best Local Similarity 84.2%; Pred. No. 2.3e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ACCCCGAGGCGACTCATG 20  
 DB 6 AGCCTCAGGCGAGTCATG 24

RESULT 10  
 ABN59176/c  
 ID ABN59176 standard; DNA; 60 BP.

AC ABN59176;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:31924.

KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

PN W0200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-1B01903.

XX 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI; 2002-257383/30.

PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of  
 PT a genome, useful for detecting tissue-, pathology-, and  
 PT developmental-specific genes

XX Example 1; SEQ ID 31924; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the  
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises  
 CC several oligonucleotides, each capable of hybridizing selectively to a  
 CC set of messenger RNAs transcribed from a given transcription unit of  
 CC the genome, which encodes one or more messenger RNA splice variants.  
 CC The oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini

CC libraries to detect transcripts of a sub-transcriptome under a  
 CC particular biological or pathological state, and so allowing the  
 CC detection of tissue- and pathology-specific genes such as those genes  
 CC only expressed in specific tissue under a specific pathological  
 CC condition; to detect developmental specific genes; and to detect RNA  
 CC transcripts and splice variants of a transcriptome of a patient suffering  
 CC from a particular disorder. ABN27253 to ABN59589 represent  
 CC oligonucleotide sequences from rats, humans and mice, which are used in  
 CC the exemplification of the present invention.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 60 BP; 15 A; 18 C; 13 G; 14 T; 0 other;

Query Match 71.0%; Score 14.2; DB 24; Length 60;  
 Best Local Similarity 84.2%; Pred. No. 2.3e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GACCCGAGGCGACTCATG 19  
 DB 30 GTCCCGAGGCGACTCATG 12

RESULT 11  
 AAL27308  
 ID AAL27308 standard; DNA; 51 BP.

AC AAL27308;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #516.

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.

OS Homo sapiens.

PN W0200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI; 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 XX Claim 1; Page 1537; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
 CC G-protein coupled receptors and thioesterases. The present sequence is  
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded

CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.

XX  
SQ Sequence 51 BP; 10 A; 16 C; 11 G; 14 T; 0 other;

Query Match 69.0%; Score 13.8; DB 22; Length 51;  
Best Local Similarity 88.2%; Pred. No. 3.5e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCCCAGGCGACTCATGG 20  
11111111111111111111  
DB 2 CCTCAGGCGAGTCAATCG 18

## RESULT 12

AAI28078/c  
ID AAI28078 standard; DNA: 51 BP.

XX  
AC AAI28078;

XX  
DT 24-JAN-2002 (first entry)

XX  
DE Human SNP oligonucleotide #1286.

XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; cholestase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.

XX  
OS Homo sapiens.

XX  
PN WO200147944-A2.

XX  
PD 05-JUL-2001.

XX  
PF 28-DEC-2000; 2000WO-US35498.

XX  
PR 28-DEC-1999; 99US-0173419.

XX  
PR 27-DEC-2000; 2000US-0173419.

XX  
PA (CURA-) CURAGEN CORP.

XX  
PI Shimkets RA, Leach M;

XX  
DR WPI; 2001-465210/50.

XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -

XX  
PS Claim 1; Page 1748; 4143pp; English.

XX  
CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include

CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.

XX  
SQ Sequence 51 BP; 15 A; 13 C; 14 G; 9 T; 0 other;

Query Match 68.0%; Score 13.6; DB 22; Length 51;  
Best Local Similarity 80.0%; Pred. No. 4.3e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GACCCCGAGGCGACTCATGG 20  
11111111111111111111  
DB 41 GTCTCCAGGCGACTACTGG 22

## RESULT 13

AAV18190  
ID AAV18190 standard; DNA: 59 BP.

XX  
AC AAV18190;

XX  
DT 28-AUG-1998 (first entry)

XX  
DE Primer for Fanconi anaemia of complementation group A gene.

XX  
KW Fanconi anaemia of complementation group A; FA-A; genetic defect;  
KW prenatal FA-A; FA-A carrier detection; disease diagnosis; PCR primer; ss.

XX  
OS Synthetic.

XX  
PN WO9814462-A1.

XX  
PD 09-APR-1998.

XX  
PF 03-OCT-1997; 97WO-US18010.

XX  
PR 04-OCT-1996; 96US-0726012.

XX  
PA (FANC-) FANCONI ANEMIA RES FUND INC.

XX  
PI Joenje H, Lo Ten Foe JR;

XX  
DR WPI; 1998-240012/21.

XX  
PT DNA for Fanconi Anemia complementation group A - useful for, e.g.  
PT developing products for diagnosis and screening of disease and gene  
PT therapy

XX  
PS Disclosure; Page 10; 63pp; English.

XX  
CC This sequence represents a PCR primer for the DNA encoding the Fanconi  
CC anaemia of complementation group A (FA-A) protein of the invention. The  
CC amplified DNA's may be used to complement a genetic defect in a cell  
CC (especially the FA-A gene). The products can be used for screening  
CC (especially prenatal FA-A), detection of FA-A carriers and FA-A disease  
CC diagnosis.

XX  
SQ Sequence 59 BP; 18 A; 16 C; 12 G; 13 T; 0 other;

Query Match 68.0%; Score 13.6; DB 19; Length 59;  
Best Local Similarity 80.0%; Pred. No. 4.4e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GACCCCGAGGCGACTCATGG 20  
11111111111111111111  
DB 27 GACCCCGAGGCGACTCATGG 46

## RESULT 14

```

ABN39793/c
ID ABN39793 standard; DNA: 60 BP.
XX
XX AC * ABN39793;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:12541.
XX
XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200210449-A2.
XX
XX PD 07-FEB-2002.
XX
XX PF 20-JUL-2001; 2001WO-IB01903.
XX
XX PR 28-JUL-2000; 2000US-221607P.
XX PR 02-MAY-2001; 2001US-287724P.
XX
XX PA (COMP-) COMPUGEN INC.
XX
XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX DR WPI; 2002-257383/30.
XX
XX PT New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes
XX
XX PS Example 1; SEQ ID 12541; 47pp; English.
XX
XX CC The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcriptome units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under a specific pathological
XX condition; to detect developmental specific genes; and to detect RNA
XX transcripts and splice variants of a transcriptome of a patient suffering
XX from a particular disorder. ABN27253 to ABN9589 represent
XX oligonucleotide sequences from rats, humans and mice, which are used in
XX the exemplification of the present invention.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX CC
XX
XX SQ Sequence 60 BP; 14 A; 14 C; 18 G; 14 T; 0 other;
XX
XX Query Match 68.0%; Score 13.6; DB 24; Length 60;
XX Best Local Similarity 80.0%; Pred. No. 4.4e-03;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0
XX
XX 1 GACCCCAAGGACATCATG 20
XX ||| ||||| || ||
XX Db 29 GACCTCCAGGCGATACAGG 10
XX
XX RESULT 15

```

```

ID AAF75272 standard; DNA: 61 BP.
AC AAF75272:
AC AAF75272:
DT 09-MAY-2001 (first entry)
DE Human PPARgamma PCR primer #1.
KW Human: peroxisome proliferator-activator receptor delta; PPARdelta;
KW RXR; cytosolic; nontropic; neuroprotective; anti-HIV; cardiant;
KW cerebroprotective; vasotropic; antitumor; immunosuppressive;
KW nephrotropic; antibacterial; antiviral; antifungal; protozoocidal;
KW non-steroidal anti-inflammatory disease; NSAID; infection;
KW Alzheimer's disease; AIDS; muscle wasting disease; autoimmune disease;
KW PCR primer; ss.
XX
XX Homo sapiens.
XX
XX MO200112858-A1.
XX
XX 22-FEB-2001.
XX
XX 16-AUG-2000; 2000MO-US22411.
XX
XX 16-AUG-1999; 99US-0148701.
XX
XX 15-AUG-2000; 2000US-0148701.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX He T, Kinzler KW, Vogelstein B:
XX
XX WPI: 2001-211236/21.
XX
XX Novel subgenomic polynucleotide having peroxisome
XX proliferator-activator receptor proliferator (PPAR-delta) and RXR
XX binding elements used to identify downregulators of PPAR-delta
XX transcriptional activity -
XX
XX Example 1: Page 21; 70pp; English.
XX
XX The present sequence is given in a specification relating to an
XX isolated subgenomic polynucleotide comprising a peroxisome
XX proliferator-activator receptor (PPAR)delta binding element and an RXR
XX binding element. The polynucleotide is useful for identifying potential
XX therapeutic agents for cancer treatment and for ameliorating negative
XX side effects of non-steroidal anti-inflammatory diseases (NSAIDs). Test
XX compounds which increase transcription of PPARdelta protein, PPARdelta
XX protein binding to a PPARdelta binding element, or expression of a
XX reporter gene which is under the control of a PPARdelta binding element,
XX are identified. These are candidates for use in encouraging cell
XX proliferation or preventing cell apoptosis in a disease state such as
XX Alzheimer's disease, AIDS, muscular dystrophy, amyotrophic lateral
XX sclerosis, or other muscle wasting diseases, autoimmune diseases, heart
XX attack, stroke, ischaemic heart disease, kidney failure, septic shock,
XX or a disease in which the cell is infected with a pathogen, such as a
XX virus, bacterium, fungus, mycoplasma, or protozoan, to promote healing
XX of the stomach or intestines, or to ameliorate negative side effects of
XX NSAIDs, such as gastric and intestinal ulceration.
XX
XX Sequence 61 BP; 20 A; 16 C; 14 G; 11 T; 0 other;
XX
XX Query Match 68.0%; Score 13.6; DB 22; Length 61;
XX Best Local Similarity 80.0%; Pred. No.4.4e+03;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
XX
XX 1 GACCCGAGGCGACATCATG 20
XX ||||| ||||| |||||
XX Db 28 GACCACCATGGCACCATGG 47

```





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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/067,615  
APPLICATION NUMBER: 08/596,387  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/596,387  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/382,454  
FILING DATE: 01-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/283,302  
FILING DATE: 29-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Pearson, Louise S.  
REGISTRATION NUMBER: 32,369  
REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 267-5300  
TELEFAX: (708) 267-5376  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
US-09-067-615-39

Query Match 63.0%; Score 12.6; DB 4; Length 40;  
Best Local Similarity 78.9%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACATCATG 19  
||| ||||| |||  
DB 38 GACACCCAGGCGCTTATG 20

RESULT 15  
PCT-US95-09816A-39/c  
Sequence 39, Application PC/TUS9509816A  
GENERAL INFORMATION:  
APPLICANT: Mong, Hung C.  
APPLICANT: Rhode, Peter R.  
APPLICANT: Widanz, Jon A.  
APPLICANT: Grammer, Susan  
APPLICANT: Edwards, Ana C.  
APPLICANT: Chavallaz, Pierre-Andre  
APPLICANT: Jiao, Jin-An  
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
NUMBER OF SEQUENCES: 123  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dade International, Inc.  
STREET: 1717 Deerfield Road  
CITY: Deerfield  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60015  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/09816A  
FILING DATE: 31-JUL-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/382,454  
FILING DATE: 01-FEB-1995  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/283,302  
FILING DATE: 29-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Pearson, Louise S.  
REGISTRATION NUMBER: 32,369  
REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 267-5300  
TELEFAX: (708) 267-5376  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
PCT-US95-09816A-39

Query Match 63.0%; Score 12.6; DB 5; Length 40;  
Best Local Similarity 78.9%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACATCATG 19  
||| ||||| |||  
DB 38 GACACCCAGGCGCTTATG 20

Search completed: November 23, 2002, 06:36:13  
Job time : 23.55 secs

Query Match 63.0%; Score 12.6; DB 4; Length 29;  
Best Local Similarity 78.9%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GACCCCGAGGCGACTCATG 19  
||| ||||| |||  
Db 29 GACACCGAGGCGCTTATG 11

## RESULT 12

US-08-670-175-7  
; Sequence 7, Application US/08670175  
; Patent No. 5854081  
; GENERAL INFORMATION:  
; APPLICANT: LINDEN, JOEL  
; APPLICANT: TAYLOR, HEIDI  
; APPLICANT: ROBEVA, ANNA  
; APPLICANT: WOODARD, ROBIN  
; APPLICANT: JIN, XIOMEI  
; TITLE OF INVENTION: STABLE EXPRESSION OF HUMAN ADENOSINE  
; TITLE OF INVENTION: RECEPTORS, AND ASSAYS EMPLOYING THE SAME  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/670,175  
; FILING DATE: 20-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 494-176-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "SYNTHETIC DNA PRIMER"  
US-08-670-175-7

Query Match 63.0%; Score 12.6; DB 2; Length 30;  
Best Local Similarity 78.9%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GACCCCGAGGCGACTCATG 19  
||| ||||| |||||  
Db 5 GATCCTGAGGACACTCTG 23

## RESULT 13

US-08-596-387B-39/C  
; Sequence 39, Application US/08596387B  
; Patent No. 5869270  
; GENERAL INFORMATION:  
; APPLICANT: Rhode, Peter R.  
; APPLICANT: Jiao, Jin-An

APPLICANT: Burkhardt, Martin  
APPLICANT: Wong, Hing  
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dade International, Inc.  
STREET: 1717 Deerfield Road  
CITY: Deerfield  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60015

## RESULT 14

US-09-067-615-39/C  
; Sequence 39, Application US/09067615  
; Patent No. 6309645  
; GENERAL INFORMATION:  
; APPLICANT: Rhode, Peter R.  
; APPLICANT: Jiao, Jin-An  
; APPLICANT: Burkhardt, Martin  
; APPLICANT: Wong, Hing  
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dade International, Inc.  
; STREET: 1717 Deerfield Road  
; CITY: Deerfield  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60015  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

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LOCATION: 1.69
US-08-352-179-10
Query Match
Best Local Similarity 64.0%; Score 12.8; DB 1: Length 69;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5 CCCAGGCGACTGATG 20
    ||||| |||||
Db 62 CCCAGGCGCTCATG 47

RESULT 9
US-08-617-874-4/C
; Sequence 4, Application US/08617874
; Patent No. 6338850
; GENERAL INFORMATION:
; APPLICANT: Jevnikar, Anthony M.
; APPLICANT: Ma, Shengwu
; APPLICANT: Stiller, Calvin R.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: George Mason Building, 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,874
; FILING DATE: 21-MAY-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 024916-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA - primer"
US-08-617-874-4
Query Match
Best Local Similarity 63.0%; Score 12.6; DB 4: Length 28;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GACCCCGAGGCGACTGATG 19
    ||| ||||| |||
Db 27 GACACCCAGGCGCTTATG 9

RESULT 10
US-08-617-874-6/C
; Sequence 6, Application US/08617874
; Patent No. 6338850
; GENERAL INFORMATION:
; APPLICANT: Jevnikar, Anthony M.
; APPLICANT: Ma, Shengwu
; APPLICANT: Stiller, Calvin R.
```

```
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: George Mason Building, 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,874
; FILING DATE: 21-MAY-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 024916-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA - primer"
US-08-617-874-6
Query Match
Best Local Similarity 63.0%; Score 12.6; DB 4: Length 28;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GACCCCGAGGCGACTGATG 19
    ||| ||||| |||
Db 27 GACACCCAGGCGCTTATG 9

RESULT 11
US-09-194-285-4/C
; Sequence 4, Application US/09194285
; Patent No. 6355479
; GENERAL INFORMATION:
; APPLICANT: Webb, Susan R.
; APPLICANT: Wingvist, Ola
; APPLICANT: Karlsson, Lars
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: MHC Class II Antigen Presenting Systems
; FILE REFERENCE: TSRI 536.1
; CURRENT APPLICATION NUMBER: US/09/194,285
; CURRENT FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: PCT/US97/08697
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: US 60/018,175
; PRIOR FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized
US-09-194-285-4
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OY 3 CCCCCAGGCACTCATGG 20  
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Db 35 CCCCCGAGGCTCAUGG 52

## RESULT 6

US-09-071-433-64  
; Sequence 64, Application US/09071433A  
; Patent No. 6197584  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Cowsett, Lex M  
; TITLE OF INVENTION: Antisense Modulation of CD40 Expression  
; FILE REFERENCE: RTS-0002  
; CURRENT APPLICATION NUMBER: US/09/071,433A  
; CURRENT FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-071-433-64

Query Match 64.0%; Score 12.8; DB 4; Length 18;  
Best Local Similarity 87.5%; Pred. No. 1.5e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACCCCAGGCACTCA 17  
||| ||||| |||||  
Db 2 ACCACGAGGCTCTCA 17

## RESULT 7

US-07-728-220C-14/C  
; Sequence 14, Application US/07728220C  
; Patent No. 6020168  
; GENERAL INFORMATION:  
; APPLICANT: MATSUO, HISAYUKI  
; APPLICANT: KANGAWA, KENJI  
; APPLICANT: TANAKA, SHOJI  
; APPLICANT: FUCHIMURA, KAYOKO  
; APPLICANT: TAMARAGI, YASUNORI  
; TITLE OF INVENTION: PORCINE CNP GENE AND PRECURSOR PROTEIN  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: ELEVENTH FLOOR, 1615 L STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036-5601

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/728,220C  
; FILING DATE: 19910712  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SCOTT, WATSON T.  
; REGISTRATION NUMBER: 26,581  
; REFERENCE/DOCKET NUMBER: WTS/9437/91816  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)861-3000  
; TELEFAX: (202)822-0944  
; TELEX: 671 4627 CUSH  
; INFORMATION FOR SEQ ID NO: 14:

## SEQUENCE CHARACTERISTICS:

LENGTH: 66 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-07-728-220C-14

Query Match 64.0%; Score 12.8; DB 3; Length 66;  
Best Local Similarity 87.5%; Pred. No. 1.5e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 CCGAGGCACTCATGG 20  
||||| ||||| |||||  
Db 62 CCGAGGCGCTCATGG 47

## RESULT 8

US-08-352-179-10/C  
; Sequence 10, Application US/08352179  
; Patent No. 5670340  
; GENERAL INFORMATION:  
; APPLICANT: YABUTA, Masayuki  
; APPLICANT: SUZUKI, Yuji  
; APPLICANT: OHSUYE, Kazuhiro  
; APPLICANT: OSHIMA, Takehiro  
; APPLICANT: ONAI, Seiko  
; APPLICANT: MAGOTA, Koji  
; APPLICANT: TANAKA, Shoji  
; TITLE OF INVENTION: PROCESS FOR PRODUCING PEPTIDE  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker and Mathis  
; STREET: The George Mason Bldg., Washington & Prince  
; STREET: Sts.  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/352,179  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/929,597  
; FILING DATE: 17-AUG-1992  
; APPLICATION NUMBER: JP 3-320769  
; FILING DATE: 19-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-223520  
; FILING DATE: 31-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crane-Feury, Sharon E  
; REGISTRATION NUMBER: 36,113  
; REFERENCE/DOCKET NUMBER: 001560-175  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: plasmid pUCNP1  
; FEATURE:  
; NAME/KEY: CDS

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RESULT 2
US-09-005-165-8/c
; Sequence 8, Application US/09005165
; Patent No. 6093542
; GENERAL INFORMATION:
; APPLICANT: ROMANO, JOSEPH
; APPLICANT: SHURLIFF, ROXANNE
; APPLICANT: PAL, RANAJIT
; TITLE OF INVENTION: ISOTHERMAL TRANSCRIPTION BASED
; TITLE OF INVENTION: AMPLIFICATION ASSAY FOR THE DETECTION AND QUANTITATION OF
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE RNA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AKZO NOBEL PATENT DEPARTMENT
; STREET: 1300 PICCARD DRIVE, SUITE 206
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,165
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KLESNER, SHARON N.
; REGISTRATION NUMBER: 36,335
; REFERENCE/DOCKET NUMBER: MDC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-948-7400
; TELEFAX: 301-948-9751
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-005-165-8

Query Match          66.0%; Score 13.2; DB 3; Length 24;
Best Local Similarity 83.3%; Pred. No. 9.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      3 CCCCCAGGCATCATGG 20
Db      23 CACCCAGGCATCTGCG 6

RESULT 3
US-09-060-756-146
; Sequence 146, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 146
; LENGTH: 75
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-060-756-146

Query Match          66.0%; Score 13.2; DB 4; Length 75;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 ACCCCAGGCATCATG 19
Db      30 ACCCCAGGCATCATG 47

RESULT 4
US-09-282-996-9/c
; Sequence 9, Application US/09282996
; Patent No. 6143502
; GENERAL INFORMATION:
; APPLICANT: Grentzmann, Guido
; APPLICANT: Gesteland, Raymond F.
; APPLICANT: Atkins, John F.
; TITLE OF INVENTION: Dual-Luciferase Reporter System
; FILE REFERENCE: T5864.NP
; CURRENT APPLICATION NUMBER: US/09/282,996
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: WordPerfect 8.0
; SEQ ID NO 9
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide luc12
US-09-282-996-9

Query Match          66.0%; Score 13.2; DB 3; Length 80;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      3 CCCCCAGGCATCATGG 20
Db      50 CCCCCGGGAGCATCATGG 33

RESULT 5
US-09-282-996-8
; Sequence 8, Application US/09282996
; Patent No. 6143502
; GENERAL INFORMATION:
; APPLICANT: Grentzmann, Guido
; APPLICANT: Gesteland, Raymond F.
; APPLICANT: Atkins, John F.
; TITLE OF INVENTION: Dual-Luciferase Reporter System
; FILE REFERENCE: T5864.NP
; CURRENT APPLICATION NUMBER: US/09/282,996
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: WordPerfect 8.0
; SEQ ID NO 8
; LENGTH: 82
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide luc11
US-09-282-996-8

Query Match          66.0%; Score 13.2; DB 3; Length 82;
Best Local Similarity 77.8%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:53:51 : Search time 21.55 Seconds  
(without alignments)  
284.619 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20

Sequence: 1 gaccccccagggcactatg 20

Scoring table: IDENTITY\_NUC

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

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Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	13.6	68.0	59	2	US-08-726-012B-5
2	13.2	66.0	24	3	US-09-005-165-8
3	13.2	66.0	75	4	US-09-060-756-146
4	13.2	66.0	80	3	US-09-282-996-9
5	13.2	66.0	82	3	US-09-282-996-8
6	12.8	64.0	16	4	US-09-071-433-64
7	12.8	64.0	66	3	US-07-728-220C-14
8	12.8	64.0	69	1	US-08-352-179-10
9	12.6	63.0	28	4	US-08-617-874-4
10	12.6	63.0	28	4	US-08-617-874-6
11	12.6	63.0	29	4	US-09-194-285-4
12	12.6	63.0	30	2	US-08-670-175-7
13	12.6	63.0	40	2	US-08-596-387B-39
14	12.6	63.0	40	4	US-09-067-615-39
15	12.6	63.0	40	5	PCT-US95-09816A-39
16	12.6	63.0	45	2	US-08-596-387B-104
17	12.6	63.0	45	4	US-09-067-615-104
18	12.6	63.0	45	5	PCT-US95-09816A-104
19	12.4	62.0	18	1	US-08-164-200-14
20	12.4	62.0	24	2	US-08-288-508C-10
21	12.4	62.0	24	3	US-08-289-222E-20
22	12.4	62.0	24	4	US-09-054-526B-20
23	12.4	62.0	33	4	US-09-110-517-28
24	12.4	62.0	37	4	US-09-263-904-7
25	12.4	62.0	38	2	US-08-292-620A-2308
26	12.4	62.0	38	3	US-09-071-845-2308
27	12.2	61.0	22	5	PCT-US95-14418-38

c	28	12.2	61.0	22	5	PCT-US95-15327-38	Sequence 38, Appl
	29	12.2	61.0	23	5	PCT-US95-14418-39	Sequence 39, Appl
	30	12.2	61.0	23	5	PCT-US95-15327-39	Sequence 39, Appl
c	31	12.2	61.0	24	1	US-07-961-268-1	Sequence 1, Appl
	32	12.2	61.0	30	2	US-08-816-605-5	Sequence 5, Appl
	33	12.2	61.0	31	3	US-08-946-914-55	Sequence 55, Appl
	34	12.2	61.0	31	4	US-08-946-914-55	Sequence 55, Appl
	35	12.2	61.0	32	3	US-08-946-914-57	Sequence 57, Appl
	36	12.2	61.0	32	4	US-09-656-450-57	Sequence 57, Appl
	37	12.2	61.0	33	4	US-09-527-236A-13	Sequence 13, Appl
	38	12.2	61.0	45	2	US-08-687-335A-14	Sequence 14, Appl
	39	12.2	61.0	45	4	US-09-407-367-14	Sequence 14, Appl
c	40	12.2	61.0	56	1	US-08-151-574-28	Sequence 28, Appl
c	41	12.2	61.0	56	2	US-08-419-448-28	Sequence 28, Appl
c	42	12.2	61.0	56	4	US-09-233-510-28	Sequence 28, Appl
c	43	12.2	61.0	60	1	US-08-470-958-14	Sequence 14, Appl
c	44	12.2	61.0	80	1	US-08-471-985A-101	Sequence 101, App
c	45	12.2	61.0	80	5	PCT-US95-12401A-101	Sequence 101, App

#### ALIGNMENTS

```
RESULT 1
US-08-726-012B-5
: Sequence 5, Application US/08726012B
: Patent No. 5952190
: GENERAL INFORMATION:
: APPLICANT: Hans Joenje, et al.
: TITLE OF INVENTION: CNA FOR FANCONI ANEMIA COMPLEMENTATION GROUP A
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESS: Kiarquist Sparkman Campbell Leigh & Whinston, LLP
: STREET: One World Trade Center, Suite 1600, 121 S.W. Salmon Street
: CITY: Portland
: STATE: OR
: COUNTRY: USA
: ZIP: 97204-2988
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Disk, 3.5-inch
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: MS DOS
: SOFTWARE: WordPerfect 5.1+, ASCII
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/726,012B
: FILING DATE: 10/04/96
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING AGENT:
: ATTORNEY/AGENT INFORMATION:
: NAME: Richard J. Polley
: REGISTRATION NUMBER: 28,107
: REFERENCE/DOCKET NUMBER: 3812-45520/RJP/DJE
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (503) 226-7391
: TELEFAX: (503) 228-9446
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 59
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-726-012B-5

Query Match 68.0%, Score 13.6, DB 2, Length 59;
Best Local Similarity 80.0%, Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Oy 1 GACCCCAAGGCATCATGG 20
Db 27 GACCAACATGCATCATGG 46
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:54:41 : Search time 17.25 Seconds  
(without alignments)  
439.108 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20  
Sequence: 1 gaccccgagcactcatg 20

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 195614

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:\*

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4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
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7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
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11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.4	72.0	39	10	US-09-879-919-16
2	13.4	67.0	78	10	US-09-938-700-25
3	13.2	66.0	92	10	US-09-923-876-3869
4	12.8	64.0	18	10	US-09-067-638B-64
5	12.8	64.0	25	10	US-09-305-856B-93
6	12.8	64.0	88	10	US-09-864-761-21663
7	12.8	64.0	94	10	US-09-864-761-21406
8	12.6	63.0	28	12	US-10-005-073-4
9	12.6	63.0	28	12	US-10-005-073-6
10	12.6	63.0	37	12	US-10-081-281-10
11	12.6	63.0	40	10	US-09-848-164-39
12	12.6	63.0	45	10	US-09-848-164-104
13	12.6	63.0	79	10	US-09-864-761-24792
14	12.6	63.0	82	10	US-09-783-590-5203
15	12.6	63.0	92	10	US-09-864-761-23498
16	12.4	62.0	37	10	US-09-264-468B-16
17	12.4	62.0	52	10	US-09-879-919-15
18	12.2	61.0	30	10	US-09-739-394-5
19	12.2	61.0	30	12	US-10-097-330-5

20	12.2	61.0	31	10	US-09-263-689-55	Sequence 55, Appl
21	12.2	61.0	32	10	US-09-263-689-57	Sequence 57, Appl
22	12.2	61.0	33	9	US-09-756-854-13	Sequence 13, Appl
23	12.2	61.0	33	9	US-10-041-574-13	Sequence 1, Appl
24	12.2	61.0	67	10	US-09-050-516-1	Sequence 62, Appl
25	12.2	61.0	72	10	US-09-918-063-62	Sequence 64, Appl
26	12.2	61.0	72	10	US-09-918-063-64	Sequence 60, Appl
27	12.2	61.0	80	9	US-09-736-457-660	Sequence 5100, Ap
28	12.2	61.0	91	10	US-09-983-965-5100	Sequence 7186, Ap
29	12.2	61.0	95	10	US-09-783-590-7186	Sequence 32598, A
30	12.2	61.0	96	10	US-09-864-761-32598	Sequence 149, App
31	12.2	61.0	100	9	US-09-728-444-149	Sequence 22, Appl
32	12.2	60.0	27	10	US-09-799-160-5	Sequence 4, Appl
33	12.2	60.0	27	10	US-09-799-160-22	Sequence 24, Appl
34	12.2	60.0	30	10	US-09-799-160-4	Sequence 1599, Ap
35	12.2	60.0	30	10	US-09-799-160-24	Sequence 32, Appl
36	12.2	60.0	31	10	US-09-801-274-1599	Sequence 255, App
37	12.2	60.0	31	10	US-09-799-160-18	Sequence 256, App
38	12.2	60.0	39	10	US-09-473-872-32	Sequence 257, App
39	12.2	60.0	47	10	US-09-179-536B-255	Sequence 258, App
40	12.2	60.0	48	10	US-09-179-536B-256	Sequence 259, App
41	12.2	60.0	49	10	US-09-179-536B-257	Sequence 260, App
42	12.2	60.0	50	10	US-09-179-536B-258	Sequence 21, Appl
43	12.2	60.0	51	10	US-09-179-536B-259	
44	12.2	60.0	52	10	US-09-179-536B-260	
45	12.2	60.0	54	9	US-09-858-332-21	

#### ALIGNMENTS

RESULT 1  
US-09-879-919-16/c  
; Sequence 16, Application US/09879919  
; Patent No. US20020064829A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang, et al.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon  
; FILE REFERENCE: PFT35PI  
; CURRENT APPLICATION NUMBER: US/09/879, 919  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 60/293, 499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277, 978  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/276, 248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/254, 875  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: 60/241, 952  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/211, 537  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 08/815, 783  
; PRIOR FILING DATE: 1997-03-12  
; PRIOR APPLICATION NUMBER: 60/016, 812  
; PRIOR FILING DATE: 1996-03-14  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-879-919-16

Query Match 72.0% Score 14.4: DB 10: Length 39;  
Best Local Similarity 93.8% Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 CCCAGGCGACTCATG 20  
DB 32 CCCAGGCGACTCATG 17

```
RESULT 2
US-09-938-700-25
; Sequence 25, Application US/09938700
; Patent No. US20020064525A1
; GENERAL INFORMATION:
; APPLICANT: Morsey, et al.
; TITLE OF INVENTION: Anti-IgE Vaccines
; FILE REFERENCE: PCI0761A
; CURRENT APPLICATION NUMBER: US/09/938,700
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 78
; TYPE: DNA
; ORGANISM: DOG CH3/CH4 NUCLEOTIDE SEQUENCE
US-09-938-700-25

Query Match      67.0%; Score 13.4; DB 10; Length 78;
Best Local Similarity 93.3%; Pred. No. 8,1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCCAGGGCAGCTCATG 19
DB      25 CCCAGGGCAGCTCATG 39

RESULT 3
US-09-923-876-3869/C
; Sequence 3869, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 3869
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700453962H1
; NAME/KEY: unsure
; LOCATION: 13, 20, 72
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-3869

Query Match      66.0%; Score 13.2; DB 10; Length 92;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 CCCCGAGGCGACTCATGG 20
DB      71 CCCGAAAGCGACTCATGG 54

RESULT 4
US-09-067-638B-64
; Sequence 64, Application US/09067638B
; Patent No. US20020028923A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
```

```
APPLICANT: Brenda F. Baker
APPLICANT: John McNeil
APPLICANT: Susan M. Freier
APPLICANT: Henri M. Sasnor
APPLICANT: Douglas G. Brooks
APPLICANT: Cara Ohashi
APPLICANT: Jacqueline R. Wyatt
APPLICANT: Alexander Borchers
APPLICANT: Timothy A. Vickers
TITLE OF INVENTION: Identification of Genetic
TITLE OF INVENTION: Targets for Modulation of Oligonucleotides and
TITLE OF INVENTION: Generation of Oligonucleotides for Gene
MODULATION
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESS: WOODCOCK WASHBURN KURTZ
ADDRESSEE: MACKIEWICZ & NORRIS LLP
STREET: 1 LIBERTY PLACE 46TH FLOOR
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: IBM
OPERATING SYSTEM: PC-Windows NT
SOFTWARE: WORD PERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,638B
FILING DATE: 28-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/081,483
FILING DATE: 13-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: ISIS-2960
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-067-638B-64

Query Match      64.0%; Score 12.8; DB 10; Length 18;
Best Local Similarity 87.5%; Pred. No. 1,4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 ACCCGGAGGCGACTCA 17
DB      2 ACCGACGAGGCGCTCA 17

RESULT 5
US-09-305-856B-93
; Sequence 93, Application US/09305856B
; Patent No. US20020061518A1
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; TITLE OF INVENTION: Genotyping the Human
; FILE REFERENCE: 4389-7 (formerly SEQ-17C1P)
; CURRENT APPLICATION NUMBER: US/09/305,856B
; CURRENT FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 60/084,807
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 124
```

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 93  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-305-856B-93

Query Match 64.0%; Score 12.8; DB 10; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.5e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCCAGGCGCATCATG 19  
|||||  
Db 3 CCCAGGCGCATCATG 18

RESULT 6  
US-09-864-761-21663/C  
Sequence 21663, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 21663  
LENGTH: 88  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:

OTHER INFORMATION: MAP TO AF152364.1  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.99  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4  
OTHER INFORMATION: NT HIT: 919506504, EVALUATE 7.20e-01  
OTHER INFORMATION: EST\_HUMAN HIT: BE970003.1, EVALUATE 4.20e+00  
US-09-864-761-21663

Query Match 64.0%; Score 12.8; DB 10; Length 88;  
Best Local Similarity 87.5%; Pred. No. 1.6e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 CCCAGGCGCATCATG 20  
|||||  
Db 52 CCCAGGCGCATCATG 37

RESULT 7  
US-09-864-761-21406  
Sequence 21406, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 21406  
LENGTH: 94  
TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:  
OTHER INFORMATION: MAP TO D87009.1  
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.98  
OTHER INFORMATION: SWISSPROT HIT: P04211, EVALUE 1.00e-07  
OTHER INFORMATION: EST HUMAN HIT: AW407157.1, EVALUE 2.00e-24  
OTHER INFORMATION: NT HIT: Z73660.1, EVALUE 3.00e-46  
US-09-864-761-21406

Query Match 64.0%; Score 12.8; DB 10; Length 94;  
Best Local Similarity 87.5%; Pred. No. 1.6e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCCCAGGACATCAT 18  
||||| |||||  
Db 62 CCCCCAGGACATCAT 77

RESULT 8  
US-10-005-073-4/c  
Sequence 4, Application US/10005073  
Patent No. US20020090371A1  
GENERAL INFORMATION:  
APPLICANT: Jevnikar, Anthony M.  
Ma, Shengwu  
Stillier, Calvin R.  
TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING  
IMMUNE RESPONSES IN MAMMALS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.  
STREET: George Mason Building, 699 Prince Street  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/005,073  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/617,874  
FILING DATE: 21-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Rea, Teresa Stanek  
REGISTRATION NUMBER: 30,427  
REFERENCE/DOCKET NUMBER: 024916-002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA - primer"  
US-10-005-073-4  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
Query Match 63.0%; Score 12.6; DB 12; Length 28;

Best Local Similarity 78.9%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCAGGACATCATG 19  
||| ||||| |||  
Db 27 GACCCAGGACATCATG 9

RESULT 9  
US-10-005-073-6/c  
Sequence 6, Application US/10005073  
Patent No. US20020090371A1  
GENERAL INFORMATION:  
APPLICANT: Jevnikar, Anthony M.  
Ma, Shengwu  
Stillier, Calvin R.  
TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING  
IMMUNE RESPONSES IN MAMMALS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.  
STREET: George Mason Building, 699 Prince Street  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/005,073  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/617,874  
FILING DATE: 21-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Rea, Teresa Stanek  
REGISTRATION NUMBER: 30,427  
REFERENCE/DOCKET NUMBER: 024916-002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA - primer"  
US-10-005-073-6

Query Match 63.0%; Score 12.6; DB 12; Length 28;  
Best Local Similarity 78.9%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCAGGACATCATG 19  
||| ||||| |||  
Db 27 GACCCAGGACATCATG 9

RESULT 10  
US-10-081-281-10/c  
Sequence 10, Application US/10081281  
Patent No. US20020151707A1  
GENERAL INFORMATION:  
APPLICANT: Kindsvogel, Wayne  
Gross, Jane A.  
Sheppard, Paul

TITLE OF INVENTION: Immune Mediators and Related Methods  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/081,281  
FILING DATE: 20-Feb-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/261,811A  
FILING DATE: 03-Mar-1999  
APPLICATION NUMBER: US 08/480,002  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/482,133  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/483,241  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 60/005,964  
FILING DATE: 27-OCT-1995  
APPLICATION NUMBER: US 08/657,581  
FILING DATE: 07-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Parent, Annette S.  
REGISTRATION NUMBER: 42,058  
REFERENCE/DOCKET NUMBER: 014058-005630US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-081-281-10  
Query Match 63.0%; Score 12.6; DB 12; Length 37;  
Best Local Similarity 78.9%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCGCTTATG 19  
||| ||||| |||  
Db 32 GACACCGAGGCGCTTATG 14

RESULT 11  
US-09-848-164-39/c  
Sequence 39, Application US/09848164  
Patent No. US20020034513A1  
GENERAL INFORMATION:  
APPLICANT: Rhode, Peter R.  
Jiao, Jin-An  
Burkhardt, Martin  
Wong, Hing  
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dade International, Inc.  
STREET: 1717 Deerfield Road  
CITY: Deerfield  
STATE: Illinois

COUNTRY: USA  
ZIP: 60015  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/848,164  
FILING DATE: 03-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/067,615  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/382,454  
FILING DATE: 01-FEB-1995  
APPLICATION NUMBER: US 08/283,302  
FILING DATE: 29-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Pearson, Louise S.  
REGISTRATION NUMBER: 32,369  
REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 267-5300  
TELEFAX: (708) 267-5376  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-848-164-39  
Query Match 63.0%; Score 12.6; DB 10; Length 40;  
Best Local Similarity 78.9%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCGCTTATG 19  
||| ||||| |||  
Db 38 GACACCGAGGCGCTTATG 20

RESULT 12  
US-09-848-164-104  
Sequence 104, Application US/09848164  
Patent No. US20020034513A1  
GENERAL INFORMATION:  
APPLICANT: Rhode, Peter R.  
Jiao, Jin-An  
Burkhardt, Martin  
Wong, Hing  
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dade International, Inc.  
STREET: 1717 Deerfield Road  
CITY: Deerfield  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60015  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/848,164  
FILING DATE: 03-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/067,615  
FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/382,454  
FILING DATE: 01-FEB-1995  
APPLICATION NUMBER: US 08/283,302  
FILING DATE: 29-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Pearson, Louise S.  
REGISTRATION NUMBER: 32,369  
REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 267-5300  
TELEFAX: (708) 267-5376  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 104:  
US-09-848-164-104  
Query Match 63.0%; Score 12.6; DB 10; Length 45;  
Best Local Similarity 78.9%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GACCCCGAGGCGCTCATG 19  
||| ||||| |||  
Db 20 GACACCCAGGCGCTTATG 38  
RESULT 13  
US-09-864-761-24792  
Sequence 24792, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecmca-x-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 24792  
LENGTH: 79  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC011483.2  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.1  
OTHER INFORMATION: SWISSPROT HIT: P48046, EVALU 9.60e+00  
OTHER INFORMATION: NT HIT: U37672.1, EVALU 3.00e-12  
US-09-864-761-24792  
Query Match 63.0%; Score 12.6; DB 10; Length 79;  
Best Local Similarity 78.9%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GACCCCGAGGCGCTCATG 19  
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Db 53 GACTACCGAGGCGCTCATG 71  
RESULT 14  
US-09-783-590-5203/C  
Sequence 5203, Application US/09783590  
Patent No. US20020110850A1  
GENERAL INFORMATION:  
APPLICANT: Dillon, Patrick J.  
APPLICANT: Haseltine, William A.  
APPLICANT: Li, Haodong  
APPLICANT: Rosen, Craig A.  
APPLICANT: Ruben, Steven M.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
FILE REFERENCE: PO-16,261  
CURRENT APPLICATION NUMBER: US/09/783,590  
CURRENT FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 08/420,856  
PRIOR FILING DATE: 1995-04-12  
PRIOR APPLICATION NUMBER: 08/346,731  
PRIOR FILING DATE: 1994-11-21  
NUMBER OF SEQ ID NOS: 12485  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5203  
LENGTH: 82  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (45)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-783-590-5203  
Query Match 63.0%; Score 12.6; DB 10; Length 82;  
Best Local Similarity 78.9%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GACCCCGAGGCGCTCATG 19  
||| ||||| |||||  
Db 21 GGCTCCAGGCGCTCATG 3

## RESULT 15

US-09-864-761-23498/C

Sequence 23498, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aecmlca-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

SEQ ID NO 23498

LENGTH: 92

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AL139352.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EST HUMAN HIT: BE697302.1, EVALUATE 1.80e-02

OTHER INFORMATION: EST HUMAN HIT: P36130, EVALUATE 9.50e+00

OTHER INFORMATION: NT HIT: AF193612.1, EVALUATE 1.20e-02

US-09-864-761-23498

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACCCCGAGGGGACTCATCG 20

Db 62 ACCCCGAGGGGAGCCCTGG 44

Search completed: November 23, 2002, 06:42:09  
Job time : 18.25 secsQuery Match 63.0%; Score 12.6; DB 10; Length 92;  
Best Local Similarity 78.9%; Pred. No. 2e+03;

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: November 25, 2002, 09:10:06 : Search time 755.55 Seconds

(without alignments)  
428.707 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20

Sequence: 1 gacccccgggcactcatg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estcov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_tod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	74.0	24	17	A2428700 1M0212L16
2	14.2	71.0	76	9	AL304064
3	13.8	69.0	100	9	AL595750
4	13.6	68.0	50	9	AU105199
5	13.6	68.0	50	9	AU105201
6	13.6	68.0	50	9	AU105204

C 7	13.6	68.0	50	9	AU105205
C 8	13.6	68.0	50	9	AU105206
C 9	13.6	68.0	50	9	AU105207
C 10	13.6	68.0	57	9	AU259073
C 11	13.6	68.0	70	9	A1829164
C 12	13.4	67.0	70	9	AL800251
C 13	13.2	66.0	66	14	BQ248668
C 14	13.2	66.0	92	9	AA525068
C 15	13.2	66.0	97	9	A1756476
C 16	12.8	64.0	52	9	A1310821
C 17	12.8	64.0	52	14	W90057
C 18	12.8	64.0	57	17	B01045
C 19	12.8	64.0	57	17	B06891
C 20	12.8	64.0	58	17	A2767622
C 21	12.8	64.0	78	9	AA558370
C 22	12.6	63.0	35	14	N94609
C 23	12.6	63.0	38	17	BH751579
C 24	12.6	63.0	45	17	BH619149
C 25	12.6	63.0	46	9	A1744340
C 26	12.6	63.0	46	17	BH753339
C 27	12.6	63.0	49	17	BH171096
C 28	12.6	63.0	49	17	BH213409
C 29	12.6	63.0	62	9	AA489456
C 30	12.6	63.0	62	17	A2819711
C 31	12.6	63.0	63	17	BH617146
C 32	12.6	63.0	71	14	F37653
C 33	12.6	63.0	71	17	A2308894
C 34	12.6	63.0	72	17	BH750287
C 35	12.6	63.0	85	9	AA245159
C 36	12.6	63.0	86	9	A1783748
C 37	12.6	63.0	87	17	BH633158
C 38	12.6	63.0	88	17	BH804906
C 39	12.6	63.0	91	9	AA559317
C 40	12.6	63.0	93	9	AA623528
C 41	12.6	63.0	94	10	BE059176
C 42	12.6	63.0	95	17	CNS031GR
C 43	12.6	63.0	98	12	BG793956
C 44	12.6	63.0	98	17	BH750078
C 45	12.6	63.0	100	9	AA779639

## ALIGNMENTS

RESULT 1  
LOCUS A2428700 24 bp DNA  
DEFINITION 1M0212L16f Mouse 10kb plasmid UGCC1M library Mus musculus genomic clone UGCC1M0212L16 F, DNA sequence.  
ACCESSION A2428700  
VERSION A2428700.1 GI:10552713  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE  
AUTHORS Dunn,D., Moyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00



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ORIGIN									
Query Match		69.0%;	Score 13.6;		DB 9;	Length 100;			
Best Local Similarity		88.2%;	Pred. No. 4.2e+04;						
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		11111111111111111111							
Db	41	GCGCCCGCGGGCAGCTCA	57						
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LOCUS		AU105199/c	50	bp	mRNA	linear	EST 30-AUG-2001		
DEFINITION		AU105199 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone							
ACCESSION		HRC00642. mRNA sequence.							
VERSION		AU105199							
KEYWORDS		AU105199.1 GI:13554720							
SOURCE		EST.							
ORGANISM		human.							
REFERENCE		Homo sapiens							
AUTHORS		Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
TITLE		1 (bases 1 to 50)							
JOURNAL		Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata							
MEDLINE		,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki							
COMMENT		,Y., Nakamura,Y., Suyama,A. and Sugano,S.							
		Diverse transcriptional initiation revealed by fine, large-scale							
		mapping of mRNA start sites							
		EMBO Rep. 2 (5), 388-393 (2001)							
		21270072							
		Contact: Yutaka Suzuki							
		Department of Virology							
		Institute of Medical Science, University of Tokyo							
		4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan							
		Email: yusuzuki@ims.u-tokyo.ac.jp							
		Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano							
		,S. Construction and characterization of a full length-enriched and							
		a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).							
FEATURES									
source		Location/Qualifiers							
		1..50							
		/organism="Homo sapiens"							
		/db_xref="taxon:9606"							
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		/clone_lib="Sugano Homo sapiens cDNA library"							
		/note="Differential display comparison of untreated and							
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ORIGIN									
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Best Local Similarity		80.0%;	Pred. No. 4.1e+04;						
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Db	35	GCGCTCGAGCGCTCCATG	16						
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LOCUS		AU105201/c	50	bp	mRNA	linear	EST 30-AUG-2001		
DEFINITION		AU105201 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone							
ACCESSION		HRC04501. mRNA sequence.							
		AU105201							

**VERSION** AU105201.1 GI:13554722  
**KEYWORDS** EST.  
**SOURCE** human.

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**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)

---

**REFERENCE** Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,  
'H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

---

**TITLE** Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp

---

**JOURNAL** Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
MEDLINE S., Construction and characterization of a full length-enriched and  
COMMENT a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/clone\_lib="Sugano Homo sapiens cDNA library"  
/note="Differential display comparison of untreated and  
dimethylflumate treated U937 cells"

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ORIGIN

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OY      1 GACCCCGAGGCCTCATGG 20
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DB       41 GGCTTCAGGCCGTCCCATTG 22

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**RESULT 6** AU105204/c 50 bp mRNA linear EST 30-AUG-2001

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**LOCUS** AU105204 Sugano Homo sapiens cDNA library Homo sapiens CDNA clone  
DEFINITION HRC06024, mRNA sequence.  
ACCESSION AU105204  
VERSION AU105204.1 GI:13554725  
KEYWORDS EST.  
SOURCE human.

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**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)

---

**REFERENCE** Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,  
AUTHORS 'H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
21270072

---

**TITLE** Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp

---

**JOURNAL** Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
MEDLINE S., Construction and characterization of a full length-enriched and  
COMMENT a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"

		/db_xref="taxon:9608"
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		/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"
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Query Match	68.0%;	Score 13.6; DB 9; Length 50;
Best Local Similarity	80.0%;	Pred. No. 4.1e+04;
Matches	16; Conservative	0; Mismatches 4; Indels 0; Gaps 0.
OY	1 GACCCCGAGGCGACTCATGG 20	
	I I I I I I I I I I I I I I I I	
Db	34 GGCTTCGAGGGCTCCCATGG 15	
RESULT 7		
AUI05205/c		50 bp mRNA linear EST 30-AUG-2001
LOCUS		
DEFINITION	AUI05205 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC07843, mRNA sequence.	
ACCESSION	AUI05205	
VERSION	AUI05205.1 GI:13554726	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 50)	
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,T., Hataki,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.	
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites	
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)	
MEDLINE	21270072	
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. 'S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers 1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_1lb="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylfumarate treated U937 cells" 5 a 21 c 16 g 8 t	
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ORIGIN		
Query Match	68.0%;	Score 13.6; DB 9; Length 50;
Best Local Similarity	80.0%;	Pred. No. 4.1e+04;
Matches	16; Conservative	0; Mismatches 4; Indels 0; Gaps 0.
OY	1 GACCCCGAGGCGACTCATGG 20	
	I I I I I I I I I I I I I I I I	
Db	35 GGCTTCGAGGGCTCCCATGG 16	
RESULT 8		
AUI05206/c		50 bp mRNA linear EST 30-AUG-2001
LOCUS		
DEFINITION	AUI05206 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC08436, mRNA sequence.	
ACCESSION	AUI05206	
VERSION	AUI05206.1 GI:13554727	
KEYWORDS	EST.	

SOURCE ORGANISM	human.
REFERENCE AUTHORS	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 50) Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)
TITLE	
JOURNAL MEDLINE COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES source	1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="HRC08436" /clone_lib="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylflumate treated U937 cells" 6 a 18 c 17 g 9 t BASE COUNT ORIGIN
Query Match	68.0%; Score 13.6; DB 9; Length 50;
Best Local Similarity	80.0%; Pred. No. 4.1e+04;
Matches	16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1. GACCCGAGGGCAGCTCATGG 20                               Db 41 GGCTTCGAGGGCTCCCATCG 22
LOCUS	AU105207/c
DEFINITION	AU105207 50 bp mRNA Linear EST 30-AUG-2001
ACCESSION	AU105207 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
VERSION	KAT01893, mRNA sequence.
KEYWORDS	AU105207 AU105207.1 GI:13554728 EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homniidae; Homo. 1 (bases 1 to 50) Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)
REFERENCE AUTHORS	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers 1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="KAT01893"
TITLE	
JOURNAL MEDLINE COMMENT	
FEATURES source	

```

/clone_11b="Sugano Homo sapiens cDNA library"
/notes="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT      5 a      16 g      8 t
ORIGIN          21 c

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Query Match	68.0%	Score 13.6	DB 9	length 50
Best Local Similarity	80.0%	Pred. No. 4	1e+04	
Matches	16	Conservative	0	Mismatches 4
				Indels 0
				Gaps 0

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Oy      1  GACCCCAAGGGCACTCATGG  20
          | | | | | | | | | |
Db      36  GGCCCTCAGGGCTCCCATGG  17

```

RESULT 10  
AU259073

LOCUS	AU255073	57 bp	RNA	linear	EST 25-APR-2002
DEFINITION	AU255073	3'-directed mouse cDNA	library	Mus musculus	cDNA clone
FEATURES	BE00014473	3'			mRNA sequence.
KEYWORDS	BE000003				

VERSION	AU259073.1	GI:20325251
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 57)	Kato, K. and Matsuda, R.	Generation of expressed sequence tags from mouse brain	Unpublished (2002)	
	Contact: Kikuya Kato			

Graduate School of Biological Sciences  
Nara Institute of Science and Technology  
8916-5 Takayama, Ikoma, Nara 630-0101, Japan  
Tel.: 81-743-72-5581  
Fax: 81-743-72-5589  
Email: [kratoebd@ist-nara.ac.jp](mailto:kratoebd@ist-nara.ac.jp),  
[ufu@http://love2.alst-nara.ac.jp/BED/index.html](mailto:ufu@http://love2.alst-nara.ac.jp/BED/index.html)

FEATURES	Location/Qualifiers
source	1. .57

```

/Organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BED0014473"
/clone_1lb="3'-directed mouse cDNA library"
/tissue_type="brain"
/notes="Vector: pGEM-T-easy"
BASE COUNT      23 a      16 c      11 g      7 t
ORIGIN

```

Query Match	68.0%	Score 13.6:	DB 9:	Length 57:
Best Local Similarity	80.0%	Pred. No.	4.3e+04:	
Matches	16:	Conservative	0:	Mismatches 4:
				Indels 0:
				Gaps 0

Oy	1	GACCCCGAGGGCACTCATGG	20
Db	1	GATCCCGAGGACCCACATGG	20

RESULT	11
A1829164	
LOCUS	
DEFINITION	wk76a07.x1 NCI-CCAP_Pan1 Homo sapiens cDNA clone IMAGE:2421300 3'
	70 bp mRNA linear EST 07-MAR-2000
A1829164	

LOCUS  
DEFINITION  
A1829164.1 NC1\_CGAP\_Pan1 70 bp mRNA linear EST 07-MAR-2000  
IMAGE:2421300 3'  
similar to SW:CA12\_MOUSE P28481 PROOLANGIN ALPHA 1(I) CHAIN  
precursor [CONTAINS: CHONROCALIN]. [3] (TF:062031 (TF:06203)  
:contains element MSR1 repetitive element /, mRNA sequence.  
A1829164  
ACCESSION  
VERSION  
KEYWORDS  
A1829164.1 GI:5449835  
EST.

<b>ORGANISM</b>	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
-----------------	---

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 70)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strusberg, Ph.D.  
mailto:robert.strusberg@nih.gov

Email: [cgap@ltnl.llnl.gov](mailto:cgap@ltnl.llnl.gov)  
Life Technologies catalog #: 11548-013  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CGAP clone distribution Information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bdrrp/image/image.html](http://www-bio.llnl.gov/bdrrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 1747 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence step: 1.

FEATURES  
source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone IMAGE:2421300"
/clone_lib="NCI CGAP Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"

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BASE COUNT	11 a	32 c	23 g	4 t
ORIGIN	/note="Organ: pancreas; Vector: pCMV-SPORT6; site_1: SalI Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average Insert size 1.72 kb. Life Technologies catalog #: 11548-Olig"			

Query Match	68.0%	Score 13.6	DB 9	Length 70
Best Local Similarity	80.0%	Pred. No. 4.6e+04		
Matches 16	Conservative 0	Mismatches 4	Indels 0	Gaps 0

QY 1 GACCCCGAGGCACTCATGG 20  
 ||||| ||| | ||| ||  
 Db 27 GACCCCGGGGCCCCAGGG 46

RESULT 12  
AL800251

LOCUS	70 bp	mrna	linear	EST 27-JUN-2002
AL800251				
DEFINITION	AL800251 XGC-neurula silurana tropicalis cdna clone TNeu067119 5',			
DESCRIPTION	mrna sequence.			

VERSION	AL800251.1	GI:21586312
KEYWORDS	EST.	
SOURCE	western clawed frog.	

ORGANISM	REFERENCE
<i>Silurana tropicallis</i>	Taylor, R., Ashurst, J. L., Croning, M. D. R., Zorn, A. M. and Rogers, J.
<i>Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi</i>	
<i>Amphibia; Batrachia; Anura; Mesobatrachia; Pipodae; Pipidae;</i>	
<i>Xenopodinae; Silurana.</i>	
1. (bases 1 to 70)	
	Unpublished (2001)
	Contact: Taylor R

Sanger Centre  
Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: trop@sanger.ac.uk  
Sanger xenopus tropicalis EST Project 2001  
TROPICALIS\_SEQUENCE\_ID: TNE067119.plcsp6  
Sequencing primer: PLCSP6  
This sequence is from a Xenopus Gene Collection (Xc) library  
constructed by Aaron M. Zorn.  
Location/Qualifiers  
1..70

```

/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu067119"
/clone_lib="XGC-neurula"

```

/dev\_stage="neurula"  
/lab\_host="Escherichia coli DH10B"  
/note="Vector: pCS107; Site\_1: EcoRI; Site\_2: NotI; cDNA was oligo dt primed from 5' end of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

BASE COUNT 12 a 29 c 18 g 11 t

ORIGIN

Query Match 67.0%; Score 13.4; DB 9; Length 70;  
Best Local Similarity 93.3%; Pred. No. 5.6e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GACCCCGAGGCATG 15  
|||||  
Db 56 GCCCCCGAGGCACAT 70

RESULT 13  
BQ248668/c 66 bp mRNA linear EST 03-MAY-2002  
LOCUS BQ248668/c  
DEFINITION Tae25005H12F Tae25 Triticum aestivum cDNA clone Tae25005H12F, mRNA sequence.  
ACCESSION BQ248668  
VERSION BQ248668.1 GI:20444544  
KEYWORDS EST.  
SOURCE bread wheat.  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
; Triticeae; Triticum.  
1 (bases 1 to 66)  
Cloutier, S.  
Wheat functional genomics - Glenlea developing seeds cDNA libraries unpublished (2002)  
Contact: Dr. Sylvie Cloutier  
Cereal Research Centre, Agriculture and Agri-food Canada  
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9  
Tel: (204) 983-2340  
Fax: (204) 983-4604  
Email: scloutier@em.agr.ca  
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).  
Average insert size is >870 bp  
Plate: 005 row: H column: 12  
Seq primer: M13 Forward.

FEATURES  
Source  
Location/Qualifiers  
1..66  
/organism="Triticum aestivum"  
/cultivar="Glenlea"  
/db\_xref="taxon:4565"  
/clone="Tae25005H12F"  
/clone\_lib="Tae25"  
/tissue\_type="developing seeds"  
/dev\_stage="25 days after anthesis"  
/lab\_host="E. coli DH10B"  
/note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies); Site\_1: NotI; Site\_2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 25 days post-anthesis"

BASE COUNT 13 a 17 c 19 g 17 t

ORIGIN

Query Match 66.0%; Score 13.2; DB 14; Length 66;  
Best Local Similarity 83.3%; Pred. No. 6.7e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ACCCCGAGGCATCATG 19  
|||||  
Db 26 ACCCCGAGGCATCATG 9

RESULT 14  
AA525968

LOCUS AA525968 92 bp mRNA linear EST 05-AUG-1997  
DEFINITION n13906.s1 NCI CGAP Pr21 Homo sapiens cDNA clone IMAGE:584442 3' similar to g9:M33882 INTERFERON-REGULATED RESISTANCE GTP-BINDING PROTEIN (HUMAN); mRNA sequence.  
ACCESSION AA525968  
VERSION AA525968.1 GI:2268037  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 92)  
NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs@mail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNML at: [www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)

FEATURES  
Source  
Location/Qualifiers  
1..92  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:584442"  
/clone\_lib="NCI CGAP Pr21"  
/sex="male"  
/tissue\_type="normal prostate"  
/lab\_host="DH10B"  
/note="Organ: prostate; Vector: p773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 30 a 19 c 26 g 17 t

ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 92;  
Best Local Similarity 83.3%; Pred. No. 7.4e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ACCCCGAGGCATCATG 19  
|||||  
Db 50 ACACACAGGCATCATG 67

RESULT 15  
A1756476/c 97 bp mRNA linear EST 18-JAN-2000  
LOCUS A1756476/c  
DEFINITION EHESTEAL5d11.y1 Eimeria M5-6 Merozoite stage Eimeria tenella cDNA 5' similar to SW:RIAL2\_BABBO P27055 60S ACIDIC RIBOSOMAL PROTEIN P2 ; mRNA sequence.  
ACCESSION A1756476  
VERSION A1756476.1 GI:5150199  
KEYWORDS EST.  
SOURCE Eimeria tenella.  
ORGANISM Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae; Eimeria.

REFERENCE  
AUTHORS

1 (bases 1 to 97)

## AUTHORS

Liberatori, P., Diaz, C., Tang, R., Marre, M., Hillier, L., Kucaba, T., Martin, J., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swallier, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson, Y., Cardenas, M., McConn, R., Waterston, R., Wilson, R. and Sibley, D. Washu-Merck Elmeria tenella project  
Unpublished (1999)

TITLE  
JOURNAL  
COMMENT

Unpublished (1999)

**COMMENT**

Contact: David Sibley, Ph.D.  
Washu-Merck Eimeria tenella project  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

Contact David Sibley (toxoest@bcm.tmc.edu) for further information relating to organism, libraries, or clone availability. Trace considered overall poor quality. Possible reversed clone: similarity on wrong strand Seq primer: -40RP from Gibco High quality sequence stop: 1.

## FEATURES

Location/Qualifiers  
1. .97

16. T.

```

/organism="Eimeria tenella"
/strain="T619"

```

1516  
1517  
1518

```

/ab_xrel= laxon:300z
/clone 14b="Elmeria M

```

```
/dev stage="Merozoite"
```

```
/lab_host="SOLR E. coll1"
```

```
/note="Vector: Bluescrip
```

; Merozoites were obtained from ceecal scrapings of

chickens infected with *E. tenella*. The library may contain a small percentage of host or bacterial contaminants. cDNA was synthesized from poly mRNA using an oligo-dT primer containing a XhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA and products were size-selected on Sephadyl 5500. cDNAs were digested with EcoRI/XhoI and cloned into lambda Zap II (Stratagene). Clones were converted to phagemids by mass excision using Exassist helper phage and SOCR cells (Stratagene). Insert sizes range from 0.7-1.5 kb.

BASE C  
ORIGIN

66.08; Score 13.2; DB 9; Length 97;

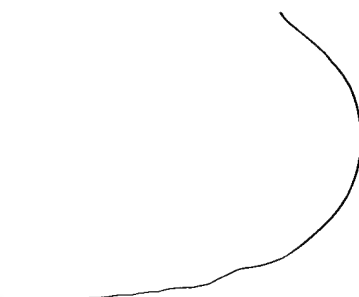
Similarity 83.38; Pred. No. 7.5e+04;

```
13; conservative 0; mismatches 3; indels 0; gaps 0;
```

QY 1 GACCCCCCAGGGCACTCAT 18

[illegible]

Search completed: November 26, 2002, 04:08:02  
Job time : 765.8 secs



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GenCore version 5.1.3  
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## OM nucleic - nucleic search, using sw model

Run on: December 3, 2002, 14:46:40 ; Search time 302.2 Seconds

(without alignments)  
1926.063 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20

Sequence: 1 cgaccacacagacagccccc 20

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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GenEmbl: *
1: gb_da: *
2: gb_htg: *
3: gb_in: *
4: gb_ov: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sy: *
12: gb_sy: *
13: gb_un: *
14: gb_un: *
15: gb_un: *
16: em_da: *
17: em_fun: *
18: em_hum: *
19: em_in: *
20: em_mu: *
21: em_mu: *
22: em_mu: *
23: em_mu: *
24: em_mu: *
25: em_mu: *
26: em_mu: *
27: em_mu: *
28: em_mu: *
29: em_mu: *
30: em_mu: *
31: em_mu: *
32: em_mu: *
33: em_mu: *
34: em_mu: *
35: em_mu: *
36: em_mu: *
37: em_mu: *
38: em_mu: *
39: em_mu: *
40: em_mu: *
41: em_mu: *
```

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	60	6	AR035484
2	13.8	69.0	25	6	AR003361
3	13.6	68.0	26	6	AR168794
4	13.6	68.0	26	6	AR168799
5	13.6	68.0	26	6	AR168801
6	13.6	68.0	26	6	AR200263
7	13.6	68.0	26	6	AR200268
8	13.6	68.0	26	6	AR200270
9	13.6	68.0	26	6	127788
10	13.6	68.0	26	6	127793
11	13.6	68.0	26	6	127795
12	13.6	68.0	45	6	AR168795
13	13.6	68.0	45	6	AR168796
14	13.6	68.0	45	6	AR200264
15	13.6	68.0	45	6	AR200265
16	13.6	68.0	45	6	127789
17	13.6	68.0	45	6	127790
18	13.6	68.0	80	9	HSD5347
19	13.6	68.0	87	6	AX282658
20	13.4	67.0	32	6	AR083991
21	13.2	66.0	27	6	AR063107
22	13.2	66.0	27	6	AR122634
23	13.2	66.0	27	6	AR164262
24	13.2	66.0	27	6	AR209834
25	13.2	66.0	28	6	AX397893
26	13.2	66.0	29	6	156811
27	13.2	66.0	78	10	HUMRMB
28	13.2	66.0	89	6	AX010661
29	13.2	66.0	89	6	AX010662
30	13.2	66.0	92	5	AF173802
31	13.2	66.0	92	11	AF042209
32	13.2	65.0	92	6	BD002386
33	13	65.0	31	6	AX298446
34	12.8	64.0	20	6	AR117105
35	12.8	64.0	51	6	AX161745
36	12.8	64.0	51	6	S57152
37	12.8	64.0	80	9	AX455995
38	12.8	64.0	90	6	E28452
39	12.6	63.0	22	6	AR070106
40	12.6	63.0	31	6	AX393601
41	12.6	63.0	36	6	A23247
42	12.6	63.0	38	6	A23248
43	12.6	63.0	38	6	AR040879
44	12.6	63.0	38	6	AR040880
45	12.6	63.0	38	6	AR040880

## ALIGNMENTS

RESULT 1  
AR035484  
LOCUS AR035484 60 bp DNA  
DEFINITION Sequence 56 from patent US 5871902.  
ACCESSION AR035484  
VERSION AR035484.1 GI:5952152  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 60)  
Weininger, S. and Weininger, A.M.  
Sequence-specific detection of nucleic acid hybrids using a  
DNA-binding molecule or assembly capable of discriminating perfect  
hybrids from non-perfect hybrids

JOURNAL Patent: US 5871902-A 56 16-FEB-1999;  
FEATURES Location/Qualifiers  
SOURCE 1..60  
BASE COUNT 16 a 23 c 13 g 8 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 60;  
Best Local Similarity 84.2%; Pred. No. 2.8e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACCCACAGACAGCCCC 20  
Db 15 GACACCCAGACAGCCCC 33

RESULT 2  
LOCUS AR003361 25 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 8 from patent US 5744303.  
ACCESSION AR003361  
VERSION AR003361.1 GI:3964620  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Iqgo, R., Friend, S.H., Frebourg, T., and Ishioka, C.  
TITLE Functional assay for transcriptional regulator genes  
JOURNAL Patent: US 5744303-A 8 28-APR-1998;  
FEATURES Location/Qualifiers  
SOURCE 1..25  
BASE COUNT 6 a 3 c 12 g 4 t  
ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 4.9e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCCCACAGACAGCCCC 20  
Db 20 CCCCACAGACAGCCCC 4

RESULT 3  
LOCUS ARI68794 26 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 20 from patent US 6288042.  
ACCESSION ARI68794  
VERSION ARI68794.1 GI:17904898  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Rando, R.F., Ojwang, J.O., Hogan, M.E., Wallace, T.L., and Cossum, P.A.  
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides  
JOURNAL Patent: US 6288042-A 20 11-SEP-2001;  
FEATURES Location/Qualifiers  
SOURCE 1..26  
BASE COUNT 0 a 0 c 17 g 9 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 6.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20  
Db 23 CGACCCACAGACAGCCCC 4

RESULT 4  
LOCUS ARI68799/c 26 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 25 from patent US 6288042.  
ACCESSION ARI68799  
VERSION ARI68799.1 GI:17904906  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Rando, R.F., Ojwang, J.O., Hogan, M.E., Wallace, T.L., and Cossum, P.A.  
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides  
JOURNAL Patent: US 6288042-A 25 11-SEP-2001;  
FEATURES Location/Qualifiers  
SOURCE 1..26  
BASE COUNT 0 a 0 c 17 g 9 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 6.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20  
Db 23 CGACCCACAGACAGCCCC 4

RESULT 5  
LOCUS ARI68801 26 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 27 from patent US 6288042.  
ACCESSION ARI68801  
VERSION ARI68801.1 GI:17904909  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Rando, R.F., Ojwang, J.O., Hogan, M.E., Wallace, T.L., and Cossum, P.A.  
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides  
JOURNAL Patent: US 6288042-A 27 11-SEP-2001;  
FEATURES Location/Qualifiers  
SOURCE 1..26  
BASE COUNT 0 a 0 c 17 g 9 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 6.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20  
Db 23 CGACCCACAGACAGCCCC 4

RESULT 6  
LOCUS AR200263/c 26 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 20 from patent US 6355785.  
ACCESSION AR200263  
VERSION AR200263.1 GI:20250337  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Rando, R.F., Fennevald, S., Zendejui, J.G., Ojwang, J.O., Hogan, M.E., Pommer, Y., and Mazumder, A.  
TITLE Guanosine-rich oligonucleotide integrase inhibitors

JOURNAL Patent: US 6355785-A 20 12-MAR-2002;  
FEATURES Location/Qualifiers  
source 1..26  
BASE COUNT 0 a 0 c 17 g 9 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 6.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20  
Db 23 CCACCCACCAACAGCCCC 4

RESULT 7  
LOCUS AR200268/c 26 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 25 from patent US 6355785.  
ACCESSION AR200268  
VERSION AR200268.1 GI:20250342  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O., Hogan,M.E.,  
Pommier,Y. and Mazumder,A.  
TITLE Guanosine-rich oligonucleotide integrase inhibitors  
JOURNAL Patent: US 6355785-A 25 12-MAR-2002;  
FEATURES Location/Qualifiers  
source 1..26  
BASE COUNT 0 a 0 c 17 g 9 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 6.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20  
Db 23 CCACCCACCAACAGCCCC 4

RESULT 8  
LOCUS AR200270/c 26 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 27 from patent US 6355785.  
ACCESSION AR200270  
VERSION AR200270.1 GI:20250344  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O., Hogan,M.E.,  
Pommier,Y. and Mazumder,A.  
TITLE Guanosine-rich oligonucleotide integrase inhibitors  
JOURNAL Patent: US 6355785-A 27 12-MAR-2002;  
FEATURES Location/Qualifiers  
source 1..26  
BASE COUNT 0 a 0 c 17 g 9 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 6.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20  
Db 23 CCACCCACCAACAGCCCC 4

Db 23 CCACCCACCAACAGCCCC 4

RESULT 9  
LOCUS I27788/c 26 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 20 from patent US 5567604.  
ACCESSION I27788  
VERSION I27788.1 GI:1818564  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Rando,R.F., Fennewald,S., Zendegui,J.G. and Ojwang,J.O.  
TITLE Anti-viral guanosine-rich oligonucleotides  
JOURNAL Patent: US 5567604-A 20 22-OCT-1996;  
FEATURES Location/Qualifiers  
source 1..26  
BASE COUNT 0 a 0 c 17 g 9 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 6.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20  
Db 23 CCACCCACCAACAGCCCC 4

RESULT 10  
LOCUS I27793/c 26 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 25 from patent US 5567604.  
ACCESSION I27793  
VERSION I27793.1 GI:1818569  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Rando,R.F., Fennewald,S., Zendegui,J.G. and Ojwang,J.O.  
TITLE Anti-viral guanosine-rich oligonucleotides  
JOURNAL Patent: US 5567604-A 25 22-OCT-1996;  
FEATURES Location/Qualifiers  
source 1..26  
BASE COUNT 0 a 0 c 17 g 9 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 6.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20  
Db 23 CCACCCACCAACAGCCCC 4

RESULT 11  
LOCUS I27795/c 26 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 27 from patent US 5567604.  
ACCESSION I27795  
VERSION I27795.1 GI:1818571  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Rando,R.F., Fennewald,S., Zendegui,J.G. and Ojwang,J.O.



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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:52:31 : Search time 98.55 Seconds  
(without alignments)  
457.027 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20  
Sequence: 1 cgacccacagacagccccc 20

Scoring table: IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_101002:\*

- 1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
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- 8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*
- 9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
- 12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*
- 13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*
- 14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*
- 15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*
- 16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*
- 17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*
- 18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*
- 19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*
- 20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*
- 21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	20	100.0	20	AA231442	Human neuropilin m
2	14.4	72.0	60	ABNA6092	Human spliced tran
3	14.2	71.0	37	ABK81254	POLYIMMUNOGLOBULIN
4	14.2	71.0	49	AA033751	upstream sequence
5	14.2	71.0	60	AAT30628	Probe nucleic acid
6	14	70.0	45	AAC82189	Human retrovirus D
7	13.8	69.0	25	AA061824	Primer for mutant
8	13.8	69.0	30	AAA0611	SHR sequence varia
9	13.8	69.0	60	AAA05788	Streptavidin displ

10	13.6	68.0	22	21	AA53503	NF-kappaB binding
11	13.6	68.0	26	15	AA079225	Guanosine rich o11
12	13.6	68.0	26	15	AA079227	Guanosine rich o11
13	13.6	68.0	26	15	AA079220	Guanosine rich o11
14	13.6	68.0	26	18	AAT51645	Viral integrase in
15	13.6	68.0	26	18	AAT51638	Viral integrase in
16	13.6	68.0	26	18	AAT51643	Viral integrase in
17	13.6	68.0	26	19	AA079227	Oligonucleotide #2
18	13.6	68.0	45	15	AA079222	Guanosine rich o11
19	13.6	68.0	45	15	AA079222	Guanosine rich o11
20	13.6	68.0	45	18	AAT51639	Viral integrase in
21	13.6	68.0	45	18	AAT51640	Viral integrase in
22	13.6	68.0	45	19	AA079228	Oligonucleotide #2
23	13.6	68.0	45	24	AA05784	Streptavidin displ
24	13.6	68.0	65	24	ABN56220	Mouse spliced tran
25	13.6	68.0	87	21	AA010414	Human secreted pro
26	13.6	68.0	87	22	AA043509	ClA35G SNP from DN
27	13.4	67.0	22	21	AAA96906	RACE PCR primer us
28	13.4	67.0	40	20	AAV82040	Moraxella lactofer
29	13.4	67.0	60	24	ABN32297	Human spliced tran
30	13.4	67.0	89	18	AAT76219	Human IL5 antisens
31	13.4	67.0	89	20	AA54024	Human IL-5 antisen
32	13.4	67.0	89	21	AA019590	Human IL5 polymucl
33	13.4	67.0	89	21	AAA33468	Low adenosine anti
34	13.2	66.0	18	24	AA518236	Rat Arginase I PCR
35	13.2	66.0	27	22	AA076134	Human Shh CA repa
36	13.2	66.0	27	22	AA010173	Human Sonic hedgeh
37	13.2	66.0	27	22	AA087099	PCR primer for con
38	13.2	66.0	27	24	ABN87571	Human sonic hedgeh
39	13.2	66.0	28	24	ABK52396	Sahh gene encoding
40	13.2	66.0	29	17	AAT07256	Oligonucleotide in
41	13.2	66.0	29	17	AAT08788	Cytokine productio
42	13.2	66.0	32	24	ABK70089	GMD PCR primer #7
43	13.2	66.0	60	24	ABN35967	Human spliced tran
44	13.2	66.0	60	24	ABN43371	Human spliced tran
45	13.2	66.0	90	22	AB048830	Human breast cell

## ALIGNMENTS

RESULT 1  
AA231442  
ID AA231442 standard; DNA: 20 BP.  
XX  
XX AA231442:  
AC  
XX  
XX  
DT 07-FEB-2000 (first entry)  
XX  
DE Human neuropilin mRNA specific antisense oligo GT13612.  
XX  
XX Neuropilin; human; growth; metastasis; tumor; neovascularisation;  
KW cancer; papilloma; diabetic retinopathy; antisense; ss.  
XX  
XX  
OS Synthetic.  
XX Homo sapiens.  
XX  
XX WO9955855-A2.  
XX  
XX  
PD 04-NOV-1999.  
XX  
XX  
PF 23-APR-1999; 99WO-CA00324.  
XX  
XX 23-APR-1998; 98US-0082791.  
XX  
XX  
PA (GENE-) GENESENSE TECHNOLOGIES INC.  
XX  
XX Wright JA, Young AH, Lee YS:  
PI  
XX  
XX WPI: 2000-023357/02.  
XX  
XX  
XX Antisense oligonucleotides that inhibit neuropilin expression, useful  
PT for treating cancer -

XX Claim 4; Page 16; 57pp; English.  
PS  
XX Sequences AA231431-460 represent antisense oligonucleotides which  
CC inhibit human neuropilin expression. The antisense oligonucleotides can  
CC be used to inhibit the growth or metastasis of a mammalian tumor and  
CC inhibit neovascularisation. The oligonucleotides may be used to treat  
CC various forms of cancers or tumors, such as sarcomas, melanomas,  
CC adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell  
CC carcinomas of the mouth, throat, larynx and lung, genitourinary cancers  
CC such as cervical and bladder cancer, hematopoietic cancers, colon cancer,  
CC breast cancer, pancreatic cancer, renal cancer, brain cancer, skin  
CC cancer, liver cancer, head and neck cancers, and nervous system cancers,  
CC as well as benign lesions such as papillomas. The methods may be used to  
CC treat neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration.  
XX  
SQ Sequence 20 BP; 5 A; 12 C; 3 G; 0 U; 0 other;  
Query Match 100.0%; Score 20; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGACCCACAGACGCCCC 20  
DB 1 CGACCCACAGACGCCCC 20  
RESULT 2  
ABN46092  
ID ABN46092 standard; DNA; 60 BP.  
XX  
AC ABN46092;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:18840.  
XX  
KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB01903.  
XX  
PR 28-JUL-2000; 2000US-221607P.  
PR 02-MAY-2001; 2001US-287724P.  
XX  
PA (COMP-) COMPUGEN INC.  
XX  
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX  
DR WPI; 2002-257383/30.  
XX  
PT New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of  
PT a genome, useful for detecting tissue-, pathology-, and  
PT developmental-specific genes.  
XX  
PS Example 1; SEQ ID 18840; 47pp; English.  
XX  
CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the  
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises  
CC several oligonucleotides, each capable of hybridising selectively to a  
CC set of messenger RNAs transcribed from a given transcription unit of  
CC the genome, which encodes one or more messenger RNA splice variants.  
CC The oligonucleotide libraries are useful for detecting mRNAs from a

CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterizing the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a  
CC particular biological or pathological state, and so allowing the  
CC detection of tissue- and pathology-specific genes such as those genes  
CC only expressed in specific tissue under a specific pathological  
CC condition; to detect developmental specific genes; and to detect RNA  
CC transcripts and splice variants of a transcriptome of a patient suffering  
CC from a particular disorder. ABN27253 to ABN59589 represent  
CC oligonucleotide sequences from rats, humans and mice, which are used in  
CC the exemplification of the present invention.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 60 BP; 15 A; 17 C; 14 G; 14 T; 0 other;  
Query Match 72.0%; Score 14.4; DB 24; Length 60;  
Best Local Similarity 93.8%; Pred. No. 2.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CGACCCACAGACGCC 16  
DB 31 CGACCCACAGACTGC 46  
RESULT 3  
ABK81254/C  
ID ABK81254 standard; DNA; 37 BP.  
XX  
AC ABK81254;  
XX  
DT 13-APR-2002 (first entry)  
XX  
DE Polymunoglobulin receptor (p1gR) related primer #44.  
XX  
KW Transcellular transport; transcytotic transport; paracellular transport;  
KW respiratory system disorder; lung cancer; tumour; asthma;  
KW pathogenic infection; allergy-related disorder;  
KW gastrointestinal tract disorder; gastrointestinal hormone disorder;  
KW Chron's disease; eating disorder; polymunoglobulin receptor; p1gR;  
KW primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200228408-A2.  
XX  
PD 11-APR-2002.  
XX  
PF 02-OCT-2001; 2001WO-US30832.  
XX  
PR 02-OCT-2000; 2000US-237929P.  
PR 13-NOV-2000; 2000US-248478P.  
PR 14-NOV-2000; 2000US-248819P.  
PR 09-FEB-2001; 2001US-267601P.  
XX  
PA (ARIZ-) ARIZEKE PHARM INC.  
XX  
PI Houston LL, Sheridan PJ, Hawley S, Glynn JM, Chaplin S, Basu A;  
XX  
DR WPI; 2002-416628/44.  
XX  
PT Complex useful for transporting active agent through epithelial  
PT barrier, has biologically active portion and target element directed to  
PT ligand that confers e.g. transcytotic properties to agent specific to  
XX  
PS Example 3; Fig 12B; 379pp; English.  
XX  
CC The invention described a complex or compound (I) comprising a  
CC biologically active portion and a target element (II) directed to a

CC ligand that confers transcellular, transcytotic or paracellular  
 CC transporting properties to an agent specifically bound to the ligand.  
 CC where (11) is not an antibody. Alternatively, (1) comprises two or more  
 CC (11) directed to one or more ligands. (1) is useful for delivering a  
 CC biologically active agent to an animal, for transporting an active agent  
 CC through an epithelial or mucosal barrier, and for treating or  
 CC identifying a disease in an animal e.g. diseases of the respiratory  
 CC system including lung cancer and tumours, asthma, pathogenic infections,  
 CC allergy-related disorders, gastrointestinal tract disorders, disorders  
 CC relating to gastrointestinal hormones, Chron's disease, eating disorders  
 CC and any disease or disorder involving polyclonal immunoglobulin receptor (pigr)  
 CC displaying cells. This sequence represents a primer associated with the  
 CC transport of biologically active agents across cellular barriers.

XX  
 SQ Sequence 37 BP; 3 A; 13 C; 14 G; 7 T; 0 other;

Query Match 71.0%; Score 14.2; DB 24; Length 37;

Best Local Similarity 84.2%; Pred. No. 3.2e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACCCACAGACAGCCCC 20  
 ||| ||||| |||||  
 DB 28 GACGCCACAGAACGCCCC 10

#### RESULT 4

AA033751/C  
 ID AA033751 standard; DNA: 49 BP.

XX AA033751;

DT 02-FEB-1993 (first entry)

XX Upstream sequence of microsatellite from clone TGLA162.

XX PCR; selection; primers; OPRIPRM; breeding; cattle; parentage;

KW genetic mapping; traits; amplification; ss.

OS Bos taurus.

PN WO9213102-A.

PD 06-AUG-1992.

PF 15-JAN-1992; 92WO-US00340.

PR 15-JAN-1991; 91US-0642342.

PA (GENM-) GENMARK.

PI Georges M, Massey JM;

DR WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification,  
 PT gene mapping, and selective breeding

XX Table 7; Page 229; 517pp; English.

XX The sequence is that upstream of a bovine microsatellite sequence  
 CC obtd. by screening a library of bovine MBOI DNA fragments of between  
 CC 250 and 500 bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe.  
 CC One out of 50 clones cross-hybridised. Assuming independent  
 CC distribution of microsatellites and MBOI sites, the frequency of  
 CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,  
 CC 000. The sequence information for ca. 230 such bovine microsatellites  
 CC is summarised in the specification and indexed herein (see below).  
 CC The sequences upstream and downstream of the microsatellite sequence  
 CC were used to generate the required PCR primers for in vitro  
 CC amplification of the corresp. microsatellite (using the program  
 CC OPTIPRM). The microsatellites may be used to identify individuals,  
 CC for parentage testing, and in the genetic mapping of economic trait  
 CC loci, or genes involved the determination of economically important

CC traits esp. in cattle, to allow selective breeding.  
 CC See also AA033501-34437.

SQ Sequence 49 BP; 12 A; 11 C; 16 G; 10 T; 0 other;

Query Match 71.0%; Score 14.2; DB 13; Length 49;

Best Local Similarity 84.2%; Pred. No. 3.2e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 19  
 ||||| ||||| |||||  
 DB 19 CGACCCACAGACAGCCCC 1

#### RESULT 5

AA030628  
 ID AA030628 standard; CDNA: 60 BP.

XX AA030628;

DT 21-FEB-1997 (first entry)

DE Probe nucleic acid #11.

XX Target binding assembly; nucleic acid recognition unit: NF-kappa-B; SPI;  
 KW TARA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;  
 KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
 KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
 KW virus; ss.

XX Synthetic.

OS WO9617956-A2.

PN 13-JUN-1996.

PD 07-DEC-1995; 95WO-US15944.

PF 09-DEC-1994; 94US-0353476.

PR (GENE-) GENE POOL INC.

PA Weininger AM, Weininger S;

PI WPI; 1996-287199/29.

DR Probe nucleic acids, target binding assemblies, etc - for detection

PT and localisation of specific nucleic acid sequences, esp. HIV and

HPV

XX Disclosure; Page 82; 172pp; English.

XX AA030615-730634 represent probe nucleic acids of the invention. The  
 CC probe of the invention contains a target binding region (TBR), a booster  
 CC binding region (BBR), and an optional support or attachment (OSA). The  
 CC target binding assembly (TBA) recognised by the TBR (see  
 CC AA030581-730614) of the probe, contains at least one nucleic acid  
 CC recognition unit (NAR), and optionally a linker sequence, an assembly  
 CC sequence (see AAR95994-R95998), an asymmetry sequence (see AAR96007),  
 CC and an OSA. The assembly sequence and asymmetry sequences are  
 CC responsible for the folding and association of the NARs. The NARs (see  
 CC AAR95965-R95993) are selected from NF-kappa-B, SPI, TARA, human  
 CC papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR  
 CC and Tat binding units. The linker sequence is an oligopeptide, which  
 CC does not interfere with NAR function, but provides stability and control  
 CC over the spacing of the NAR from the rest of the TBA. The OSA is an  
 CC attached support or indicator, or other means of localisation of the  
 CC probe. The probe can be used in a method for detecting or localising a  
 CC specific target nucleic acid sequence (TNA). The method is highly  
 CC sensitive, and has a high degree of specificity. The method can be used  
 CC for detecting specific nucleic acid sequences, including those found in  
 CC human cells, in HIV, HPV, and other nucleic acid containing systems,

CC Including bacteria and viruses.  
 XX Sequence 60 BP; 16 A; 23 C; 13 G; 8 T; 0 other;  
 SQ

Query Match  
 Best Local Similarity 71.0%; Score 14.2; DB 17;  
 Best Local Similarity 84.2%; Pred. No. 3.2e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACCCACAGACAGCCCC 20  
 ||| ||||| ||| |||  
 Db 15 GACACACAGACAGCCCC 33

RESULT 6  
 AAC82189  
 ID AAC82189 standard; DNA; 45 BP.  
 XX  
 AC AAC82189;  
 XX  
 DT 08-MAR-2001 (first entry)  
 XX  
 DE Human retrovirus DNA probe 2J #1.  
 XX  
 KW Detection; infection; disease; diagnosis; risk assessment; probe;  
 KW PCR primer; ss.  
 XX  
 OS Human retrovirus.  
 XX  
 PN DEL19921419-A1.  
 PD 16-NOV-2000.  
 XX  
 PF 08-MAY-1999; 99DE-1021419.  
 XX  
 PR 08-MAY-1999; 99DE-1021419.  
 XX  
 PA (UWHE-) UNIV HEIDELBERG RUDRECHT-KARLS.  
 XX  
 PI Selfarth W, Leib-Moesch C, Baust C;  
 XX  
 DR WPI; 2001-000507/01.  
 XX  
 PT Specific detection of retroviral nucleic acid, useful e.g. for early  
 PT diagnosis of disease, comprises amplification with universal primers  
 PT then reverse dot blot hybridization -  
 XX  
 PS Example 3; Page 11; 22pp; German.  
 XX  
 CC This invention describes a novel method for the specific detection and  
 CC identification of retroviral nucleic acid (or retroviruses) comprising  
 CC isolation of DNA and/or RNA, subjecting this to reverse  
 CC transcription-polymerase chain reaction (RT-PCR) with one of two  
 CC specified primer pairs (or both pairs), purifying the amplicons and  
 CC analyzing them by reverse dot blot hybridization (RDBH) using  
 CC immobilized, synthetic oligonucleotide probes. The method is used to  
 CC detect retroviruses (or their nucleic acid) in cell cultures (or  
 CC supernatants); body samples or other biological materials. It produces an  
 CC expression pattern of all retroviruses in a single experiment,  
 CC particularly for large scale surveys to determine any correlations  
 CC between diseases and activity of selected retroviruses. If such a  
 CC correlation is found, the method will allow early diagnosis, or  
 CC assessment of risk. An efficient, reliable and rapid method for detecting  
 CC all presently known endogenous and exogenous retroviruses of human or  
 CC animal origin with very low detection limit. The amplification primers  
 CC are universal and inclusion of a clamp and restriction enzyme recognition  
 CC site in them (i) improves primer/matrix binding kinetics and allows  
 CC amplification of Rase templates even if there is not an exact match and  
 CC (ii) facilitates subsequent cloning. Using probes that do not overlap  
 CC with primers overcomes the problem of amplicons reacting, to some extent,  
 CC with all probes in the array.  
 XX  
 SQ Sequence 45 BP; 12 A; 17 C; 4 G; 12 T; 0 other;

Query Match  
 Best Local Similarity 70.0%; Score 14; DB 22; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 CACAGACAGCCCC 20  
 ||||| ||||| |||||  
 Db 3 CACAGACAGCCCC 16

RESULT 7  
 AA061824/C  
 ID AA061824 standard; DNA; 25 BP.  
 XX  
 AC AA061824;  
 XX  
 DT 19-SEP-1994 (first entry)  
 XX  
 DE Primer for mutant p53 sequence.  
 XX  
 KW Fragment A; RGC; transcriptional regulator; TR; germ line mutation;  
 KW assay; cancer; PCR; amplification; sense; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9408049-A.  
 PD 14-APR-1994.  
 XX  
 PF 28-SEP-1993; 93WO-US09259.  
 XX  
 PR 01-OCT-1992; 92US-0956696.  
 XX  
 PR 12-APR-1993; 93US-0046033.  
 XX  
 PA (GEO) GEN HOSPITAL CORP.  
 PA (SURE-) INST SUISSE RECH EXPERIMENTALE.  
 XX  
 PI Frebourg T, Friend SH, Iggo R, Ishioka C;  
 XX  
 DR WPI; 1994-135609/16.  
 XX  
 PT Assay for mutations in a transcriptional regulator gene - using  
 PT cells transfected with the gene and DNA encoding a detectable  
 PT protein expressed in response to the gene.  
 XX  
 PS Example; Page 21; 51pp; English.  
 XX  
 CC The sequence is that of a sense PCR primer for amplification of a  
 CC mutant p53 gene. The PCR prod. can be used in an assay to directly  
 CC assess whether a germ-line mutation in a gene which is a trans-  
 CC criptional regulator results in the prodn. of a non functional gene.  
 CC This may be used in screening individuals at risk of cancer or in cancer  
 CC prognosis.  
 CC See also AA061818-23.  
 XX  
 SQ Sequence 25 BP; 6 A; 3 C; 12 G; 4 T; 0 other;

Query Match  
 Best Local Similarity 69.0%; Score 13.8; DB 15;  
 Best Local Similarity 88.2%; Pred. No. 4.7e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCCCACAGACAGCCCC 20  
 ||||| ||||| |||  
 Db 20 CCCCACAGACAGCCTCC 4

RESULT 8  
 AAA40611  
 ID AAA40611 standard; DNA; 30 BP.  
 XX  
 AC AAA40611;  
 XX  
 DT 15-AUG-2000 (first entry)  
 XX



DE SHR sequence variant number 2 SEQ ID NO:11.

XX Human; rat; CD36; SHR; spontaneous hypertensive rat; diagnosis;  
 KW therapy; screening; polymorphism; variant; detection; mutant;  
 KW blood; mutation; insulin; glucose metabolism; fatty acid metabolism;  
 KW catecholamine; malaria; infection; parasite; antiparasitic;  
 KW antidiabetic; primer; ss.

XX Rattus sp.  
 OS Synthetic.  
 XX WO200019883-A2.

XX 13-APR-2000.

XX 07-OCT-1999; 99WO-US23418.

XX 07-OCT-1998; 98US-0167750.  
 PR 28-DEC-1998; 98US-0221222.  
 PR 17-MAR-1999; 99US-0270542.

XX (MEDT-) MEDICAL RES COUNCIL.  
 PA (SCIO-) SCIOS INC.  
 PA (ATM/) ALTMAN T J.  
 PA (SCOT/) SCOTT J.  
 PA (SPAN/) STANTON L W.

XX Altman TJ, Scott J, Stanton LW;  
 PI WPI: 2000-303596/26.

XX Nucleic acids encoding mutant CD36 proteins useful for preventing,  
 PT diagnosing and treating parasitic infections, especially malaria -  
 PT Example 4; Page 83; 167pp; English.

XX The present invention describes isolated nucleic acid molecules (A)  
 CC encoding mutant CD36 proteins (B). Parasites such as Plasmodium  
 CC falciparum (the major cause of malaria) are unable to utilize the  
 CC mutated proteins to gain entry to, and infect cells. The mutant CD36  
 CC proteins do not function correctly preventing parasites utilizing them  
 CC to infect cells. The nucleic acids may be used for the recombinant  
 CC production of mutant CD36 proteins according to standard methodologies.  
 CC They may be used in this way to prevent and treat parasitic infections  
 CC that utilize the CD36 protein to infect cells, such as P. falciparum,  
 CC the major cause of malaria. For example, the protein may be used to  
 CC identify modulators of CD36 expression and activity or a patient's CD36  
 CC DNA may be screened to determine whether there are any mutations present  
 CC that may confer resistance to parasitic infections. The proteins and  
 CC nucleic acids may also be used to prevent, diagnose and treat diseases  
 CC associated with defects in insulin action and/or glucose metabolism  
 CC and/or fatty acid metabolism and/or catecholamine action in subjects  
 CC possessing mutations in the CD36 genes. AAA40606 to AAA40759, and  
 CC AAB02315 to AAB02564, represent nucleotide and amino acid sequences  
 CC respectively which are used in the exemplification of the present  
 CC invention.

XX Sequence 30 BP; 10 A; 10 C; 5 G; 5 T; 0 other;  
 SQ

Query Match 69.0%; Score 13.8; DB 21; Length 30;  
 Best Local Similarity 88.2%; Pred. No. 4.7e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GACCCACAGACAGCC 18  
 Db 9 GACCCCAAGACAGACAC 25

RESULT 9  
 ID AAA05788 standard; DNA: 60 BP.  
 XX AAA05788;  
 AC AAA05788;

XX 05-JUN-2000 (first entry)

DE Streptavidin display linker DNA, SEQ ID NO:250.

XX Phage display; bacteriophage M13; fusion protein; major coat protein;  
 KW protein VIII; phagemid vector; electroporation; combinatorial library;  
 KW streptavidin; SAV; ss.

XX Synthetic.  
 OS  
 XX WO200006717-A2.

XX 10-FEB-2000.

XX 22-JUL-1999; 99WO-US16596.

XX 27-JUL-1998; 98US-0094291.  
 PR 08-OCT-1998; 98US-0103514.  
 PR 10-MAY-1999; 99US-0133296.  
 PR 19-MAY-1999; 99US-0134870.

XX (GETH ) GENENTECH INC.  
 PA Sidhu SS, Weiss GA, Wells JA;  
 PI WPI: 2000-183122/16.  
 DR P-PSDB: AAY81345.

XX Fusion proteins comprising a heterologous protein and a viral variant  
 PT major coat protein useful in phage display systems for improving  
 PT transformation efficiency -  
 PT Disclosure; Fig 7B; 118pp; English.

XX The invention relates to novel fusion proteins comprising a heterologous  
 CC polypeptide fused to a variant (non-wild type) bacteriophage  
 CC major coat protein (protein VIII). The invention also relates to  
 CC replicable expression vectors which contain a gene encoding the fusion  
 CC protein; host cells containing the expression vectors; phages which  
 CC display the fusion protein on their surface; phage libraries displaying  
 CC a plurality of different fusion proteins on viral surfaces; and methods  
 CC of using these compositions. The fusion proteins the invention are well  
 CC tolerated in phage display systems. Variants of the major coat proteins  
 CC can be used to alter the number of fusion proteins incorporated into a  
 CC virus particle. Hyper-functional variants can be used to increase the  
 CC number of fusion proteins incorporated into a virus particle.  
 CC Conversely, hypo-functional variants can be used to decrease fusion  
 CC protein incorporation. This is useful for tailoring the incorporation of  
 CC fusion proteins into virus particles to achieve a desired level of  
 CC valency. The variant replicable plasmid/phagemid vectors are useful for  
 CC producing polypeptides of interest. The methods are useful for improving  
 CC the transformation of cells by highly purifying DNA. The present  
 CC invention uses affinity DNA purification to reduce ionic impurities and  
 CC thus reduce the conductance associated with a unit mass of DNA. This is  
 CC an advantageous in electroporation methods for increasing the  
 CC concentration of DNA present. The increase in DNA entering the host cell  
 CC provides a greater number of transformants per electroporation and allows  
 CC one to prepare larger combinatorial libraries which overcomes the prior  
 CC art problem of small library size using recombinant DNA. Sequences  
 CC AAA05768-A05795 represent DNA encoding linkers selected for display  
 CC of streptavidin (SAV).

XX Sequence 60 BP; 10 A; 44 C; 6 G; 0 U; 0 other;  
 SQ

Query Match 69.0%; Score 13.8; DB 21; Length 60;  
 Best Local Similarity 88.2%; Pred. No. 4.8e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCCCACAGACAGCCCC 20  
 Db 6 CCCCAGCAGACAGCCCC 22

```

RESULT 10
AA53503
ID AAA53503 standard; DNA: 22 BP.
XX
AC AAA53503;
XX
DE 05-OCT-2000 (first entry)
XX
DE NF-kappa binding phosphotetrahioate aptamer #3.
XX
XX Phosphotetrahioate aptamer; NF-kappa; bacterial pathogenesis; AIDS;
XX SY-40; rheumatoid arthritis; Crohn's disease; asbestos lung disease;
XX generalised inflammatory bowel disease; Hodgkin's disease; cancer;
XX lung injury; atherosclerosis; cytomegalovirus; herpes simplex virus;
XX rhinovirus; influenza; neurological disorder; JCV; ds.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..22
FT /tag= a
FT /note= "all A nucleotides are 5' monophosphorothioated"
XX
PN WO200024404-A1.
XX
PD 04-MAY-2000.
XX
PF 26-OCT-1999; 99WO-US24058.
XX
PR 26-OCT-1998; 98US-0105600.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Gorenstein DG, Aronson J, Luxon B, Herzog N;
XX
DR WPI: 2000-350578/30.
XX
PT Preparing achiral nuclear factor-kappa specific aptamers for
PT generating high binding, nuclease resistant aptamers that retain their
PT specificity comprises synthesizing amplifying random phosphodiester
PT oligonucleotide combinatorial library -
XX
PS Example 3; Page 31; 63pp; English.
XX
XX The present sequence is a randomly generated sequence created so that
XX each A residue is 5' monophosphorothioated. It has a high affinity for
XX the p65 homodimer, which forms part of the nuclear factor kappaB
XX (NF-kappaB) transcription factor. This sequence can be used in the
XX production of aptamers which are stable and nuclease resistant, and can
XX be used to treat diseases involving the transcription factor, such as
XX bacterial pathogenesis, rheumatoid arthritis, Crohn's disease,
XX generalised inflammatory bowel disease, asbestos lung disease, Hodgkin's
XX disease, prostate cancer, ventilator induced lung injury, cancer, AIDS,
XX human cutaneous T-cell lymphoma, lymphoid malignancies, HTLV-1 induced
XX adult T-cell leukemia, atherosclerosis, cytomegalovirus, herpes simplex
XX virus, JCV, SV-40, rhinovirus, influenza, neurological disorders and
XX lymphomas.
XX
SQ Sequence 22 BP; 4 A; 16 C; 2 G; 0 U; 0 other:
XX
Query Match 68.0%; Score 13.6; DB 21; Length 22;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

RESULT 11
AA079225/C
ID AA079225 standard; DNA: 26 BP.

```

```

XX
AC AA079225;
XX
DE 17-JUL-1995 (first entry)
XX
DE Guanosine rich oligonucleotide used to treat viral infection.
XX
XX Guanosine; tetrad; inhibition; replication; virus; treatment;
XX therapy; infection; herpes simplex virus; human papilloma virus;
XX Epstein-Barr virus; HIV, adenovirus; respiratory syncytial virus;
XX hepatitis B virus; human cytomegalovirus; ss.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT msc_feature 26
FT /tag= a
FT /mod_base=
FT /note= "Cholesterol moiety attached to this base."
XX
PN WO9425037-A.
XX
PD 10-NOV-1994.
XX
PF 25-APR-1994; 94WO-US04529.
XX
PR 23-APR-1993; 93US-0053027.
XX
PR 28-OCT-1993; 93US-0145704.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PA (TRIP-) TRIPLEX PHARM CORP.
XX
PI Fennewald S, Hogan ME, O'wang JO, Rando RF, Zendequi JG;
XX
DR WPI: 1994-357890/44.
XX
PT Oligo-nucleotide(s) rich in guanosine which form guanosine
PT tetrads - used to treat viral infections, e.g. herpes-virus and
PT HIV
XX
PS Claim 41; Page 56; 101pp; English.
XX
XX The oligonucleotides (See AA079201-52) can be used to treat viral
XX infections. The oligonucleotides inhibit viral replication by
XX forming guanosine tetrads which form a stabilised 3D structure.
XX Preferred oligonucleotides contain at least 2 runs of at least 2
XX guanosine bases and may be capped at the 3' terminus with a modifier
XX selected from polyamine, poly-L-lysine, cholesterol and
XX propionolamine. They may also have a modified phosphodiester linkage
XX or be modified to contain a phosphorothioate linkage. They are used
XX to treat infections with viruses such as herpes simplex virus, human
XX papilloma virus, Epstein-Barr virus, HIV, adenovirus, respiratory
XX syncytial virus, hepatitis B virus or human cytomegalovirus.
XX
SQ Sequence 26 BP; 0 A; 0 C; 17 G; 9 T; 0 other:
XX
Query Match 68.0%; Score 13.6; DB 15; Length 26;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

RESULT 12
AA079227/C
ID AA079227 standard; DNA: 26 BP.
XX
AC AA079227;
XX
DE 17-JUL-1995 (first entry)
XX

```

## RESULT 15

US-08-285-936-45/C

; Sequence 45, Application US/08285936  
; Patent No. 5728821

## ; GENERAL INFORMATION:

; APPLICANT: Yelton, Dale

; APPLICANT: Glaser, Scott

; APPLICANT: Huse, William

; APPLICANT: Rosok, Mae J.

; TITLE OF INVENTION: No. 5728821el Mutant BR96 Antibodies and

; TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merchant &amp; Gould

; STREET: 11150 Santa Monica Blvd., Suite 400

; CITY: Los Angeles

; STATE: CA

; COUNTRY: USA

; ZIP: 90025-3395

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/285,936

; FILING DATE: 04-AUG-1994

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Adriano, Sarah B.

; REGISTRATION NUMBER: 34,470

; REFERENCE/DOCKET NUMBER: 30436.16US01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 310-445-1140

; TELEFAX: 310-445-9031

; INFORMATION FOR SEQ. ID NO: 45:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 51 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-285-936-45

; Query Match 66.0%; Score 13.2; DB 1; Length 51;

; Best local Similarity 83.3%; Pred. No. 1.2e+03;

; Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

; QY 2 GAGGTGGGGTGGAGTG 19

; Db 43 GAGGTCTGCTGGAGTG 26

Search completed: November 23, 2002, 06:36:09

Job time : 22.55 secs

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STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-073-353-7

Query Match      71.0%; Score 14.2; DB 9; Length 30;
Best Local Similarity 84.2%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 GAGTGGCGGCTGAGAGTGC 20
        ||||| |||||
Db      25 GAGCTGTGCTGTGAGAGTGC 7

RESULT 2
US-09-905-291A-151
; Sequence 151, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kjaer, Jennie P.
; APPLICANT: Mather, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
```

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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 151
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-905-291A-151

Query Match      71.0%; Score 14.2; DB 9; Length 50;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 TGAGTGGCGGCTGAGAGTGC 19
        ||| | ||||| |||
Db      16 TGAGGCGCGGTGAGAGTGC 34

RESULT 3
US-09-909-320-151
; Sequence 151, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
```

PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 151  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-909-320-151

Query Match 71.0% Score 14.2; DB 10; Length 50;  
Best Local Similarity 84.2%; Pred. No. 5.3e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 TGAGTGGCGGTGGAAGTG 19  
Db 16 TGAAGCGCGGTGGAAGTG 34

RESULT 4  
US-09-909-088B-151  
Sequence 151, Application US/0909088B  
Patent No. US20020146709A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paonli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT FILING DATE: 2001-07-18  
CURRENT APPLICATION NUMBER: US/09/909,088B  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 151  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-909-088B-151

Query Match 71.0% Score 14.2; DB 10; Length 50;  
Best Local Similarity 84.2%; Pred. No. 5.3e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 TGAGTGGCGGTGGAAGTG 19  
Db 16 TGAAGCGCGGTGGAAGTG 34

RESULT 5  
US-09-820-339A-26  
Sequence 26, Application US/09820339A  
Patent No. US20020081652A1  
GENERAL INFORMATION:  
APPLICANT: FUCHS, Sara  
APPLICANT: BARCHAN, Dora  
APPLICANT: SOUBOUTON, Marianne  
TITLE OF INVENTION: RECOMBINANT FRAGMENTS OF THE HUMAN ACETYLCHOLINE RECEPTOR AND  
FILE REFERENCE: FUCHS-2A  
CURRENT APPLICATION NUMBER: US/09/820,339A  
CURRENT FILING DATE: 1999-11-08  
PRIOR APPLICATION NUMBER: 09/423,398

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;; PRIOR FILING DATE: 1999-11-08
;; PRIOR APPLICATION NUMBER: PCT/IL98/00211
;; PRIOR FILING DATE: 1998-05-06
;; NUMBER OF SEQ ID NOS: 32
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 26
;; LENGTH: 24
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic
US-09-820-339A-26

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 10; Length 24;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGGAAGTGC 20
    ||||| ||||| |||||
DB 4 TGAGTGGCGGTGAGCGTGC 23

RESULT 6
US-09-733-042-4/c
; Sequence 4, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Enh-REV
US-09-733-042-4

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 9; Length 25;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGGTGGCGGTGGAAGTGC 20
    ||||| ||||| |||||
DB 22 AGGTGGCGGTGAGGTAC 5

RESULT 7
US-09-801-274-191/c
; Sequence 191, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 31
; TYPE: DNA
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;; ORGANISM: Homo sapiens
US-09-801-274-191

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 10; Length 31;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGGAAGT 18
    ||||| ||||| |||||
DB 18 TGYGAGCGCGGTGGAAGT 1

RESULT 8
US-09-864-761-18926
; Sequence 18926, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 18926
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF060568.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.7
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OTHER INFORMATION: NE HIT: AF060568.1, EVALUE 2.00e-47  
OTHER INFORMATION: EST HUMAN HIT: AA150052.1, EVALUE 8.20e-01  
OTHER INFORMATION: SWISSPROT HIT: Q00998, EVALUE 9.20e+00  
US-09-864-761-18926

Query Match 66.0%; Score 13.2; DB 10; Length 96;  
Best Local Similarity 83.3%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGTGGCGGTGGAAGTGC 20  
||||| ||||||| ||  
Db 41 AGGTGCACGTGGAAGACC 58

RESULT 9  
US-09-764-877-3114  
Sequence 3114, Application US/09764877  
Patent No. US20020147140A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC005  
CURRENT APPLICATION NUMBER: US/09/764,877  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - refer to PALM or file wrapper  
NUMBER OF SEQ ID NOS: 4031  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 3114  
LENGTH: 100  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-764-877-3114

Query Match 66.0%; Score 13.2; DB 10; Length 100;  
Best Local Similarity 83.3%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGTGGCGGTGGAAGTG 19  
||||| ||||||| |||||  
Db 12 GAGGTGCAGGTGCGAGTG 29

RESULT 10  
US-09-873-676-70  
Sequence 70, Application US/09873676  
Patent No. US20020077289A1  
GENERAL INFORMATION:  
APPLICANT: Macdonald, Nicholas J.  
TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use  
FILE REFERENCE: 05213-0378 (43170-259333)  
CURRENT APPLICATION NUMBER: US/09/873,676  
CURRENT FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: US 60/209,065  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: US 60/289,387  
PRIOR FILING DATE: 2001-05-08  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 70  
LENGTH: 33  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: binding molecule  
US-09-873-676-70

Query Match 64.0%; Score 12.8; DB 10; Length 33;  
Best Local Similarity 87.5%; Pred. No. 2.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GTGGCGGTGGAAGTGC 20  
||||| ||||||| |||

Db 17 GTGGCGGTGGAAGTGC 32

RESULT 11  
US-09-923-876-1514  
Sequence 1514, Application US/09923876  
Patent No. US20020013958A1  
GENERAL INFORMATION:  
APPLICANT: Laigudi, Raghunath V.  
APPLICANT: Kamigaki, Laura Y. (Ito)  
APPLICANT: Sherman, Bradley K.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING  
FILE REFERENCE: PL-0012-1 CON  
CURRENT APPLICATION NUMBER: US/09/923,876  
CURRENT FILING DATE: 2001-08-06  
PRIOR APPLICATION NUMBER: 09/298,329  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/085,331  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 6332  
SOFTWARE: PERL Program  
SEQ ID NO 1514  
LENGTH: 82  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No. US20020013958A1 700158952H1  
LOCATION: 2, 12-13, 37, 51, 58, 65, 67, 81  
OTHER INFORMATION: a, t, c, g, or other  
US-09-923-876-1514

Query Match 64.0%; Score 12.8; DB 10; Length 82;  
Best Local Similarity 77.8%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGTGGCGGTGGAAGTG 19  
||||| ||||||| |||||  
Db 59 GAGGTGANGTGAGAGTG 76

RESULT 12  
US-09-755-004-10/c  
Sequence 10, Application US/09755004  
Patent No. US20020110810A1  
GENERAL INFORMATION:  
APPLICANT: Shubert, Anthony  
TITLE OF INVENTION: Methods for Detecting, Grading or Monitoring an H. pylori In  
FILE REFERENCE: EXT-048  
CURRENT APPLICATION NUMBER: US/09/755,004  
CURRENT FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 10  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: APC forward primer  
US-09-755-004-10

Query Match 63.0%; Score 12.6; DB 10; Length 20;  
Best Local Similarity 78.9%; Pred. No. 2.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGGAAGTG 19  
||||| ||||||| |||||  
Db 19 TGAGAGGTGTGTGAGAGTG 1

RESULT 13  
US-09-866-108-13254

```
; Sequence 13254, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: AeoMica Sequence Listing Engine
; SEQ ID NO 13254
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-13254

Query Match      63.0%  Score 12.6:  DB 10:  Length 25:
Best Local Similarity 78.9%:  Pred. No. 2.6e+03:
Matches 15:  Conservative 0:  Mismatches 4:  Indels 0:  Gaps 0:
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```
OY      2  GAGTGCGGGTGAAGTGC 20
        |||| || || || || || ||
DB      7  GAGGAGCTGGAGAAAGTGC 25
```

```
RESULT 14
US-09-866-108-13255
; Sequence 13255, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
```

```
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: AeoMica Sequence Listing Engine
; SEQ ID NO 13255
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-13255

Query Match      63.0%  Score 12.6:  DB 10:  Length 25:
Best Local Similarity 78.9%:  Pred. No. 2.6e+03:
Matches 15:  Conservative 0:  Mismatches 4:  Indels 0:  Gaps 0:
```

```
OY      2  GAGTGCGGGTGAAGTGC 20
        |||| || || || || || ||
DB      6  GAGGAGCTGGAGAAAGTGC 24
```

```
RESULT 15
US-09-866-108-13256
; Sequence 13256, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
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? PRIOR APPLICATION NUMBER: PCT/US01/00666
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00667
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00664
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? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 60/266,860
? PRIOR FILING DATE: 2001-02-05
? NUMBER OF SEQ ID NOS: 15752
? SOFTWARE: Acomica Sequence Listing Engine
? SEQ ID NO 13256
? LENGTH: 25
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-866-108-13256
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Query Match	63.0%	Score 12.6	DB 10	Length 25
Best Local Similarity	78.9%	Pred. No. 2.6e+03		
Matches 15; Conservative	0; Mismatches 4; Indels 0; Gaps 0;			
OY	2	GAGTGGCGGTGGAAGTGC	20	
db	5	GAGGAGCTGGAGAAAGTGC	23	

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Job time : 17.25 secs

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OM nucleic - nucleic search, using sw model

Run on: November 25, 2002, 09:10:06 : Search time 755.55 Seconds  
(without alignments)  
428.707 Million cell updates/sec

Title: US-09-296-264-9  
Sequence: 1 tgaaggtcgcgcgtgaggtgc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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EST:  
1: em\_estba:\*  
2: em\_esthm:\*  
3: em\_estln:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrc:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	14.4	72.0	75	17	BH790276 SALK-0567
3	14.2	71.0	61	12	BF507253 5923P-29
4	14.2	71.0	73	10	BE130245 L48-385T3
5	14.2	71.0	82	9	AA646813 vn37b09.r
6	14.2	71.0	86	12	BG402252 602465822

c	7	14.2	71.0	99	9	AT559239	tg32e03.x
	8	13.8	69.0	50	9	AT102737	AT102737
	9	13.6	68.0	60	17	A2982649	2M0263H04
	10	13.6	68.0	61	9	AA659447	nu24b08.s
	11	13.6	68.0	69	17	DR17P215	Dan10_rer
	12	13.6	68.0	88	9	AA500773	vg01b07.r
	13	13.6	68.0	92	14	H55398	CHR220337.C
	14	13.6	68.0	96	14	220250	HSAABRWT.P
	15	13.2	66.0	72	17	AQ248436	TTM22-Sp6
	16	13.2	66.0	73	12	BG879136	1b70h10.y
	17	13.2	66.0	76	9	A1221944	qh01a03.x
	18	13.2	66.0	84	10	AV848064	AV848064
	19	13.2	66.0	88	14	W29984	mc23d02.r1
	20	13.2	66.0	90	17	BH233613	1006174G0
	21	13.2	66.0	91	17	AF190831	AF190831
	22	13.2	66.0	95	14	BQ753757	EBca01_SQ
	23	13.2	66.0	97	9	AA097217	mk10a12.r
	24	13.2	66.0	99	9	AA704622	zf86a04.s
	25	13	65.0	19	17	A2782026	2M0021I23
	26	13	65.0	31	9	AT021071	ua99f05.r
	27	12.8	64.0	50	9	AT104342	AT104342
	28	12.8	64.0	61	9	A1877694	fc30e10.y
	29	12.8	64.0	68	13	B1763776	603049718
	30	12.8	64.0	77	10	AM022596	d41b06.y
	31	12.8	64.0	82	14	R69402	y183d10.r1
	32	12.8	64.0	96	9	AT263688	qx67h11.x
	33	12.8	64.0	96	17	TA192C04P	AL477388.T
	34	12.6	63.0	35	17	A2986475	2M0268N09
	35	12.6	63.0	43	14	T63536	yc07c10.s1
	36	12.6	63.0	47	17	A2373977	1M0126A05
	37	12.6	63.0	47	17	A2949602	2M0213H20
	38	12.6	63.0	48	17	A2496155	1M0332K15
	39	12.6	63.0	49	14	R53501	yj70d10.r1
	40	12.6	63.0	50	9	AU106147	AU106147
	41	12.6	63.0	57	17	A2344037	1M0077A19
	42	12.6	63.0	58	17	AL758979	AREb1d0ps
	43	12.6	63.0	67	12	BG892810	de56e02.y
	44	12.6	63.0	68	17	A2660373	1M0538K22
	45	12.6	63.0	69	9	AA215059	mu97e04.r

## ALIGNMENTS

RESULT 1  
LOCUS AT198185 100 bp mRNA EST 02-DEC-1998  
DEFINITION g151f03.x1 NCI\_CGAP\_Brn25 Homo sapiens CDNA clone IMAGE:1860029 3',  
mRNA sequence.  
ACCESSION AT198185  
VERSION AT198185.1 GI:3750791  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 100)  
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CCAP/BRGAP), Tumor Gene Index  
UNPUBLISHED (1998)  
CONTACT: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonalio, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.lnl.gov/bdrrp/image/image.html

Insert Length: 1236    Std Error: 0.00  
Seq primer: -40UP from GIBCO  
High quality sequence stop: 82.

BASE COUNT	35 a	13 c	31 g	21 t
ORIGIN				

RESULT 2	LOCUS	DEFINITION
BH790276	BH790276	75 bp DNA linear GSS 02-Apr-2002
		SALK_056721.50.40.x Arabidopsis thaliana RNA insertion lines
		Arabidopsis thaliana genomic clone SALK_056721.50.40.x, DNA
		sequence.

BASE COUNT      19 a      11 c      25 g      20 t

ORIGIN

directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at <http://signal.salk.edu/ttna-protocols.html>"

Query Match	72.0%	Score 14.4	DB 17	Length 75
Best Local Similarity	93.8%	Pred. No. 5	2e+04	
Matches 15; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0
Qy	4	GGTGGGGGTGCAAGTC	19	
Db	45	GGTGGGGGTGCAAGTC	60	

RESULT	3
LOCUS	BF507253
DEFINITION	BF507253 61 bp mRNA linear EST 07-DEC-2001 593P-29, Pooled green leaf and root tissue Sorghum bicolor cDNA clone 5923P-29, mRNA sequence.
ACCESSION	BF507253
VERSION	BF507253.1 GI:1159051
KEYWORDS	EST.
SOURCE	Sorghum, bicolor
ORGANISM	Sorghum bicolor [Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheobionta; Equisetopsida; Poales; Poaceae]

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
SOURCE

1 (bases 1 to 61)  
Childs,K.L., Klein,R.R., Klein,P.E., Morishige,D.T. and Mullet,J.E  
Mapping Genes on an Integrated Sorghum Genetic and Physical Map  
Using cDNA Selection Technology  
Unpublished (2001)  
Contact: Kevin Childs  
Department of Biochemistry and Biophysics  
Texas A&M University  
College Station, TX 77843, USA  
Tel: 979 845 0832  
Fax: 979 862 4718  
Email: kchilds@unix.tamu.edu  
location/qualifiers  
1..61

```

/organism="Sorghum bicolor"
/cultivar="BRx623"
/db_xref="taxon:4558"
/clone="5923P-29"
/clone_1bp="Pooled green leaf and root tissue"
/tissue_type="green leaf and root tissue"
/notes="Vector: pBluescript II (SK); Site_1: EcoRI; Site_2:
EcoRI"

```

RESULT 4	LOCUS	DEFINITION	ACCESION	VERSION	KEYWORDS	SOURCE	ORGANISM
BEI30245	BEI30245	73 bp mRNA linear EST 20-FEB-2001	BEI30245	BEI30245.1	GI:8577608	common iceplant	Mesembryanthemum crystallinum
		L48-385T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours NCI treatment Mesembryanthemum crystallinum CDNA clone L48-385 5', mRNA sequence.					

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Alzaceae; Mesembryanthemum. 1 (bases 1 to 73)

Cushman, J.C.  
An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum  
Unpublished (1997)  
Contact: Cushman JC  
Department of Biochemistry  
University of Nevada  
MS200, Reno, NV 89557-0014, USA  
Tel: 775-784-1918  
Fax: 775-784-1650  
Email: jcushman@unr.edu

PCR Primers  
FORWARD: T7  
BACKWARD: T3  
Plate: L48-4 row: H column: 1  
Seq primer: T3  
High quality sequence stop: 73  
POLYA-No.  
Location/Qualifiers

FEATURES  
SOURCE

1. .73  
/organism="Mesembryanthemum crystallinum"  
/db\_xref="taxon:3544"  
/clone="L48-385"  
/clone\_lib="ice plant Lambda Uni-Zap XR expression library", 48 hours NaCl treatment"  
/tissue\_type="Leaf, 48 h 0.4M NaCl"  
/dev\_stage="Six week old"  
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"  
BASE COUNT 16 a 6 c 30 g 21 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 10; Length 73;  
Best Local Similarity 84.2%; Pred. No. 6.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TGAGTCGGGTGGAAGTG 19  
|||||  
Db 42 TGAAGTCGGGTGGAATG 60

RESULT 5  
AA646813/c 82 bp mRNA linear EST 28-OCT-1997  
LOCUS vn37b09.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone  
DEFINITION IMAGE:1023353 5' similar to SW:ANXA\_RABIT P33477 ANNEXIN XI ;, mRNA  
sequence.  
AA646813  
VERSION AA646813.1 GI:2573242  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 82)  
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., and Waterston, R.  
The Washu-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Maria M/Mouse EST Project  
Washu-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. MGI:574129  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28ml3 rev1 ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
SOURCE

1. .82  
/organism="Mus musculus"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1023353"  
/clone\_lib="Stratagene mouse skin (#937313)"  
/sex="females"  
/tissue\_type="whole skin"  
/dev\_stage="11 weeks old"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: skin; Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-Zap XR Vector: -5' adaptor sequence: 5' GAATTCGACACGAG 3' -3' adaptor sequence: 5' CTCGACGTTTTTTTTTTTTTTT 3'."  
BASE COUNT 19 a 25 c 18 g 20 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 9; Length 82;  
Best Local Similarity 84.2%; Pred. No. 6.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TGAGTCGGGTGGAAGTG 19  
|||||  
Db 41 TGAGAGCCGCTGGAAGTG 23

RESULT 6  
BG402252 86 bp mRNA linear EST 12-MAR-2001  
LOCUS 602465822F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4593941 5',  
DEFINITION mRNA sequence.  
BG402252  
VERSION BG402252.1 GI:13295700  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 86)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs@remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LCM1334 row: 1 column: 06  
High quality sequence stop: 42.  
Location/Qualifiers

FEATURES  
SOURCE

1. .86  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4593941"  
/clone\_lib="NIH\_MGC\_75"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggcgctcgcc); Site\_2: SfiI (ggcgctatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGCGC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech laboratories (Palo Alto, CA). Note: this is a NIH\_MGC library."

BASE COUNT 20 a 11 c 23 g 32 t

Query Match 71.0%; Score 14.2; DB 12; Length 86;

Best Local Similarity 84.2%; Pred. No. 6.2e+04; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 3;

QY 1 TGAGGTGGCGGTGGAAGTG 19  
||||| |||||||

Db 45 TGAGGTGATGTGGAAAGTG 63

RESULT 7  
AI559239/c 99 bp mRNA linear EST 24-MAR-1999

LOCUS tq32e03.x1 NCI\_CGAP utl Homo sapiens cDNA clone IMAGE:2210524 3'

DEFINITION similar to gb:X77738.rnal BAND 3 ANION TRANSPORT PROTEIN (HUMAN);,  
mRNA sequence.

ACCESSION AI559239 GI:4509444

VERSION AI559239

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 99)

AUTHORS NCI-CGAP

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Journal Tumor Gene Index

COMMENT Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapdb-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40bp from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..99

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2210524"

/clone\_lib="NCI\_CGAP-utl"

/tissue\_type="well-differentiated endometrial

adenocarcinoma, 7 pooled tumors"

/lab\_host="DH10B"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1; Salt;

Site: 2; Note: Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Life Technologies catalog #:

11538-014"

BASE COUNT 12 a 25 c 30 g 31 t 1 others

ORIGIN

Query Match 71.0%; Score 14.2; DB 9; Length 99;

Best Local Similarity 84.2%; Pred. No. 6.2e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGGTGGCGGTGGAAGTG 20

||||| ||| |||||||

Db 88 GAGGTGGCGGTGGAAGTG 70

RESULT 8  
AU102737 50 bp mRNA linear EST 30-AUG-2001

DEFINITION AU102737 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

LOCUS HEP13330, mRNA sequence.

ACCESSION AU102737.1 GI:13552258

VERSION AU102737

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata

,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki

,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

CONTACT: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano

,S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

Location/Qualifiers

1..50

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="HEP13330"

/clone\_lib="Sugano Homo sapiens cDNA library"

/note="Differential display comparison of untreated and

dimethylfumarate treated U937 cells"

BASE COUNT 7 a 14 c 19 g 10 t

ORIGIN

Query Match 69.0%; Score 13.8; DB 9; Length 50;

Best Local Similarity 88.2%; Pred. No. 8.8e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGGTGGCGGTGGAAGTG 19

||||| |||||||

Db 1 AGGTGGCGGTGGAAGTG 17

RESULT 9

LOCUS AZ982649 60 bp DNA linear GSS 27-APR-2001

DEFINITION 2M0263HH04R Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0263HH04 R, DNA sequence.

ACCESSION AZ982649

VERSION AZ982649.1 GI:13853876

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 60)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Relilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah







Clinical Research Centre  
 Watford Road, Harrow, Middlesex HA1 3UJ, U.K.  
 Email: biophelp@hmp.mrc.ac.uk  
 single read.

## FEATURES

source

Location/Qualifiers  
 1. .96

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"

/clone\_lib="P", Human foetal Brain Whole tissue"

/note="Vector: Bluescript; clone\_library=P, Human foetal  
 Brain Whole tissue; cloning vector is Bluescript."

## BASE COUNT

26 a 29 c 22 g 17 t 2 others

## ORIGIN

## Query Match

68.0%; Score 13.6; DB 14; Length 96;

Best Local Similarity 80.0%; Pred. No. 1.1e+05;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TGAGTCGCGGTGAGAGTC 20

Db 40 TGAGTCGCGGTGAGAGGC 21

## RESULT 15

AQ248436 72 bp DNA linear GSS 06-OCT-1998

LOCUS T7M22-SP6 T7MU Arabidopsis thaliana genomic clone T7M22, DNA

DEFINITION

sequence.

ACCESSION AQ248436

VERSION AQ248436.1

KEYWORDS GI:3698519

SOURCE

ORGANISM

thale cress.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 72)

Peng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and

Ecker, J.

BAC End Sequences at ATGC

Unpublished (1997)

Contact: Ecker J.

Arabidopsis Thaliana Genome Center

Dept. of Biology, University of Pennsylvania, Philadelphia, PA

19104

Tel: 215-898-9384

Fax: 215-898-8780

Email: jecker@atgenom.bio.upenn.edu

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1. .72

/organism="Arabidopsis thaliana"

/strain="Columbia"

/db\_xref="taxon:3702"

/clone="T7M22"

/clone\_lib="T7MU"

/sex="hermaphrodite"

/note="Vector: BelOAPCII; Site\_1: HindIII; Site\_2: HindIII

; Produced by Rod Wing"

BASE COUNT

8 a 39 c 4 g 21 t

## ORIGIN

## Query Match

66.0%; Score 13.2; DB 17; Length 72;

Best Local Similarity 83.3%; Pred. No. 1.5e+05;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GAGTCGCGGTGAGAGTG 19

Db 61 GAGTCGCGGTGAGAGG 44

Search completed: November 26, 2002, 04:07:48  
 Job time : 766.8 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: December 3, 2002, 14:46:40 : Search time 302.2 Seconds  
(without alignments)  
1926.063 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20

Sequence: 1 gtcgcgacgtggaccacaga 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pal:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pin:\*  
35: em\_htg\_mam:\*  
36: em\_htg\_rod:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_higo\_hum:\*  
40: em\_higo\_mus:\*  
41: em\_higo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.6	88.0	21	6	AX097265
C 2	13.8	69.0	27	6	AX188785
C 3	13.6	68.0	27	6	A98650
C 4	13.6	68.0	51	6	AX162818
C 5	13.2	66.0	27	6	AX002713
C 6	13.2	66.0	33	6	AR127237
C 7	13.2	66.0	33	6	AR127238
C 8	13.2	66.0	35	6	AX358674
C 9	13.2	66.0	35	6	AX358675
C 10	13.2	66.0	44	6	AR143578
C 11	13.2	66.0	44	6	AR168947
C 12	13.2	66.0	90	9	HSEXT82
C 13	12.8	64.0	22	6	E11187
C 14	12.8	64.0	24	6	AX019309
C 15	12.8	64.0	25	6	AR065111
C 16	12.8	64.0	25	6	E09880
C 17	12.8	64.0	30	9	HUMPLTP12
C 18	12.8	64.0	48	6	A97298
C 19	12.8	64.0	53	6	E11189
C 20	12.8	64.0	62	6	AR127979
C 21	12.8	64.0	70	6	E03982
C 22	12.8	64.0	100	10	RATMAL01
C 23	12.6	63.0	20	6	AR121581
C 24	12.6	63.0	30	6	AX173016
C 25	12.6	63.0	30	6	AX173171
C 26	12.6	63.0	30	6	AX174698
C 27	12.6	63.0	45	6	AR168071
C 28	12.6	63.0	45	6	AR204842
C 29	12.6	63.0	51	6	AX162807
C 30	12.6	63.0	51	6	AX162817
C 31	12.6	63.0	51	6	AX162819
C 32	12.6	63.0	51	6	AX162820
C 33	12.6	63.0	83	9	HSRNP72515
C 34	12.6	63.0	84	10	S56855
C 35	12.6	63.0	92	9	HUMPK30
C 36	12.4	62.0	50	6	AX159092
C 37	12.4	62.0	50	6	AX427051
C 38	12.4	62.0	51	6	AX427050
C 39	12.4	62.0	80	10	MMDNDS9
C 40	12.2	61.0	19	6	AX132262
C 41	12.2	61.0	20	6	AR206645
C 42	12.2	61.0	20	6	AR206646
C 43	12.2	61.0	23	6	AR137741
C 44	12.2	61.0	30	6	A95831
C 45	12.2	61.0	34	6	AR108658

## ALIGNMENTS

RESULT 1  
AX097265 21 bp DNA linear PAT 30-MAR-2001  
LOCUS Sequence 2443 from Patent WO0118250.  
DEFINITION AX097265  
ACCESSION AX097265 GI:13513682  
VERSION  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 21)  
Lander, E.S., Gargill, M., Ireland, J.S., Bolik, S., Daley, G.O. and  
McCarthy, J.J.  
TITLE Single nucleotide polymorphisms in genes

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JOURNAL Patent: WO 0118250-A 2443 15-MAR-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium  
Pharmaceuticals, Inc. (US)  
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source 1..21  
Location/Qualifiers  
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BASE COUNT 3 a 8 c 5 g 4 t 1 others  
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Best Local Similarity 94.4%; Pred. No. 1.8e+02;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCCGACGTGGAGCCCA 18  
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Db 18 GTGCCGACGTGGAGCCCA 1

RESULT 2  
AX188785 27 bp DNA linear PAT 08-AUG-2001  
LOCUS  
DEFINITION Sequence 32 from Patent WO0148228.  
ACCESSION AX188785  
VERSION AX188785.1 GI:15142326  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequences.  
REFERENCE  
AUTHORS 1 (bases 1 to 27)  
Chater,K.F., Bruton,C.J., O'Rourke,S.J. and Wietzorrek,A.W.  
TITLE Methods and materials relating to gene expression  
JOURNAL Patent: WO 0148228-A 32 05-JUL-2001;  
Plant Bioscience Limited (GB)  
FEATURES  
source 1..27  
Location/Qualifiers  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer"  
BASE COUNT 3 a 12 c 9 g 3 t  
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Best Local Similarity 88.2%; Pred. No. 1.7e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GCCGACGTGGAGCCAG 19  
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Db 3 GCCGACGTGGAGCCAG 19

RESULT 3  
A98650 27 bp DNA linear PAT 26-JAN-2000  
LOCUS  
DEFINITION Sequence 6 from Patent WO910500.  
ACCESSION A98650  
VERSION A98650.1 GI:6781694  
KEYWORDS  
SOURCE  
ORGANISM  
unidentified.  
unclassified.  
REFERENCE  
AUTHORS 1 (bases 1 to 27)  
Schlichter,U. and Steinbiss,H.  
TITLE NUCLEIC ACID MOLECULES CODING FOR A CYSTEINE PROTEINASE OF PLANT  
ORIGIN AND THEIR REGULATING REGIONS  
JOURNAL Patent: WO 9910500-A 6 04-MAR-1999;  
MAX PLANCK GESELLSCHAFT (DE); SCHLICHTER URSULA (DE)  
FEATURES  
source 1..27  
Location/Qualifiers  
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/db\_xref="taxon:32644"  
BASE COUNT 6 a 6 c 11 g 4 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 27;  
Best Local Similarity 80.0%; Pred. No. 2.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 6 GTGTGGACCTGGAGCCAGA 25

RESULT 4  
AX162818 51 bp DNA linear PAT 22-JUN-2001  
LOCUS  
DEFINITION Sequence 6146 from Patent WO0140521.  
ACCESSION AX162818  
VERSION AX162818.1 GI:14544149  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 51)  
Shinkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0140521-A 6146 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES  
source 1..51  
Location/Qualifiers  
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misc\_feature 26  
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Accession number cg44914955"  
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Db 45 GTTCAGACGTGGGTGCAGCA 26

RESULT 5  
AX002713 27 bp DNA linear PAT 21-AUG-2000  
LOCUS  
DEFINITION Sequence 5 from Patent WO9900490.  
ACCESSION AX002713  
VERSION AX002713.1 GI:9885040  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequences.  
REFERENCE  
AUTHORS 1 (bases 1 to 27)  
Wainberg,M.A.  
TITLE Attenuated human immunodeficiency virus vaccine  
JOURNAL Patent: WO 9900490-A 5 07-JAN-1999;  
WAINBERG MARK A (CA); SIR MORTIMER B DAVIS JEWISH GE (CA)  
FEATURES  
source 1..27  
Location/Qualifiers  
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/db\_xref="taxon:32630"  
BASE COUNT 3 a 7 c 11 g 6 t  
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Best Local Similarity 83.3%; Pred. No. 3.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 GCCGACGTGGAGCCAGA 20

RESULT 6  
AF090124 78 bp mRNA linear INV 07-OCT-1998  
LOCUS Helix aspersa shaw-like potassium channel Kv3.1 (Kv3.1) mRNA,  
DEFINITION partial cds.  
ACCESSION AF090124  
VERSION AF090124.1 GI:3703091  
KEYWORDS  
SOURCE Helix aspersa.  
ORGANISM Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;  
Stylommatophora; Helicacea; Helicidae; Helix.  
REFERENCE 1 (bases 1 to 78)  
AUTHORS Witcheh,H.J., Davies,D. and Meech,R.W.  
TITLE Immunological identification of a putative potassium channel  
subunit from a short (9) amino acid sequence  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 78)  
AUTHORS Witcheh,H.J., Davies,D. and Meech,R.W.  
TITLE Direct Submission  
JOURNAL Submitted (03-SEP-1998) Physiology, Medical School, University of  
Bristol, Bristol BS8 1TD, England  
FEATURES  
source 1..78  
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CDS <1..>78  
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Best Local Similarity 93.3%; Pred. No. 5.1e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 3 TGGGCGCCCTGTGCC 17  
Db 36 TGGGCGCCCTGTGCC 50

RESULT 7  
ARI63949/c 20 bp DNA linear PAT 17-OCT-2001  
LOCUS ARI63949  
DEFINITION Sequence 147 from patent US 6271030.  
ACCESSION ARI63949  
VERSION ARI63949.1 GI:16234807  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monla,B.P., Butler,M.M. and Wyatt,J.  
TITLE Antisense inhibition of C/EBP beta expression  
JOURNAL Patent: US 6271030-A 147 07-AUG-2001;  
FEATURES  
source 1..20  
/organism="unknown"  
BASE COUNT 6 a 7 c 6 g 1 t  
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Query Match 66.0%; Score 13.2; DB 6; Length 20;  
Best Local Similarity 83.3%; Pred. No. 7.2e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2 ATGGCGCCCTGTGCCG 19

Db 20 ATGGCGCCCTGTGCCG 3  
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RESULT 8  
AX326934/c 20 bp DNA linear PAT 07-JAN-2002  
LOCUS AX326934  
DEFINITION Sequence 130 from Patent WO0178894.  
ACCESSION AX326934  
VERSION AX326934.1 GI:18097645  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Keith,T.  
TITLE Novel human gene relating to respiratory diseases, obesity, and  
inflammatory bowel disease  
JOURNAL Patent: WO 0178894-A 130 25-OCT-2001;  
Genome Therapeutics Corp. (US)  
FEATURES  
source 1..20  
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/note="Primer"  
BASE COUNT 7 a 3 c 7 g 3 t  
ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 20;  
Best Local Similarity 83.3%; Pred. No. 7.2e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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Db 18 AATGGTCCTGTGCC 1

RESULT 9  
A60217 34 bp DNA linear PAT 06-MAR-1998  
LOCUS A60217  
DEFINITION Sequence 13 from Patent WO9708330.  
ACCESSION A60217  
VERSION A60217.1 GI:3715225  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 34)  
AUTHORS Collins,M.K., Weiss,R.A., Takeuchi,Y. and Cosset,F.  
TITLE EXPRESSION SYSTEMS  
JOURNAL Patent: WO 9708330-A 13 06-MAR-1997;  
CANCER RES CAMPAIGN TECH (GB)  
FEATURES  
source 1..34  
/organism="unidentified"  
/db\_xref="taxon:32644"  
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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Db 5 ATGGCGCCCTATGCGTCG 22  
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RESULT 10  
ARI22293 34 bp DNA linear PAT 16-MAY-2001  
LOCUS ARI22293  
DEFINITION Sequence 13 from patent US 6165715.  
ACCESSION ARI22293

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VERSION      AR122293.1 GI:14106610
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 34)
AUTHORS     Collins,M,Katherine,Levinge., Weiss,R,Anthony., Takeuchi,Y. and
            Cosset,F.-L.
TITLE       Expression systems
JOURNAL     Patent: US 6165715-A 13 26-DEC-2000;
FEATURES    Location/Qualifiers
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Best Local Similarity 83.3%; Pred. No. 6.9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGGCGCCCTGTGTCCCG 19
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Db 5 ATGGCGCCCTATGCGCTCG 22

RESULT 11
LOCUS       AR135209 40 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 35 from patent US 6194559.
ACCESSION  AR135209
VERSION     AR135209.1 GI:14124114
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 40)
AUTHORS     Kim,S,Young.
TITLE       Abscisic acid responsive element-binding transcription factors
JOURNAL     Patent: US 6194559-A 35 27-FEB-2001;
FEATURES    Location/Qualifiers
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ORIGIN
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Best Local Similarity 83.3%; Pred. No. 6.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTGGCGCCCTGTGTCCCGA 20
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Db 26 TTGGCGCCACGTGTCCCGA 9

RESULT 12
LOCUS       AR146705 40 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 35 from patent US 6218527.
ACCESSION  AR146705
VERSION     AR146705.1 GI:15109894
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 40)
AUTHORS     Kim,S,Young.
TITLE       Nucleic acid molecule encoding abscisic acid responsive
            element-binding factor 3
JOURNAL     Patent: US 6218527-A 35 17-APR-2001;
FEATURES    Location/Qualifiers
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BASE COUNT   9 a          11 c          14 g          6 t
ORIGIN

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ORIGIN
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Best Local Similarity 83.3%; Pred. No. 6.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTGGCGCCCTGTGTCCCGA 20
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Db 26 TTGGCGCCACGTGTCCCGA 9

RESULT 13
LOCUS       AR152276 40 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 35 from patent US 6232461.
ACCESSION  AR152276
VERSION     AR152276.1 GI:15118326
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 40)
AUTHORS     Kim,S,Young.
TITLE       Nucleic acid molecule encoding abscisic acid responsive
            element-binding factor 4
JOURNAL     Patent: US 6232461-A 35 15-MAY-2001;
FEATURES    Location/Qualifiers
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BASE COUNT   9 a          11 c          14 g          6 t
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Query Match 66.0%; Score 13.2; DB 6; Length 40;
Best Local Similarity 83.3%; Pred. No. 6.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 26 TTGGCGCCACGTGTCCCGA 9

RESULT 14
LOCUS       AR157814 40 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 35 from patent US 6245905.
ACCESSION  AR157814
VERSION     AR157814.1 GI:16218827
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 40)
AUTHORS     Kim,S,Young.
TITLE       Nucleic acid molecule encoding abscisic acid responsive
            element-binding factor 2
JOURNAL     Patent: US 6245905-A 35 12-JUN-2001;
FEATURES    Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 26 TTGGCGCCACGTGTCCCGA 9

RESULT 15
HSA403877

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**LOCUS** HSA403877 45 bp mRNA linear PRI 24-MAY-2000  
**DEFINITION** Homo sapiens partial mRNA for histone specific T-cell receptor beta chain, V-D-J region (TCRBV12.1-J1.2 gene).  
**ACCESSION** AJ403877  
**VERSION** AJ403877.1 GI:8217172  
**KEYWORDS** diversity region; joining segment; T-cell receptor beta; TCR beta chain; TCRBV12.1-J1.2 gene; variable region.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
**REFERENCE** 1 (bases 1 to 45)  
**AUTHORS** Andreassen, K., Bendixsen, S., Moens, U., Van Ghelue, M. and Rekvig, O.  
**TITLE** Comparison of precursor frequencies and receptor structures of histone specific T cells from SLE patients and from normal individuals reveals no major differences  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 45)  
**AUTHORS** Andreassen, K.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (03-MAY-2000) Andreassen K., Molecular Genetics, Medical Biology, University of Tromsøe, Mh, 9037 Tromsøe, NORWAY  
**FEATURES** Location/Qualifiers  
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 /rearranged  
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 BASE COUNT 10 a 16 c 12 g 7 t  
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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4	13.8	69.0	44	21	AAA47032
5	13.8	69.0	45	21	AAA47033
6	13.6	68.0	30	22	AAAD21726
7	13.6	68.0	47	21	AAZ69022
8	13.6	68.0	65	24	ABN58471
9	13.4	67.0	31	22	AAI30331

10	13.4	67.0	33	22	AAH44305
11	13.4	67.0	90	24	ABK36795
12	13.2	66.0	20	24	ABL94381
13	13.2	66.0	34	18	AAT90699
14	13.2	66.0	40	22	AAAD14566
15	13.2	66.0	40	22	AAAD07861
16	13.2	66.0	40	22	AAAD08929
17	13.2	66.0	40	22	AAAD08929
18	13.2	66.0	40	22	AAAD08929
19	13.2	66.0	40	22	AAAD08929
20	13.2	66.0	48	15	AAO58903
21	12.8	64.0	21	13	AAQ22357
22	12.8	64.0	21	13	AAQ22382
23	12.8	64.0	21	16	AAQ11952
24	12.8	64.0	21	16	AAQ12015
25	12.8	64.0	21	16	AAQ12015
26	12.8	64.0	21	19	AAQ17869
27	12.8	64.0	21	19	AAQ17869
28	12.8	64.0	31	16	AAQ16888
29	12.8	64.0	31	19	AAQ16700
30	12.8	64.0	31	20	AAQ39267
31	12.8	64.0	53	19	AAQ70985
32	12.8	64.0	53	21	AAQ00045
33	12.8	64.0	57	18	AAQ70206
34	12.8	64.0	60	24	ABN43652
35	12.6	63.0	27	21	AAQ17586
36	12.6	63.0	60	24	ABN37294
37	12.6	63.0	60	24	ABN40783
38	12.6	63.0	60	24	ABN44841
39	12.6	63.0	65	24	ABN52637
40	12.6	63.0	72	18	AAQ68554
41	12.6	63.0	90	24	ABK36689
42	12.6	63.0	93	13	AAQ27938
43	12.4	62.0	41	22	AAH73403
44	12.4	62.0	51	22	AAI27440
45	12.4	62.0	51	22	AAI28285

## ALIGNMENTS

RESULT 1  
ID: AAZ31437 standard; DNA: 20 BP.

AC: AAZ31437;

DE: 07-FEB-2000 (first entry)

XX: Human neurotrophin mRNA specific antisense oligo CT13607.

KW: Neurotrophin; human; growth; metastasis; tumor; neovascularisation;  
cancer; papilloma; diabetic retinopathy; antisense; ss.

OS: Synthetic.

XX: Homo sapiens.

PN: W09955855-A2.

PD: 04-NOV-1999.

PF: 23-APR-1999; 99WO-CA00324.

PR: 23-APR-1998; 98US-0082791.

(GENE-) GENENSENSE TECHNOLOGIES INC.

Wright JA, Young AH, Lee YS;  
WPI; 2000-023357/02.

Antisense oligonucleotides that inhibit neurotrophin expression, useful  
for treating cancer -

XX Claim 4; Page 16; 57pp; English.  
PS  
XX  
CC Sequences AA231431-460 represent antisense oligonucleotides which  
CC inhibit human neuropilin expression. The antisense oligonucleotides can  
CC be used to inhibit the growth or metastasis of a mammalian tumor and  
CC inhibit neovascularisation. The oligonucleotides may be used to treat  
CC various forms of cancers or tumors, such as sarcomas, melanomas,  
CC adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell  
CC carcinomas of the mouth, throat, larynx and lung, genitourinary cancers  
CC such as cervical and bladder cancer, hematopoietic cancers, colon cancer,  
CC breast cancer, pancreatic cancer, renal cancer, brain cancer, skin  
CC cancer, liver cancer, head and neck cancers, and nervous system cancers,  
CC as well as benign lesions such as papillomas. The methods may be used to  
CC treat neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration.  
XX  
SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 other;  
  
Query Match 100.0%; Score 20; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AATGGCGCCGTGTCCCGA 20  
Db 1 AATGGCGCCGTGTCCCGA 20  
|||||  
  
RESULT 2  
AAQ92990  
ID AAQ92990 standard; DNA; 25 BP.  
AC AAQ92990;  
XX  
XX  
DT 02-APR-1996 (first entry)  
XX  
DE Pre-Invasive human breast cancer marker gene PCR primer.  
KW BRCAl; breast cancer; diagnosis; prognosis; gene therapy;  
KW non-comedo DCIS; ductal carcinoma in situ; intraductal carcinoma;  
KW pre-invasive human breast tissue; marker gene; RT-PCR; primer;  
KW randomly selected; ss.  
XX  
OS Synthetic.  
XX  
XX W09519369-A1.  
PN  
XX  
PD 20-JUL-1995.  
XX  
PF 17-JAN-1995; 95WO-US00608.  
XX  
PR 17-JAN-1995; 95US-0373799.  
PR 14-JAN-1994; 94US-0182961.  
XX  
PA (UYVA-) UNIV VANDERBILT.  
XX  
PI Holt JT, Jensen RA, Obermiller PS, Page DL, Robinson-Benton CL,  
PI Thompson ME;  
XX  
DR WPI; 1995-269208/35.  
XX  
PT Detection, diagnosis and treatment of pre-invasive breast cancer  
PT by identifying differentially expressed marker genes, also use of  
PT BRCAl gene in therapy of breast cancer.  
XX  
PS Claim 13; Page 106; 149pp; English.  
XX  
CC In a novel method, differentially expressed cDNA clones are  
CC identified by comparing cDNA obtained from abnormal breast tissue  
CC (e.g. ductal carcinoma in situ (DCIS)) samples with those obtained  
CC from normal breast epithelial cells. Such clones are useful as  
CC marker genes for pre-invasive human breast tissue. In a prefd.  
CC version of the method, differential expression of the marker gene

CC is confirmed by using PCR amplification. The present sequence is  
CC that of a randomly selected PCR primer for use in the amplification.  
XX  
SQ Sequence 25 BP; 4 A; 8 C; 8 G; 5 T; 0 other;  
  
Query Match 71.0%; Score 14.2; DB 16; Length 25;  
Best Local Similarity 84.2%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 ATGGCGCCGTGTCCCGA 20  
Db 3 ATGGCGTCCTATAACCGA 21  
|||||  
  
RESULT 3  
AAH44307  
ID AAH44307 standard; DNA; 41 BP.  
AC AAH44307;  
XX  
XX  
DT 25-SEP-2001 (first entry)  
XX  
DE Human fibrinogen 9 probe SEQ ID NO:8.  
XX  
XX Human; fibrinogen 9; cytosolic; haemostatic; antiinflammatory;  
KW immunomodulatory; virucide; malignant tumour; haemopathy;  
KW HIV infection; immunological disease; inflammation; probe; ss.  
XX  
OS Homo sapiens.  
XX  
XX W0200148196-A1.  
PN  
XX  
PD 05-JUL-2001.  
XX  
PF 18-DEC-2000; 2000MO-CN00611.  
XX  
PR 24-DEC-1999; 99CN-0125762.  
XX  
PA (BIOW-) B10WINDOW GENE DEV LTD SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2001-418278/44.  
XX  
XX Fibrinogen 9 and encoded polynucleotide, applicable in diagnosis and  
PT treatment of malignant tumor, hemopathy, HIV infection, immunological  
PT diseases and various inflammations -  
XX  
PS Example 7; Page 14; 27pp; Chinese.  
XX  
XX The present sequence represents a probe for human fibrinogen 9.  
CC Human fibrinogen 9 has cytosolic, haemostatic, antiinflammatory,  
CC immunomodulatory and virucide activities. The human fibrinogen 9 protein  
CC and polynucleotide sequences are applicable in the diagnosis and  
CC treatment of malignant tumour, haemopathy, HIV infection, immunological  
CC diseases and various inflammations.  
XX  
SQ Sequence 41 BP; 11 A; 9 C; 11 G; 10 T; 0 other;  
  
Query Match 69.0%; Score 13.8; DB 22; Length 41;  
Best Local Similarity 88.2%; Pred. No. 2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 GGGCGCCGTGTCCCGA 20  
Db 8 GGAGCCCTGTGTCCCGA 24  
|||||  
  
RESULT 4  
AAA47032  
ID AAA47032 standard; DNA; 44 BP.  
XX  
AC AAA47032;

XX 03-OCT-2000 (first entry)  
 XX PCR primer used to introduce mutations S19A/S23A in TRIP.  
 DE Human: IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen;  
 KW PCR primer; ss.  
 XX Homo sapiens.  
 OS WO200039308-A1.  
 PN 06-JUL-2000.  
 PD 24-DEC-1999; 99MO-JP07286.  
 XX 24-DEC-1998; 98GB-0028704.  
 PR (GLAX ) GLAXO WELLCOME KK.  
 PA Takemoto Y, Sakai Y, Hashimoto Y;  
 PI WPI; 2000-475700/41.  
 DR New IKK3 kinase protein and nucleotides encoding it, useful for  
 XX screening for IKK3 protein modulators for treating inflammation, e.g.  
 PT arthritis, atopic dermatitis or systemic lupus erythematosus  
 CC Example 1; Page 17; 102pp; English.  
 PS PCR primers AAA47032-33 were used to modify DNA encoding a human  
 CC TRIP9. The specification describes an IKK3 protein. The protein  
 CC is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein  
 CC is useful for screening for agents with anti-inflammatory activity.  
 CC Compounds which exhibit IKK3 kinase modulating activity may be used  
 CC in formulating a treatment or prophylaxis of a disorder responsive  
 CC to the modulation of IKK3 kinase activity in a mammal. The proteins,  
 CC their variants or fragments, derivatives, analogues or cells  
 CC expressing them can also be used as immunogens to produce antibodies  
 CC against IKK3 protein, which may further be used to locate the protein  
 CC in tissues expressing that protein.  
 XX Sequence 44 BP; 6 A; 14 C; 18 G; 6 T; 0 other;  
 SQ

Query Match 69.0%; Score 13.8; DB 21; Length 44;  
 Best Local Similarity 88.2%; Pred. No. 2e+03; Mismatches 0; Gaps 0;  
 Matches 15; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 4 GGCCTGTGTCCCGA 20  
 ||||||| |||||  
 Db 24 GGCCTGTGTCCCGA 40

RESULT 5  
 AAA47033/c  
 ID AAA47033 standard; DNA; 45 BP.  
 XX AAA47033;  
 AC 03-OCT-2000 (first entry)  
 DT PCR primer used to introduce mutations S19A/S23A in TRIP9.  
 DE Human: IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen;  
 KW PCR primer; ss.  
 XX Homo sapiens.  
 OS WO200039308-A1.  
 PN 06-JUL-2000.  
 PD 24-DEC-1999; 99MO-JP07286.

XX 24-DEC-1998; 98GB-0028704.  
 PR (GLAX ) GLAXO WELLCOME KK.  
 PA Takemoto Y, Sakai Y, Hashimoto Y;  
 PI WPI; 2000-475700/41.  
 DR New IKK3 kinase protein and nucleotides encoding it, useful for  
 XX screening for IKK3 protein modulators for treating inflammation, e.g.  
 PT arthritis, atopic dermatitis or systemic lupus erythematosus  
 CC Example 1; Page 17; 102pp; English.  
 PS PCR primers AAA47032-33 were used to modify DNA encoding a human  
 CC TRIP9. The specification describes an IKK3 protein. The protein  
 CC is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein  
 CC is useful for screening for agents with anti-inflammatory activity.  
 CC Compounds which exhibit IKK3 kinase modulating activity may be used  
 CC in formulating a treatment or prophylaxis of a disorder responsive  
 CC to the modulation of IKK3 kinase activity in a mammal. The proteins,  
 CC their variants or fragments, derivatives, analogues or cells  
 CC expressing them can also be used as immunogens to produce antibodies  
 CC against IKK3 protein, which may further be used to locate the protein  
 CC in tissues expressing that protein.  
 XX Sequence 45 BP; 6 A; 19 C; 14 G; 6 T; 0 other;  
 SQ

Query Match 69.0%; Score 13.8; DB 21; Length 45;  
 Best Local Similarity 88.2%; Pred. No. 2e+03; Mismatches 0; Gaps 0;  
 Matches 15; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 4 GGCCTGTGTCCCGA 20  
 ||||||| |||||  
 Db 21 GGCCTGTGTCCCGA 5

RESULT 6  
 AAD21726/c  
 ID AAD21726 standard; DNA; 30 BP.  
 XX AAD21726;  
 AC 28-JAN-2002 (first entry)  
 DT Alternative version of mouse SCR-1 cDNA amplifying PCR primer.  
 DE Mouse: stem cell growth factor-like protein; anti-inflammatory; neutrotrophic;  
 XX neuroprotective; vulnary; cytostatic; anticonvulsant; immunostimulant;  
 KW vasotrophic; vituicide; dermatological; cranulliser; cerebroprotective;  
 KW osteopathic; immunodeficiency syndrome; chronic granulomatous disease;  
 KW duplicated immunodeficiency syndrome; Wiskott-Aldrich syndrome; AIDS;  
 KW Gaucher's disease; lysosomal storage disease; mucopolysaccharidosis;  
 KW adrenal white matter degeneration; anaemia; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; thrombocytopaenia; SCID;  
 KW severe combined immunodeficiency; immune disorder; autoimmune disorder;  
 KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;  
 KW autoimmune pulmonary inflammation; cancer; tumour; gene therapy; SCR-1;  
 XX supporting factor for the proliferation of stem cell; PCR primer; ss.  
 OS Mus musculus.  
 XX WO200177169-A2.  
 PN 18-OCT-2001.  
 PD 05-APR-2001; 2001MO-US11208.  
 XX 05-APR-2000; 2000US-0543774.  
 PR 28-JUN-2000; 2000US-215733P.  
 PR 09-JAN-2001; 2001US-0757562.

```

PR 05-FEB-2001: 2001US-266514P.
XX
PA (HYSE-) HYSEQ INC.
PA (KIRI) KIRIN BEER KK.
XX
PI Tang WY, Labat I, Tillinghast JS, Sinku A, Liu C, Dirmanac RT;
PI Stache-Grain B, Dickson M, Mize NK, Nishikawa M;
XX
XX WPI: 2001-657166/75.
XX
XX
XX Novel stem cell growth factor like polypeptides and polynucleotides for
PT identifying modulators useful for treating diseases such as Alzheimer's
PT disease, cancer, rheumatoid arthritis, osteoporosis
XX
XX
XX Example 12, Page 221, 232pp: English.
XX
XX The patent discloses novel stem cell growth factor-like proteins and
XX polynucleotides encoding them. Proteins of the invention are also known
XX as supporting factor for the proliferation of stem cells (SCR-1). Stem
XX cell growth factor-like proteins are useful for supporting proliferation
XX or survival of a stem cell or germ cell which is preferably primordial
XX germ cell, germ line stem cell, embryonic stem cell, haematopoietic stem
XX cell, haematopoietic progenitor cell, pluripotent cell or totipotent
XX cell. The haematopoietic progenitor cell cultured using stem cell
XX growth factor-like proteins can replace as a graft for the bone marrow
XX transplantation or cord blood transplantation for treating a variety
XX of diseases such as immunodeficiency syndrome, chronic granulomatous
XX disease, duplicated immunodeficiency syndrome, agammaglobulinemia,
XX Wiskott-Aldrich syndrome, acquired immune deficiency syndrome (AIDS),
XX thalassemia, haemolytic anaemia due to enzyme defect, congenital
XX anaemia such as sickle cell anaemia, Gaucher's disease, lysosomal
XX storage diseases such as mucopolysaccharidosis, adrenal white matter
XX degeneration, a variety of cancer and tumours. Proteins of the
XX invention are useful for treating diseases such as Parkinson's
XX disease, Alzheimer's disease and other neurodegenerative diseases,
XX thrombocytopaenia, immune deficiencies and disorders such as severe
XX combined immunodeficiency (SCID) and autoimmune disorders such as
XX multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis,
XX and autoimmune pulmonary inflammation. Sequences of the invention are
XX also useful in gene therapy. The present DNA sequence is the alternative
XX version of mouse SCR-1 cDNA amplifying PCR primer.
XX Note: This sequence is stated to be the same as that shown as SEQ ID
XX CC No: 30 in page 179 of the specification. However these sequences differ
XX at many locations.
XX
XX Sequence 30 BP; 5 A; 6 C; 11 G; 8 T; 0 other;
XX
XX Query Match 68.0%; Score 13.6; DB 22; Length 30;
XX Best Local Similarity 80.0%; Pred. No. 2.5e+03;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0
XX
XX 1 AATGCGCCCTGTGTCGCA 20
XX | | | | | | | | | | | | | |
XX Db 21 AATGCGCGCTTCTCCCA 2
XX
XX
XX RESULT 7
XX AAZ69022
XX ID AAZ69022 standard; DNA; 47 BP.
XX
XX AAZ69022;
XX
XX 10-SEP-2001 (first entry)
XX
XX Human map-related diallelic marker SEQ ID NO:3378.
XX
XX Human genome; diallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX diagnosis; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX

```

FT	Key	Location/Qualifiers
FT	Variation	replace(24,T)
FT		/*tag=
FT		a
FT		/standard_name= "single nucleotide polymorphism"
XX		
XX	W09954500-A2.	
XX		
XX	28-0CT-1999.	
XX		
XX	21-APR-1999;	99W0-IB00822.
XX		
XX	21-APR-1998;	98U5-0082614.
XX	23-NOV-1998;	98U5-0109732.
XX		
XX	(GEST ) GENSET.	
XX		
XX	Cohen D, Blumenfeld M, Chumakov I;	
XX		
XX	WPI; 2000-013267/01.	
XX		
XX	Novel diallelic markers used to construct a high density disequilibrium	
XX	map of the human genome	
XX		
XX	Claim 3; Page 951; 2745pp; English.	
XX		
XX	AAZ65654 to AAZ69578 represent human diallelic markers from the present	
XX	invention, which contain a polymorphic base at position 24 of their	
XX	nucleotide sequences. AAZ69579 to AAZ77440 represent amplification	
XX	primers for the diallelic markers. The diallelic markers of the	
XX	invention have a variety of uses: they can be used for high density	
XX	mapping of the human genome, and in complex association studies and	
XX	haployping studies which are useful in determining the genetic basis	
XX	for disease states. Compositions and methods of the invention can also	
XX	be useful for the identification of the targets for the development of	
XX	pharmaceutical agents and diagnostic methods, as well as the	
XX	characterisation of the differential efficacious responses to and side	
XX	effects from pharmaceutical agents acting on a disease as well as other	
XX	treatment.	
XX	N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297	
XX	and 3367, are not actually given a sequence in the Sequence Listing	
XX	from the present invention.	
XX		
XX	Sequence 47 BP; 6 A; 14 C; 18 G; 9 T; 0 other;	
XX		
XX	Query Match	68.0%; Score 13.6; DB 21; Length 47;
XX	Best Local Similarity	80.0%; Pred. NO. 2.5e+03;
XX	Matches 16; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
QY	1 AATGGCGCCCTGTGCCGA 20	
DB	7 AAGGCCGTCCTGTGCCCGA 26	
	RESULT 8	
	ABN58471/C	
ID	ABN58471 standard; DNA; 65 BP.	
XX		
XX	ABN58471;	
XX		
XX	15-JUL-2002 (first entry)	
XX		
XX	Mouse spliced transcript detection oligonucleotide SEQ ID NO:31219.	
DE		
XX	Human; mouse; rat; splice transcript; detection; RNA transcript;	
XX	splice variant; transcriptome; oligonucleotide library; ss.	
KW		
XX	Mus musculus.	
OS		
XX		
XX	W0200210449-AZ.	
PN		
XX		
XX	07-FEB-2002.	
PD		
XX		
XX	20-JUL-2001; 2001WO-IB01903.	

```

XX 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Falgler S;
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes -
XX
XX Example 1; SEQ ID 31219; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under a specific pathological
XX condition; to detect developmental specific genes; and to detect RNA
XX transcripts and splice variants of a transcriptome of a patient suffering
XX from a particular disorder. ABN27253 to ABN59589 represent
XX oligonucleotide sequences from rats, humans and mice, which are used in
XX the exemplification of the present invention.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 65 BP; 15 A; 21 C; 13 G; 16 T; 0 other;
XX
XX Query Match 68.0%; Score 13.6; DB 24; Length 65;
XX Best Local Similarity 80.0%; Pred. No. 2.6e+03;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 AATGGCGCCGTGTGCCGA 20
XX ||||| ||| | ||||| ||
XX Db 60 AATGGTGCCTTCTCTCTGA 41
XX
XX RESULT 9
XX AAI30331/c
XX ID AAI30331 standard; DNA: 31 BP.
XX
XX AAI30331;
XX
XX 18-OCR-2001 (first entry)
XX
XX Human single nucleotide polymorphism (SNP) RPS6KA1 5.
XX
XX Human; resequence; genotype; disease; forensic; paternity testing;
XX single nucleotide polymorphism; SNP; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Variation replace(16,A)
XX /*tag= a
XX /standard_name= "single nucleotide polymorphism"
XX

```

```

PN WO200166600-A2.
XX
XX 13-SEP-2001.
XX
XX 07-MAR-2001; 2001WO-US07268.
XX
XX 07-MAR-2000; 2000US-0187510.
XX 22-MAY-2000; 2000US-0206129.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Cargill M, Ireland JS, Lander ES;
XX WPI; 2001-522952/57.
XX
XX Nucleic acid molecules from the human genome which include polymorphic
XX sites, useful in methods for predicting the presence, absence or
XX severity of a particular phenotype or disorder (e.g. diabetes)
XX associated with a particular genotype -
XX
XX Claim 1; Page 79; 145pp; English.
XX
XX The invention relates to the identification of nucleic acid molecules
XX (AAI29513-AAI3314) from the human genome which include polymorphic sites
XX which can predispose individuals to disease. Various genes from a number
XX of individuals were resequenced and single nucleotide polymorphisms
XX (SNPs) in these genes discovered. The method is useful for predicting the
XX presence, absence or severity of a particular phenotype or disorder (e.g.
XX diabetes) associated with a particular genotype. The nucleic acids
XX containing the polymorphic sites may be useful in forensics and paternity
XX testing.
XX
XX Sequence 31 BP; 5 A; 9 C; 14 G; 3 T; 0 other;
XX
XX Query Match 67.0%; Score 13.4; DB 22; Length 31;
XX Best Local Similarity 93.3%; Pred. No. 3.1e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 6 CGCCCTGTGCCGA 20
XX ||||| ||| |||||
XX Db 28 CGCCCTGTGCCGA 14
XX
XX RESULT 10
XX AAH44305
XX ID AAH44305 standard; DNA: 33 BP.
XX
XX AAH44305;
XX
XX 25-SEP-2001 (first entry)
XX
XX Human fibrinogen 9 PCR primer SEQ ID NO:5.
XX
XX Human; fibrinogen 9; cytosolic; haemostatic; antiinflammatory;
XX immunomodulatory; virucide; malignant tumor; haemopathy;
XX HIV infection; immunological disease; inflammation; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200148196-A1.
XX
XX 05-JUL-2001.
XX
XX 18-DEC-2000; 2000WO-CN00611.
XX
XX 24-DEC-1999; 99CN-0125762.
XX
XX (BIOW-) BIOWINDOM GENE DEV LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX WPI; 2001-418278/44.
XX

```

PT	Fibrinogen 9 and encoded polynucleotide, applicable in diagnosis and
PT	treatment of malignant tumor, hemopathy, HIV infection, immunological
PT	diseases and various inflammations -
XX	
PS	Example 5; Page 12; 27pp; Chinese.
XX	
CC	The present sequence represents a PCR primer for human fibrinogen 9.
CC	Human fibrinogen 9 has cytosstatic, haemostatic, antiinflammatory, protein
CC	immunomodulatory and virucide activities. The human fibrinogen 9
CC	and polynucleotide sequences are applicable in the diagnosis and
CC	treatment of malignant tumour, haemopathy, HIV infection, immunological
CC	diseases and various inflammations.
XX	
SO	Sequence 33 BP; 6 A; 10 C; 10 G; 7 T; 0 other;
QY	
DB	
Query Match	67.0%; Score 13.4; DB 22; Length 33;
Best Local Similarity	93.3%; Pred. No. 3.1e+03;
Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0
4 GGGCCCTGTGTCC 18	
11	
18 GGAGCCCTGTGTCCC 32	
RESULT 11	
ABK36795	
ID	ABK36795 standard; DNA; 90 BP.
XX	
AC	ABK36795;
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Human DNA encoding MC1R segment 18.
XX	
KM	Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KM	viral infection; human immunodeficiency virus; melanoma;
KW	bacterial infection; Salmonella; Legionella; parasitic infection;
KW	Typanosoma; Toxoplasma; Giardia; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200190197-A1.
XX	
PD	29-NOV-2001.
XX	
PE	25-MAY-2001; 2001WO-AU00622.
XX	
PR	26-MAY-2000; 2000AU-0007761.
XX	
PA	(AUSU ) UNIV AUSTRALIAN NAT.
XX	
PI	Thomson SA, Ramshaw IA;
XX	
DR	WPI: 2002-147575/19.
DR	P-PSDB; AA084975.
XX	
PT	New synthetic polypeptides having several different segments of at
PT	least one parent polypeptide linked together differently compared to
PT	the linkage in the parent polypeptide, for inducing immune response
PT	against a pathogen or cancer
XX	
PS	Example 3; Fig 27; 364pp; English.
XX	
CC	The invention relates to a new synthetic polypeptide (I) comprising
CC	several different segments of at least one parent polypeptide linked
CC	together in a different relationship relative to their linkage in the
CC	parent polypeptide to impede, abrogate or otherwise alter at least one
CC	function associated with the parent polypeptide and for inducing an
CC	immune response against a pathogen or cancer. Also included are a
CC	synthetic polynucleotide encoding and a computer system for
CC	designing the synthetic polypeptides. The synthetic polypeptides and
CC	polynucleotides are referred to as a Savine. The synthetic polypeptide is
CC	useful for modulating immune responses preferably directed against a

CC	pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix,
CC	colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone
CC	liver, oesophagus, brain, testicle, uterus), as potentiating agents.
CC	Compositions comprising the polypeptide may be used in the treatment or
CC	prophylaxis against viral (such as infections caused by HIV (human
CC	immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC	virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC	(e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC	Salmonella, Streptococcal, Legionella and Mycobacterium) or parasitic
CC	(e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC	Trypanosoma, Toxoplasma and Giardia) infections. The present
CC	sequence encodes a peptide derived from a parent protein used to
CC	construct a vaccine of the invention.
SQ	Sequence 90 BP; 15 A; 30 C; 14 G; 31 T; 0 other;
Query Match	67.0% Score 13.4; DB 24; Length 90;
Best Local Similarity	93.3%; Pred. No. 3.2e+03;
Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps
OY	6 GCACCTGTGTCGCCGA 20     33 CGTCTGTGTCCCA 47
DB	
RESULT 12	
ID	ABL94381/c
AC	ABL94381 standard; DNA; 20 BP.
XX	ABL94381;
DE	29-JUL-2002 (first entry)
XX	Mouse C/EBP beta phosphorothioate antisense oligonucleotide, SEQ ID:147.
XX	
KW	Mouse; murine; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EBP2;
KW	LAP; TCFF5; CBP2; NFIL6; IL6BP; NF-M; AGP/EBP; ApC/EBP;
KW	transcription factor; tissue development; cellular function;
KW	proliferation; differentiation; hormone responsiveness;
KW	oxidative stress response; IL-6 signalling mediator; interleukin-6;
KW	carbohydrate metabolism; immunity; Th1 response; female fertility;
KW	glucocorticoids; ovarian; cancer; tumour formation; type II; diabetes;
KW	infection; inflammation; expression inhibition; phosphorothioate;
KW	antisense oligonucleotide; ss.
OS	Mus musculus.
XX	
FH	Key Location/Qualifiers
FT	modified_base 1..20
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "Phosphorothioate linkages"
FT	modified_base 1..5
FT	/tag= b
FT	/mod_base= OTHER
FT	/note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT	cytosines are 5-methylcytosine"
FT	modified_base 16..20
FT	/tag= c
FT	/mod_base= OTHER
FT	/note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT	cytosines are 5-methylcytosine"
PN	US6271030-B1.
XX	
PD	07-AUG-2001.
XX	
PP	14-JUN-2000; 2000US-0593711.
XX	
PR	14-JUN-2000; 2000US-0593711.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	



PI Monla BP, Butler MM, Wyatt J;  
 XX WPI: 2002-214451/27.  
 DR  
 XX  
 PT Novel antisense compound targeted to nucleic acids encoding human or  
 PT mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro for  
 PT inhibiting expression of human or mouse C/EBP beta in cells/tissues -  
 XX  
 PS Claim 1: Column 49-50; 69pp; English.  
 XX  
 CC Sequences ABL94252-ABL94476 represent antisense oligonucleotides targeted  
 CC to the human or mouse CCAAT/enhancer-binding protein alpha (C/EBP alpha)  
 CC gene, which inhibit its expression. The antisense oligonucleotides were  
 CC designed to target different regions of the human and/or mouse C/EBP  
 CC alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels  
 CC by quantitative real-time PCR. The C/EBP family of proteins are a family  
 CC of genes that control normal tissue development, cellular function,  
 CC cellular proliferation and functional differentiation. C/EBP beta (also  
 CC known as C/EBP2, LAP, TCF5, CRP2, NR1H6, IL6BP, NF-W, AGP/EBP and  
 CC Apc/EBP) primarily regulates hormone responsiveness and oxidative stress  
 CC responses and is a mediator of IL-6 (Interleukin-6) signalling. C/EBP  
 CC beta is thought to be involved in carbohydrate metabolism, immunity, the  
 CC Th1 response, female fertility and gluconeogenic pathways. C/EBP beta is  
 CC expressed in the liver, lung, spleen, kidney, brain, and testis, with the  
 CC highest expression found in the lung. It is also expressed at a higher  
 CC level in malignant ovarian tissue compared with normal ovarian tissue,  
 CC and its expression in pancreas is upregulated in response to chronic  
 CC elevated levels of glucose, indicating that it is involved in the  
 CC impairment of insulin secretion in type II diabetes. The oligonucleotides  
 CC of the invention are useful for diagnosis, prevention and treatment of  
 CC conditions associated with C/EBP beta expression, such as cancer  
 CC (particularly ovarian cancer), tumour formation, diabetes (particularly  
 CC type II diabetes), infection, or inflammation.  
 CC  
 SQ Sequence 20 BP; 6 A; 7 C; 6 G; 1 T; 0 other;  
 XX  
 QY Query Match 66.0%; Score 13.2; DB 24; Length 20;  
 Db Best Local Similarity 83.3%; Pred. No. 3.8e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 2 ATGGCGCCCTGTGTCCG 19  
 ||||| || || |||||  
 20 ATGGCGCCGCTTCCG 3  
 RESULT 13  
 AAT90699  
 ID AAT90699 standard; DNA: 34 BP.  
 XX  
 AC AAT90699;  
 XX  
 DT 05-JAN-1998 (first entry)  
 XX  
 DE Primer #4 for env containing plasmid construction.  
 XX  
 KW Packaging-deficient construct; viral gag-pol gene; packaging cell line;  
 KW moloney murine leukaemia virus; MoMuV; viral env gene; helper construct;  
 KW gene therapy; polymerase chain reaction; primer; amplify; PCR; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9708330-A1.  
 PN  
 PD 06-MAR-1997.  
 PD  
 PF 23-AUG-1996; 96MO-GH02061.  
 PF  
 PR 23-AUG-1995; 95GB-0017263.  
 PR  
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 PA  
 PI Collins MKL, Cosset F, Takeuchi Y, Weiss RA;

XX  
 DR WPI: 1997-179287/16.  
 XX  
 PT Selectable retroviral packaging cell lines and expression constructs  
 PT - comprise selectable gene downstream of gene of interest, are  
 PT selectable due to the in-efficiency associated with translation  
 PT re-initiation  
 XX  
 PS Example 2; Page 19; 79pp; English.  
 XX  
 CC AAT90696-T90701 represent amplification primers used in the construction  
 CC of viral env gene containing recombinant expression vectors (REV) of the  
 CC invention. The vectors are used to create a packaging cell line. The  
 CC REV's of the invention comprise a gene of interest (GOI) and a SM gene.  
 CC The SM gene is arranged downstream of the GOI and a GOI associated stop  
 CC codon is spaced from a start codon of the SM gene to ensure that the SM  
 CC protein is expressed as a result of translation reinitiation. The cell  
 CC lines are transformed with two REV's, both are replication deficient, one  
 CC contains the viral gag-pol gene, the other the viral env gene. By using  
 CC helper constructs, such as the REV's, which are directly selectable and  
 CC which provide for high expression of the viral gene, high titre  
 CC retroviral vectors may be obtained. The packaging cell lines are useful  
 CC for gene therapy. Prior packaging cell lines using full length retroviral  
 CC genomes as helper genomes were isolated by cotransfecting them with  
 CC plasmids encoding selectable markers. However, the helper functions can  
 CC be lost during the passages of the cells in culture and the current  
 CC packaging systems provide limited titres of infectious retroviral  
 CC vectors. Co-transfection with a plasmid encoding a SM does not directly  
 CC select the best gag-pol-env-expressing cells. The new retroviral  
 CC packaging cell lines overcome these problems.  
 CC  
 SQ Sequence 34 BP; 6 A; 10 C; 9 G; 9 T; 0 other;  
 XX  
 QY Query Match 66.0%; Score 13.2; DB 18; Length 34;  
 Db Best Local Similarity 83.3%; Pred. No. 3.9e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 2 ATGGCGCCCTGTGTCCG 19  
 ||||| || || |||||  
 5 ATGGCGCCCTATGCTCG 22  
 RESULT 14  
 AAD14556/C  
 ID AAD14556 standard; DNA: 40 BP.  
 XX  
 AC AAD14556;  
 XX  
 DT 01-NOV-2001 (first entry)  
 XX  
 DE Arabidopsis thaliana ABF binding sequence #3.  
 XX  
 KW Abscisic acid responsive element; ABRE; ABRE-binding factor; ABF;  
 KW stress treatment; transgenic plant; environmental stress; ds.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 FH Key Location/Qualifiers  
 FH misc\_feature 12..22  
 FT /\*tag= a  
 FT /note= "Conserved region"  
 FT  
 PN US6232461-B1.  
 PN  
 PD 15-MAY-2001.  
 PD  
 PF 19-SEP-2000; 2000US-0665309.  
 PF  
 PR 12-OCT-1999; 99US-0416050.  
 PR  
 PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.  
 PA  
 PI Kim SY;

```
XX DR WPI; 2001-366358/38.
XX PT New nucleic acid encoding abscisic acid responsive element binding
XX PT factor 4, useful for generating transgenic plants, which are tolerant
XX PT to multiple environmental stresses -
XX PS Disclosure; Fig 5B; 42pp; English.
XX CC The invention relates to nucleic acid encoding the Abscisic acid
CC responsive element (ABRE)-binding factor 4 (ABF4). ABF4 belongs to
CC the ABF family of factors which bind abscisic acid responsive elements
CC in plants. Expression of ABFs is inducible by abscisic acid and various
CC stress treatments. ABFs have the potential to activate a large number
CC of abscisic acid/stress responsive genes and thus a nucleic acid
CC molecule encoding ABF4 is useful for generating transgenic plants
CC that are tolerant to multiple environmental stresses. The present
CC sequence is Arabidopsis thaliana ABF binding sequence which contains
CC the group IA consensus sequence.
XX SQ Sequence 40 BP; 9 A; 11 C; 14 G; 6 T; 0 other;
XX
XX Query Match 66.0%; Score 13.2; DB 22; Length 40;
XX Best Local Similarity 83.3%; Pred. No. 3.9e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 3 TGGCGCCCTGTGCCGA 20
DB 26 TTGGCCACGCTGCCGA 9
AA07861/C
ID AA07861 standard; DNA; 40 BP.
XX AC AA07861;
XX DT 23-OCT-2001 (first entry)
XX DE Binding site selection assay group IA sequence #3.
XX KW Abscisic acid responsive element binding factor; ABF; bZIP; ss; G/ABRE;
XX KW G-box-like ABRE; coupling element-like ABRE; C/ABRE; transgenic plant;
XX KW stress responsive gene; environmental stress; cress;
XX KW binding site selection assay.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX FT misc_feature 13..22
XX FT /*tag= a
XX FT /note= "Group IA consensus sequence"
XX PN EPI097999-A2.
XX PD 09-MAY-2001.
XX PF 29-JUN-2000; 2000EP-0305459.
XX PR 04-NOV-1999; 99KR-0048477.
XX PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX PI Kim SY;
XX DR WPI; 2001-337113/36.
XX PT Nucleic acid encoding novel transcription factors that bind to various
XX PT abscisic acid responsive elements, for generating stress tolerant
XX PT transgenic plants -
XX PS Disclosure; Fig 5B; 37pp; English.
XX
```

```
CC CC The sequence represents an oligonucleotide studied in a binding site
CC selection assay, for studying abscisic acid responsive element binding
CC factor (ABF) proteins. The oligonucleotide contains the IA consensus
CC sequence. ABFs are bZIP class transcription factors that can bind to two
CC classes of ABRE, namely G-box-like ABREs (G/ABRE) and coupling
CC element-like ABREs (C/ABRE). Expression of ABF is inducible by abscisic
CC acid and various stress treatments and they can transactivate an
CC ABRE-containing reporter gene in yeast. Therefore, the ABFs are useful
CC for activating a large number of abscisic acid or stress responsive genes
CC and for generating transgenic plants that are tolerant to multiple
XX environmental stresses.
XX SQ Sequence 40 BP; 9 A; 11 C; 14 G; 6 T; 0 other;
XX
XX Query Match 66.0%; Score 13.2; DB 22; Length 40;
XX Best Local Similarity 83.3%; Pred. No. 3.9e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 3 TGGCGCCCTGTGCCGA 20
DB 26 TTGGCCACGCTGCCGA 9
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Search completed: November 23, 2002, 06:28:48  
Job time : 102.6 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:53:51 : Search time 21.55 Seconds  
(without alignments)  
284.619 Million cell updates/sec

Title: US-09-296-264-7

Perfect score: 20

Sequence: 1 aaigcgcgcctgttcccca 20

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

1: /cgn2\_6/ptodata/1/1na/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/1na/5B\_COMB.seq:\*  
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4: /cgn2\_6/ptodata/1/1na/6B\_COMB.seq:\*  
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6: /cgn2\_6/ptodata/1/1na/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	25	1	US-08-182-961B-10 Sequence 10, Appl
2	14.2	71.0	25	4	US-09-007-678B-10 Sequence 10, Appl
3	13.2	66.0	20	4	US-09-593-711A-147 Sequence 147, App
4	13.2	66.0	34	4	US-09-011-745-13 Sequence 13, Appl
5	13.2	66.0	40	4	US-09-416-050A-35 Sequence 35, Appl
6	13.2	66.0	40	4	US-09-664-800-35 Sequence 35, Appl
7	13.2	66.0	40	4	US-09-665-309-35 Sequence 35, Appl
8	13.2	66.0	40	4	US-09-661-569-35 Sequence 35, Appl
9	12.8	64.0	21	1	US-08-009-263C-9 Sequence 9, Appl
10	12.8	64.0	21	1	US-08-009-263C-72 Sequence 9, Appl
11	12.8	64.0	21	1	US-07-927-506-9 Sequence 9, Appl
12	12.8	64.0	21	3	US-08-838-715B-9 Sequence 9, Appl
13	12.8	64.0	21	3	US-08-838-715B-72 Sequence 72, Appl
14	12.8	64.0	21	5	PCT-US91-05815-9 Sequence 9, Appl
15	12.6	63.0	65	2	US-08-418-848A-70 Sequence 70, Appl
16	12.6	63.0	72	2	US-08-748-852-48 Sequence 48, Appl
17	12.6	63.0	70	3	US-08-748-852-50 Sequence 50, Appl
18	12.2	61.0	20	3	US-09-428-584-13 Sequence 13, Appl
19	12.2	61.0	86	1	US-07-964-624D-82 Sequence 82, Appl
20	12.2	61.0	86	1	US-08-442-062-82 Sequence 82, Appl
21	12.2	61.0	86	1	US-08-748-697A-82 Sequence 82, Appl
22	12.2	61.0	86	4	US-09-165-616-82 Sequence 82, Appl
23	12.2	60.0	40	4	US-09-416-050A-37 Sequence 37, Appl
24	12.2	60.0	40	4	US-09-664-800-37 Sequence 37, Appl
25	12.2	60.0	40	4	US-09-665-309-37 Sequence 37, Appl
26	12.2	60.0	40	4	US-09-661-569-37 Sequence 37, Appl
27	12.2	60.0	45	3	US-08-612-973-98 Sequence 98, Appl

c 28	12	60.0	45	4	US-08-927-597-98	Sequence 98, Appl
c 29	12	60.0	58	5	PCT-US95-02917-3	Sequence 3, Appl
c 30	12	60.0	62	2	US-08-850-049-14	Sequence 14, Appl
c 31	12	60.0	62	2	US-08-050-478-14	Sequence 14, Appl
c 32	12	60.0	62	4	US-07-858-747B-14	Sequence 14, Appl
c 33	12	60.0	62	4	US-09-414-117-14	Sequence 14, Appl
c 34	12	60.0	62	4	US-09-678-437-14	Sequence 14, Appl
c 35	12	60.0	70	1	US-08-400-440A-82	Sequence 82, Appl
c 36	12	60.0	70	1	US-08-463-093A-82	Sequence 82, Appl
c 37	12	60.0	70	2	US-08-460-888A-82	Sequence 82, Appl
c 38	12	60.0	70	2	US-08-894-578-82	Sequence 82, Appl
c 39	12	60.0	70	4	US-09-412-017-82	Sequence 39, Appl
c 40	12	60.0	71	2	US-08-465-591A-39	Sequence 39, Appl
c 41	12	60.0	71	2	US-08-465-594A-39	Sequence 39, Appl
c 42	12	60.0	71	4	US-08-973-124-224	Sequence 224, App
c 43	12	60.0	71	5	PCT-US96-08014-224	Sequence 224, App
c 44	11.8	59.0	27	4	US-09-253-356A-134	Sequence 134, App
c 45	11.8	59.0	28	4	US-09-552-322-60	Sequence 60, Appl

#### ALIGNMENTS

RESULT 1  
US-08-182-961B-10  
Sequence 10, Application US/08182961B  
Patent No. 5677125  
GENERAL INFORMATION:  
APPLICANT: HOLT, JEFFREY T.  
APPLICANT: JENSEN, ROY A.  
APPLICANT: PAGE, DAVID L.  
APPLICANT: OBERMILLER, PATRICE S.  
APPLICANT: ROBINSON-BENION, CHERYL L.  
TITLE OF INVENTION: METHOD OF DETECTION AND DIAGNOSIS OF PRE-INVASIVE CANC  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: I. C. WADDEY, JR.  
STREET: 27TH FLOOR, L & C TOWER, 401 CHURCH  
CITY: NASHVILLE  
STATE: TENNESSE  
COUNTRY: USA  
ZIP: 37219  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: MS-DOS (version 5.0)  
SOFTWARE: WordPerfect 5.1/WordPerfect Editor  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,961B  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: I. C. WADDEY, JR.  
REGISTRATION NUMBER: 25,180  
REFERENCE/DOCKET NUMBER: 0216-9409  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (615) 242-2400  
TELEFAX: (615) 242-2221  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25  
TYPE: nucleic acid  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
DESCRIPTION: PCR primer  
HYPOTHETICAL: yes  
ANTI-SENSE: no  
FRAGMENT TYPE: oligonucleotide

US-08-182-961B-10

Query Match 71.0%; Score 14.2; DB 1; Length 25;  
Best Local Similarity 84.2%; Pred. No. 2.2e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ATGGCGCCCTGTGCCGA 20  
||||| ||||| |||||  
Db 3 ATGGCGTCTGTACCCGA 21

RESULT 2  
US-09-007-678B-10  
; Sequence 10, Application US/09007678B  
; Patent No. 6342483  
; GENERAL INFORMATION:

; APPLICANT: HOLT, JEFFREY T.  
; APPLICANT: JENSEN, ROY A.  
; APPLICANT: PAGE, DAVID L.  
; APPLICANT: OBERMILLER, PATRICE S.  
; APPLICANT: ROBINSON-BENION, CHERYL L.  
; APPLICANT: THOMPSON, MARIAN E.  
; TITLE OF INVENTION: METHOD FOR DETECTION AND TREATMENT OF BREAST CANCER  
; FILE REFERENCE: Attorney Docket No. 6342483 1242-1-2-2  
; CURRENT FILING DATE: 1998-01-15  
; PRIOR APPLICATION NUMBER: 08/373,799  
; PRIOR FILING DATE: 1995-01-17  
; PRIOR APPLICATION NUMBER: 08/182,961  
; PRIOR FILING DATE: 1994-01-14  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: Microsoft Wordpad  
; SEQ ID NO 10  
; LENGTH: 25

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized PCR primer  
US-09-007-678B-10

Query Match 71.0%; Score 14.2; DB 4; Length 25;  
Best Local Similarity 84.2%; Pred. No. 2.2e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ATGGCGCCCTGTGCCGA 20  
||||| ||||| |||||  
Db 3 ATGGCGTCTGTACCCGA 21

RESULT 3  
US-09-593-711A-147/C  
; Sequence 147, Application US/09593711A  
; Patent No. 6271030  
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia  
; APPLICANT: Madeline M. Butler  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION  
; FILE REFERENCE: RFS-0118  
; CURRENT APPLICATION NUMBER: US/09/593,711A  
; CURRENT FILING DATE: 2000-06-14  
; NUMBER OF SEQ ID NOS: 244  
; SEQ ID NO 147  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-593-711A-147

Query Match 66.0%; Score 13.2; DB 4; Length 20;  
Best Local Similarity 83.3%; Pred. No. 6.6e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ATGGCGCCCTGTGCCG 19  
||||| ||||| |||||  
Db 20 ATGGCGCGCGGTTCGCC 3

RESULT 4  
US-09-011-745-13  
; Sequence 13, Application US/09011745  
; Patent No. 6165715  
; GENERAL INFORMATION:  
; APPLICANT: Collins, Mary KL  
; APPLICANT: Weiss, Robin A  
; APPLICANT: Takeuchi, Yasuhiro  
; APPLICANT: Cosset, Francois-Joic  
; TITLE OF INVENTION: Expression systems  
; FILE REFERENCE: 09/011,745  
; CURRENT APPLICATION NUMBER: US/09/011,745  
; CURRENT FILING DATE: 1998-06-22  
; EARLIER APPLICATION NUMBER: PCT/GB96/02061  
; EARLIER FILING DATE: 1996-08-23  
; EARLIER APPLICATION NUMBER: GB9517263.1  
; EARLIER FILING DATE: 1995-08-23  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 34  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
US-09-011-745-13

Query Match 66.0%; Score 13.2; DB 4; Length 34;  
Best Local Similarity 83.3%; Pred. No. 6.7e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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||||| ||||| |||||  
Db 5 ATGGCGCCCTGTGCCG 22

RESULT 5  
US-09-416-050A-35/C  
; Sequence 35, Application US/09416050A  
; Patent No. 6194559  
; GENERAL INFORMATION:  
; APPLICANT: KIM, Soo Young  
; TITLE OF INVENTION: Abscisic Acid Responsive Element -Binding Transcription Factor  
; FILE REFERENCE: 1942/42  
; CURRENT APPLICATION NUMBER: US/09/416,050A  
; CURRENT FILING DATE: 1999-10-12  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-416-050A-35

Query Match 66.0%; Score 13.2; DB 4; Length 40;  
Best Local Similarity 83.3%; Pred. No. 6.7e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 26 TTGGCGACGCTGCCGA 9

RESULT 6  
US-09-664-800-35/C  
; Sequence 35, Application US/09664800

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; Patent No. 6218527
; GENERAL INFORMATION:
; APPLICANT: KIM, Soo Young
; TITLE OF INVENTION: Abscisic Acid Responsive Element -Binding Transcription Factor
; FILE REFERENCE: 1942/42
; CURRENT APPLICATION NUMBER: US/09/664,800
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/416,050
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-664-800-35

Query Match
Best Local Similarity 83.3%; DB 4; Length 40;
Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGCGCCCTGTGTCCGA 20
Db 26 TTGGCCACGTCGTCCGA 9

RESULT 7
US-09-665-309-35/c
; Sequence 35, Application US/09665309
; Patent No. 6232461
; GENERAL INFORMATION:
; APPLICANT: KIM, Soo Young
; TITLE OF INVENTION: Abscisic Acid Responsive Element -Binding Transcription Factor
; FILE REFERENCE: 1942/42
; CURRENT APPLICATION NUMBER: US/09/665,309
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/416,050
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-665-309-35

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 4; Length 40;
Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGCGCCCTGTGTCCGA 20
Db 26 TTGGCCACGTCGTCCGA 9

RESULT 8
US-09-661-569-35/c
; Sequence 35, Application US/09661569
; Patent No. 6245905
; GENERAL INFORMATION:
; APPLICANT: KIM, Soo Young
; TITLE OF INVENTION: Abscisic Acid Responsive Element -Binding Transcription Factor
; FILE REFERENCE: 1942/42
; CURRENT APPLICATION NUMBER: US/09/661,569
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 09/416,050
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
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US-09-661-569-35

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 4; Length 40;
Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGCGCCCTGTGTCCGA 20
Db 26 TTGGCCACGTCGTCCGA 9

RESULT 9
US-08-009-263C-9/c
; Sequence 9, Application US/08009263C
; Patent No. 5442049
; GENERAL INFORMATION:
; APPLICANT: Kevin Anderson, Kenneth Draper, Brenda Baker
; TITLE OF INVENTION: Oligonucleotides for Modulating the
; EFFECT OF SEQUENCES: Effects of Cytomegalovirus Infections
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5442049-1s
; STREET: One Liberty Place -- 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/009,263C
; FILING DATE: January 25, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 927,506
; FILING DATE: No. 5442049ember 19, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISIS-0844
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-009-263C-9

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 1; Length 21;
Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCGCCCTGTGTCCGA 20
Db 21 GCGCCCGTGTCCGA 6

RESULT 10
US-08-009-263C-72
; Sequence 72, Application US/08009263C
; Patent No. 5442049
; GENERAL INFORMATION:
; APPLICANT: Kevin Anderson, Kenneth Draper, Brenda Baker
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: TITLE OF INVENTION: Oligonucleotides for Modulating the
: TITLE OF INVENTION: Effects of Cytomegalovirus Infections
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz
: ADDRESSEE: Mackiewicz & No. 54420491s
: STREET: One Liberty Place -- 46th floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: PC-DOS
: SOFTWARE: WORDPERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/009,263C
: FILING DATE: January 25, 1993
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 927,506
: FILING DATE: No. 5442049ember 19, 1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Jane Massey Licata
: REGISTRATION NUMBER: 32,257
: REFERENCE/DOCKET NUMBER: ISIS-0844
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 72:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 21 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: US-08-009-263C-72

Query Match      64.0%; Score 12.8; DB 1; Length 21;
Best Local Similarity 87.5%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGGCCCTGTGTCCGA 20
   ||||| ||||| ||
DB 1 GGGCCCGGTGTCCGA 16

RESULT 11
US-07-927-506-9/c
: Sequence 9, Application US/07927506
: Patent No. 5591720
: GENERAL INFORMATION:
: APPLICANT: Anderson, Kevin P.
: APPLICANT: Draper, Kenneth G.
: TITLE OF INVENTION: Oligonucleotides for Modulating
: TITLE OF INVENTION: the Effects of Cytomegalovirus Infections
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
: ADDRESSEE: No. 55917201s
: STREET: One Liberty Place -- 46th floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
: MEDIUM TYPE: STORAGE
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: PC-DOS
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```

: SOFTWARE: WORDPERFECT 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/927,506
: FILING DATE: 19921119
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Licata, Jane M.
: REGISTRATION NUMBER: 32,257
: REFERENCE/DOCKET NUMBER: ISIS-0408
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 21 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: YES
: US-07-927-506-9

Query Match      64.0%; Score 12.8; DB 1; Length 21;
Best Local Similarity 87.5%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGGCCCTGTGTCCGA 20
   ||||| ||||| ||
DB 21 GGGCCCGGTGTCCGA 6

RESULT 12
US-08-838-715B-9/c
: Sequence 9, Application US/08838715B
: Patent No. 6153595
: GENERAL INFORMATION:
: APPLICANT: Draper, Chapman, Kisner, Anderson
: TITLE OF INVENTION: Composition and Method for Treatment
: TITLE OF INVENTION: of CMV Infection
: NUMBER OF SEQUENCES: 90
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Jane Massey Licata, Esq.
: STREET: 66 E. Main Street
: CITY: Marlon
: STATE: NJ
: COUNTRY: USA
: ZIP: 08053
: COMPUTER READABLE FORM:
: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
: COMPUTER: IBM 486
: OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
: SOFTWARE: WORDPERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,715B
: FILING DATE: April 9, 1997
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/568,366
: FILING DATE: 8/16/90
: APPLICATION NUMBER: 07/927,506
: FILING DATE: 11/19/92
: APPLICATION NUMBER: 08/009,263
: FILING DATE: 1/25/93
: APPLICATION NUMBER: 08/233,711
: FILING DATE: 4/26/94
: ATTORNEY/AGENT INFORMATION:
: NAME: Jane Massey Licata
: REGISTRATION NUMBER: 32,257
: REFERENCE/DOCKET NUMBER: ISPH-0204
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (609) 779-2400
: TELEFAX: (609) 810-1454
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INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-838-715B-9

Query Match 64.0%; Score 12.8; DB 3; Length 21;  
Best Local Similarity 87.5%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 GCGCCCTGTGCCGA 20  
||||| ||||| ||  
Db 21 GCGCCCGGTGCCGA 6

RESULT 13  
US-08-838-715B-72  
Sequence 72, Application US/08838715B  
Patent No. 6153595  
GENERAL INFORMATION:  
APPLICANT: Draper, Chapman, Kiser, Anderson  
TITLE OF INVENTION: Composition and Method for Treatment  
TITLE OF INVENTION: Of CMV Infection  
NUMBER OF SEQUENCES: 90  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,715B  
FILING DATE: April 9, 1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/568,366  
FILING DATE: 8/16/90  
APPLICATION NUMBER: 07/927,506  
FILING DATE: 11/19/92  
APPLICATION NUMBER: 08/009,263  
FILING DATE: 1/25/93  
APPLICATION NUMBER: 08/233,711  
FILING DATE: 4/26/94  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0204  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 810-1454  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-838-715B-72  
Query Match 64.0%; Score 12.8; DB 3; Length 21;

Best Local Similarity 87.5%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 GCGCCCTGTGCCGA 20  
||||| ||||| ||  
Db 1 GCGCCCGGTGCCGA 16

RESULT 14  
PCT-US91-05815-9/c  
Sequence 9, Application PC/TUS9105815  
GENERAL INFORMATION:  
APPLICANT: Anderson, Kevin P.  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: Oligonucleotides for Modulating  
TITLE OF INVENTION: the Effects of Cytomegalovirus Infections  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
STREET: One Liberty Place -- 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB  
MEDIUM TYPE: STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/05815  
FILING DATE: 19910814  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Licata, Jane M.  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISIS-0408  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
PCT-US91-05815-9  
Query Match 64.0%; Score 12.8; DB 5; Length 21;  
Best Local Similarity 87.5%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 15  
US-08-418-848A-70/c  
Sequence 70, Application US/08418848A  
Patent No. 5847096  
GENERAL INFORMATION:  
APPLICANT: SCHUBERT, MANFRED, HARMISON II,  
APPLICANT: GEORGE G., CHANG-JIE, CHEN, BANJERJEA, AKHIL  
TITLE OF INVENTION: DEFECTIVE, INTERFERING  
TITLE OF INVENTION: HIV PARTICLES  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
COUNTRY: U.S.A.  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/418,848A  
FILING DATE: 07-APR-1995  
CLASSIFICATION: 526  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/936,849  
FILING DATE: 28-AUG-1992  
CLASSIFICATION: 526  
ATTORNEY/AGENT INFORMATION:  
NAME: RICHARD W. BORK  
REGISTRATION NUMBER: 36,459  
REFERENCE/DOCKET NUMBER: 2026-4091US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 65 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-418-848A-70

Query Match 63.0%; Score 12.6; DB 2; Length 65;  
Best Local Similarity 78.9%; Pred No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0;  
Gaps 0;

OY 1 AATGGCGCCCTGTGTCCG 19  
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Db 56 AATGGCACCACGTGTTCG 38

Search completed: November 23, 2002, 06:36:06  
Job time : 22.55 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:54:41 ; Search time 17.25 Seconds  
(without alignments)  
439.108 Million cell updates/sec

Title: US-09-296-264-7

Perfect score: 20  
Sequence: 1 aatggcgcctgtgtcccca 20

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 195614

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:\*

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- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
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- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
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- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	12.2	61.0	41	10	US-09-778-175-17
4	12.2	61.0	41	10	US-09-335-218-17
5	11.8	59.0	30	12	US-10-028-051-17
6	11.8	59.0	31	10	US-09-801-274-867
7	11.8	59.0	52	10	US-09-146-157-2
8	11.8	59.0	72	10	US-09-242-980-32
9	11.6	58.0	87	10	US-09-873-075A-5
10	11.4	57.0	20	10	US-09-780-172-54
11	11.4	57.0	28	10	US-09-987-967-3
12	11.4	57.0	52	9	US-10-046-935-1880
13	11.4	57.0	87	10	US-09-864-761-32231
14	11.2	56.0	16	10	US-09-420-433-34
15	11.2	56.0	25	12	US-10-007-805-554
16	11.2	56.0	28	9	US-09-905-291A-24
17	11.2	56.0	28	10	US-09-909-320-24
18	11.2	56.0	28	10	US-09-909-088B-24
19	11.2	56.0	34	10	US-09-801-368-13

c	20	11.2	56.0	75	10	US-09-864-761-20571	Sequence 20571, A
c	21	11.2	56.0	76	10	US-09-783-590-3546	Sequence 3546, Ap
c	22	11.2	56.0	85	10	US-09-864-761-24620	Sequence 24620, A
c	23	11.2	56.0	89	9	US-09-933-797-225	Sequence 225, App
c	24	11.2	56.0	91	10	US-09-864-761-21111	Sequence 21111, A
c	25	11.2	56.0	94	10	US-09-864-761-31201	Sequence 31201, A
c	26	11.2	56.0	96	10	US-09-864-761-29606	Sequence 29606, A
c	27	11.2	56.0	97	10	US-09-864-761-19857	Sequence 19857, A
c	28	11.2	55.0	24	10	US-09-865-703-65	Sequence 65, Appl
c	29	11.2	55.0	32	10	US-09-896-852-39	Sequence 39, Appl
c	30	11.2	55.0	36	9	US-09-251-330-6	Sequence 39, Appl
c	31	11.2	55.0	42	10	US-09-795-006A-5	Sequence 5, Appl1
c	32	11.2	55.0	42	10	US-09-795-006A-14	Sequence 14, Appl
c	33	11.2	55.0	51	9	US-10-027-806-105	Sequence 105, App
c	34	11.2	55.0	64	10	US-09-822-217-1029	Sequence 1029, Ap
c	35	11.2	55.0	64	10	US-09-833-263-1029	Sequence 1029, Ap
c	36	11.2	55.0	96	10	US-09-815-343-1109	Sequence 1009, Ap
c	37	11.2	55.0	96	10	US-09-815-343-1137	Sequence 1137, Ap
c	38	11.2	55.0	98	10	US-09-864-761-26075	Sequence 26075, A
c	39	10.8	54.0	24	10	US-09-853-830-119	Sequence 119, App
c	40	10.8	54.0	30	10	US-09-886-191-5	Sequence 5, Appl1
c	41	10.8	54.0	30	10	US-09-886-191-7	Sequence 7, Appl1
c	42	10.8	54.0	31	10	US-09-801-274-88	Sequence 88, Appl
c	43	10.8	54.0	31	10	US-09-801-274-893	Sequence 893, App
c	44	10.8	54.0	37	10	US-09-250-611-106	Sequence 106, Appl
c	45	10.8	54.0	40	9	US-09-826-025-19	Sequence 19, Appl

#### ALIGNMENTS

RESULT 1  
US-09-801-274-819/c  
Sequence 819, Application US/09801274  
Patent No. US20020032319A1  
GENERAL INFORMATION:  
APPLICANT: Carigill, Michele  
APPLICANT: Ireland, James S.  
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
FILE REFERENCE: 2825.2009-001  
CURRENT APPLICATION NUMBER: US/09/801.274  
CURRENT FILING DATE: 2001-03-07  
PRIOR APPLICATION NUMBER: US 60/187,510  
PRIOR FILING DATE: 2000-03-07  
PRIOR APPLICATION NUMBER: US 60/206,129  
PRIOR FILING DATE: 2000-05-22  
NUMBER OF SEQ ID NOS: 1802  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 819  
LENGTH: 31  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-801-274-819

Query Match 65.0%; Score 13; DB 10; Length 31;  
Best Local Similarity 86.7%; Pred. No. 6.4e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCCTGTGTCCCGA 20  
Db 28 CGCCTGTGTCCCGA 14

RESULT 2  
US-09-778-168-17/c  
Sequence 17, Application US/09778168  
Patent No. US20010009761A1  
GENERAL INFORMATION:  
APPLICANT: Wright, David J.  
APPLICANT: Milla, Maria A.  
APPLICANT: Nadeau, James G.  
APPLICANT: Walker, G. Terrance

```

RESULT 6
US-09-801-274-867/C
; Sequence 867, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele

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; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 867
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-801-274-867
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Query Match          59.0%; Score 11.8; DB 10; Length 31;
Best Local Similarity 86.7%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 4 GGGCCCTGTGTCC 18
    |||||||
Db 31 GGAGCCCTGTCTC 17
```

```
RESULT 7
; US-09-146-157-2/c
; Sequence 2, Application US/09146157
; Patent No. US20010009760A1
; GENERAL INFORMATION:
; APPLICANT: HORN, Thomas
; APPLICANT: SCHROEDER, Hartmut R.
; APPLICANT: WARNER, Brian D.
; APPLICANT: FISS, Ellen
; APPLICANT: SELLS, Todd
; APPLICANT: LAM, Say-Jong
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES BEARING QUENCHABLE FLUORESCENT LABELS,
; FILE REFERENCE: 1411.002
; CURRENT APPLICATION NUMBER: US/09/146,157
; CURRENT FILING DATE: 1998-09-03
; EARLIER APPLICATION NUMBER: 60/057,810
; EARLIER FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This information
; OTHER INFORMATION: is not available.
; US-09-146-157-2
```

```
Query Match          59.0%; Score 11.8; DB 10; Length 52;
Best Local Similarity 86.7%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 4 GGGCCCTGTGTCC 18
    |||||||
Db 39 GGCGCTCTGTATCC 25
```

```
RESULT 8
; US-09-242-980-32
; Sequence 32, Application US/09242980
; Patent No. US20010021073A1
; GENERAL INFORMATION:
; APPLICANT: Ogil, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
```

```
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,980
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 32
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Human
; US-09-242-980-32
```

```
Query Match          59.0%; Score 11.8; DB 10; Length 72;
Best Local Similarity 86.7%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 4 GGGCCCTGTGTCC 18
    |||||||
Db 34 GGCGCCCTGGGTCC 48
```

```
RESULT 9
; US-09-873-075A-5/c
; Sequence 5, Application US/09873075A
; Patent No. US20020123123A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Schroder Glad, Sanne
; APPLICANT: Fukuyama, Shiro
; APPLICANT: Matsui, Tomoko
; TITLE OF INVENTION: Cutinase variants
; FILE REFERENCE: 10038.200-US
; CURRENT APPLICATION NUMBER: US/09/873,075A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: misc_feature
; LOCATION: (43)..(43)
; OTHER INFORMATION: n denotes a, g, c or t
; NAME/KEY: misc_feature
; LOCATION: (46)..(46)
; OTHER INFORMATION: n denotes a, g, c or t
; NAME/KEY: misc_feature
; LOCATION: (49)..(49)
; OTHER INFORMATION: n denotes a, g, c or t
; US-09-873-075A-5
```

```
Query Match          58.0%; Score 11.6; DB 10; Length 87;
Best Local Similarity 70.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
OY 1 AATGGCCCTGTGTCCGA 20
    |:|||||
Db 27 ASYGACGCCCTGGATCCAGA 8
```

```
RESULT 10
; US-09-780-172-54/c
; Sequence 54, Application US/09780172
; Patent No. US20020147163A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wrayt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
; FILE REFERENCE: RTS-0159
; CURRENT APPLICATION NUMBER: US/09/780,172
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-09-780-172-54

Query Match          57.0%; Score 11.4; DB 10; Length 20;
Best Local Similarity 92.3%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8  CCCTGTCGCCGA 20
Db      13 CCCTGTGTACGA 1

RESULT 11
US-09-987-967-3/C
; Sequence 3, Application US/09987967
; Patent No. US20020055144A1
; GENERAL INFORMATION:
; APPLICANT: Wei et al.
; TITLE OF INVENTION: Human Hematopoietic - Specific Protein
; FILE REFERENCE: PF268D1C1
; CURRENT APPLICATION NUMBER: US/09/987,967
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: PCT/US96/04930
; PRIOR FILING DATE: 1996-04-11
; PRIOR APPLICATION NUMBER: 08/837,029
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 09/265,977
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Primer-Bind
; OTHER INFORMATION: Synthetic primer containing a Bam HI restriction site
; OTHER INFORMATION: encoding a start AUG, followed by 19 nucleotides of the hHSP
; OTHER INFORMATION: coding sequence beginning with the first base of the 23rd codon.
US-09-987-967-3

Query Match          57.0%; Score 11.4; DB 10; Length 28;
Best Local Similarity 92.3%; Pred. No. 3.9e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  AATGGCGCCCTGT 13
Db      23 AATGGCGCCCTGT 11

RESULT 12
US-10-046-935-1880/C
; Sequence 1880, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
```

```
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1880
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 18, 19, 20
; OTHER INFORMATION: n = A,T,C or G
US-10-046-935-1880

Query Match          57.0%; Score 11.4; DB 9; Length 52;
Best Local Similarity 92.3%; Pred. No. 4.1e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  CGCCTGTGTCCC 18
Db      52 CGCCTGTGTCCC 40

RESULT 13
US-09-864-761-32231
; Sequence 32231, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Gene Expression Analysis by Microarray
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
```

PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 32231  
LENGTH: 87  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AF186997.2  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94  
OTHER INFORMATION: EST\_HUMAN HIT: AV761450.1, EVALUE 2.70e-01  
US-09-864-761-32231

Query Match 57.0%; Score 11.4; DB 10; Length 87;  
Best Local Similarity 92.3%; Pred. No. 4.3e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 GCGCCTGTGTCGG 19  
DB 25 GCGCCTGTGTCGG 37

## RESULT 14

US-09-420-433-34  
Sequence 34, Application US/09420433  
Patent No. US20020098480A1  
GENERAL INFORMATION:  
APPLICANT: Sidransky, David  
TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION IN  
NUMBER OF SEQUENCES: 82  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Judas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/420,433  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/181,664  
FILING DATE: JANUARY 14, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D., John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-3055  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..16  
US-09-420-433-34  
Query Match 56.0%; Score 11.2; DB 10; Length 16;

Best Local Similarity 81.2%; Pred. No. 4.7e+03;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCGCCCTGTGTCGG 19  
DB 1 GGTGCGCTGTGACCG 16

## RESULT 15

US-10-007-805-554  
Sequence 554, Application US/10007805  
Patent No. US20020150581A1  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yugu  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Durham, Margarita  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.470C10  
CURRENT APPLICATION NUMBER: US/10/007,805  
CURRENT FILING DATE: 2001-12-07  
NUMBER OF SEQ ID NOS: 593  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 554  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR primer  
US-10-007-805-554

Query Match 56.0%; Score 11.2; DB 12; Length 25;  
Best Local Similarity 81.2%; Pred. No. 4.9e+03;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4 GCGCCCTGTGTCGG 19  
DB 4 GCGCCATGAGTCGG 19

Search completed: November 23, 2002, 06:42:06  
Job time : 18.25 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2002, 09:10:06 ; Search time 755.55 Seconds  
(without alignments)  
428.707 Million cell updates/sec

Title: US-09-296-264-7

Perfect score: 20  
Sequence: 1 aatgcgcctgtgtccgca 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809743376 residues  
Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estda:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlun:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hlc:\*  
12: gb\_estl3:\*  
13: gb\_estl4:\*  
14: gb\_estl5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_lun:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vlc:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	14.2	71.0	88	AM826045 us20f01.x
2	13.8	69.0	65	AZ922880 SICot6C05
3	13.8	69.0	87	AA612425 v005912.r
4	13.8	69.0	91	W13623 ma93f03.r1
5	13.8	69.0	92	AA257852 MBL2S4C8
6	13.4	67.0	26	TA376C02P
			17	TA376C02P

Result No.	Score	Query Match Length	DB ID	Description
7	13.4	67.0	82	AI942604
8	13.2	66.0	73	AI768372
9	13.2	66.0	63	BI256496
10	13.2	66.0	97	BI764407
11	13.2	66.0	97	BI764407
12	13.2	66.0	97	BI764407
13	13.2	66.0	97	BI764407
14	13.2	66.0	97	BI764407
15	13.2	66.0	97	BI764407
16	13.2	66.0	97	BI764407
17	13.2	66.0	97	BI764407
18	13.2	66.0	97	BI764407
19	13.2	66.0	97	BI764407
20	13.2	66.0	97	BI764407
21	13.2	66.0	97	BI764407
22	13.2	66.0	97	BI764407
23	13.2	66.0	97	BI764407
24	13.2	66.0	97	BI764407
25	13.2	66.0	97	BI764407
26	13.2	66.0	97	BI764407
27	13.2	66.0	97	BI764407
28	13.2	66.0	97	BI764407
29	13.2	66.0	97	BI764407
30	13.2	66.0	97	BI764407
31	13.2	66.0	97	BI764407
32	13.2	66.0	97	BI764407
33	13.2	66.0	97	BI764407
34	13.2	66.0	97	BI764407
35	13.2	66.0	97	BI764407
36	13.2	66.0	97	BI764407
37	13.2	66.0	97	BI764407
38	13.2	66.0	97	BI764407
39	13.2	66.0	97	BI764407
40	13.2	66.0	97	BI764407
41	13.2	66.0	97	BI764407
42	13.2	66.0	97	BI764407
43	13.2	66.0	97	BI764407
44	13.2	66.0	97	BI764407
45	13.2	66.0	97	BI764407

# ALIGNMENTS

RESULT 1  
AM826045/c  
LOCUS  
DEFINITION  
us20f01.x1 Soares\_NMGBC\_B-cell Mus musculus cDNA clone  
IMAGE:3167641.3' similar to SW:PAN\_MOUSE 035242 PROTEIN FAN ;, mRNA  
Sequence  
AM826045  
VERSION  
AM826045.1 GI:7919122  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus  
house mouse.  
EST.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Mus.  
1 (bases 1 to 88)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Other-ESTs: us20f01.y1  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
, Ph.D.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov/image/html/resources.shtml>





ORIGIN	Query Match	69.0%;	Score 13.8;	DB 9;	Length 87;
	Best Local Similarity	88.2%;	Pred. No. 1.4e+04;		
	Matches 15;	Conservative	0;	Mismatches 2;	Indels 0;
OY	4 GGCGCCGCTGTGCCGA 20				
	Db	51 GGAGCCGCTGTGCCAA 35			
RESULT 4					
W13623					
DEFINITION	ma33f03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone	91 bp	mrna	linear	EST 02-OCT-1997
	IMAGE:318269 5' similar to SW:KRB2, COATA P02447 KERATIN,				
	HIGH-SULFUR MATRIX PROTEIN, IIB2 ;				
	W13623				
ACCESSION	W13623.1	GI:1287661			
VERSION					
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
	Eukaryota; Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 91)				
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,D., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thelsting,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Waterson,R.				
TITLE	The Mashu-HMI Mouse EST Project				
JOURNAL	Unpublished (1996)				
COMMENT	Contact: Marra M/Mouse EST Project Mashu-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI: 208885 Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: ETPRimer High quality sequence stop: 1. Location/Qualifiers 1. 91 /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:318269" /clone_1lb="Soares mouse p3NMF19.5" /dev_stage="19.5 dpc total fetus" /lab_host="DH10B (ampicillin resistant)" /note="Vector: pRT3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAAAGTGGAGCGCGCCGATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."				
BASE COUNT	19 a	36 c	20 g	16 t	
ORIGIN					
Query Match	69.0%;	Score 13.8;	DB 14;	Length 91;	
Best Local Similarity	88.2%;	Pred. No. 1.4e+04;			
Matches 15;	Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
OY	4 GGCGCCGCTGTGCCGA 20				

DB	70	GGAGCCCTGTCTCCAA	86
RESULT 5	AA257852	92 bp	mRNA
LOCUS	MB12SJ4C8T3	Brugia malayi second stage	larvae JHU96SL-Bml2 Brugia
DEFINITION	malayi cDNA clone LZSJ4C8 5', mRNA sequence.		
ACCESSION	AA257852		
VERSION	AA257852.1	GI:1893368	
KEYWORDS	EST.		
SOURCE	Brugia malayi.		
ORGANISM	Brugia malayi.		
REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchoercidae; Brugia.		
AUTHORS	1 (bases 1 to 92) Blaxter, M.L., Waterfall, M., Daub, J., Lizotte, M., Baron, L. and Jones, S.J.		
TITLE	Genes expressed in adult female Brugia malayi		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Blaxter ML Institute of Cell, Animal and Population Biology University of Edinburgh Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JF, UK. Tel: +44 131 650 6760 Fax: +44 131 670 5450 Email: mark.blaxter@ac.uk The ABI trace of this sequence can be viewed at <a href="http://www.sanger.ac.uk/brugia/LZ5/MB12SJ4C8T3.html">http://www.sanger.ac.uk/brugia/LZ5/MB12SJ4C8T3.html</a> Seq primer: T3.		
FEATURES	Location/Qualifiers		
SOURCE	1..92 /organism="Brugia malayi" /strain="IRS Labs" /db_xref="taxon:6279" /clone="LZSJ4C8" /clone_id="Brugia malayi second stage larvae JHU96SL-Bml2" /sex="mixed" /dex_stage="mosquito derived, second stage larvae (L2)" /lab_host="E. coli XL1-blue MRP-" /note="Vector: lambdaZapII; Site_1: Eco R I (5' end); Site_2: Xho I (3' end); Brugia malayi is a lymphatic filarial nematode parasite of humans. Full length cDNA was prepared by long-range RT-PCR from mRNA from L2 larvae of the human filarial nematode parasite Brugia malayi using nematode spliced leader (SL, 5' end) and oligo-d(T) (3' end) primers. The library had an unamplified titer of ~1 x 10E6 per ml and ~95% of clones have inserts (mean length ~900 bp). The library is available from The Filarial Genome Project Resource Center; contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, MA 01063 USA phone +1 413 585 3826 fax +1 413 585 3786 email genome@smith.edu"		
BASE COUNT	20 a	33 c	20 g
ORIGIN			19 t
Query Match	69.0%	Score 13.8	DB 9; Length 92;
Best Local Similarity	88.2%	Pred. No. 1.5e+04;	
Matches 15; Conservative	0;	Mismatches 2;	Indels 0;
Gaps	0;		
0Y	4 GGCGCCCTGTCTCCGA	20	
DB	3 GGCGCCCTGTCTCCGA	19	
RESULT 6	TA376C02P	26 bp	DNA
LOCUS	T. brucei sheared genomic		
DEFINITION	clone 376C02, forward sequence,		
	genomic survey sequence.		

ACCESSION A1497551  
 VERSION A1497551.1 GI:11873273  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei.  
 ORGANISM Trypanosoma brucei.  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.  
 REFERENCE 1 (bases 1 to 26)  
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
 COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
 FEATURES  
 source  
 1..26  
 /organism="Trypanosoma brucei"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="376c02"  
 BASE COUNT 5 a 6 c 6 g 9 t  
 ORIGIN  
 Query Match 67.0%; Score 13.4; DB 17; Length 26;  
 Best Local Similarity 93.3%; Pred. No. 1.4e+04;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AATGGCGCCTGTGT 15  
 Db 6 AATGGCGCCTGTGT 20  
 RESULT 7  
 A1942604 82 bp mRNA linear EST 07-JUN-2001  
 A1942604/c fc73e04.y1 zebrafish washu mpimg EST Danio rerio cDNA clone  
 LOCUS IMAGE:327038 5' similar to TR:Q13518 Q13518 PROTEIN KINASE  
 DEFINITION C-BINDING PROTEIN RACK8 ;, mRNA sequence.  
 ACCESSION A1942604  
 VERSION A1942604.1 GI:5707260  
 KEYWORDS EST.  
 SOURCE zebrafish.  
 ORGANISM Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes  
 REFERENCE 1 (bases 1 to 82)  
 AUTHORS Clark, M., Johnson, S.L., Lehnach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurr, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
 TITLE Washu zebrafish EST Project 1998  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Stephen L. Johnson  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800

Fax: 314 286 1810  
 Email: zbrfish@watson.wustl.edu  
 CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone Distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourceZentrumPrimaDatenbank, Berlin, Germany (web address: www.rzpd.de)  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seg primer: T3 ET from Amersham  
 High quality sequence stop: 1.  
 FEATURES  
 source  
 1..82  
 /organism="Danio rerio"  
 /db\_xref="taxon:7955"  
 /clone="IMAGE:327038"  
 /clone\_1b="zebrafish washu mpimg EST"  
 /sex="mixed"  
 /tissue\_type="26 somite embryos, adult livers, shield stage embryos"  
 /lab\_host="X11-blue MRF"  
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer (5' pGACTGATCTTCTGATCGGAGCGGCCCTTTTCTTTTCTTTT3.1); double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehnach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."  
 BASE COUNT 16 a 24 c 24 g 18 t  
 ORIGIN  
 Query Match 67.0%; Score 13.4; DB 9; Length 82;  
 Best Local Similarity 93.3%; Pred. No. 2.2e+04;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 GCGCCCTGTGTCCG 19  
 Db 31 GCGCCCTGTGTCTGT 17  
 RESULT 8  
 A1768372 63 bp mRNA linear EST 20-DEC-1999  
 A1768372 wg84f09.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone  
 LOCUS IMAGE:2371817 3' similar to SW:MY18\_HUMAN 075293 NEGATIVE  
 DEFINITION GROWTH-REGULATORY PROTEIN MYD118 ;, mRNA sequence.  
 ACCESSION A1768372  
 VERSION A1768372.1 GI:5234881  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 63)  
 AUTHORS NCI-CGAP htlp://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.



Db 80 ACTGGCGCCCTGTGTCC 63

# RESULT 11

AZ830008 65 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0109B05F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCG2M0109B05 F, DNA sequence.

ACCESSION AZ830008  
VERSION AZ830008.1 GI:12999916

KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota: Metazoa: Chordata: Craniala: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathu: Muridae: Murine; Mus.  
1 (bases 1 to 65)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0109 row: B column: 05  
Seq primer: CGTTGTAACGACGCGCCACT  
Class: plasmid ends  
High quality sequence stop: 65.  
Location/Qualifiers

# FEATURES

source 1. .65  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG2M0109B05"  
/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PMD42nv: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 17 a 15 c 15 g 18 t  
ORIGIN

Query Match 65.0%; Score 13; DB 17; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.1e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGGCGCCCTGT 13

Db 50 AATGGCGCCCTGT 62

# RESULT 12

BH865695 85 bp DNA linear GSS 05-AUG-2002  
LOCUS SALK\_096695 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
DEFINITION thaliana genomic clone SALK\_096695, DNA sequence.

ACCESSION BH865695  
VERSION BH865695.1 GI:22101593

KEYWORDS GSS.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids II: Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 85)

AUTHORS Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.  
A Sequence-indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (Signal)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g32820.  
Class: TDNA tagged.  
Location/Qualifiers

# FEATURES

source 1. .85  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_096695"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna\_protocols.html"

BASE COUNT 20 a 19 c 20 g 24 t 2 others  
ORIGIN

Query Match 65.0%; Score 13; DB 17; Length 85;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGGCGCCCTGT 13  
Db 31 AATGGCGCCCTGT 19

# RESULT 13

A1465146 92 bp mRNA linear EST 09-MAR-1999  
LOCUS mw82h01.x1 GuayWoodford Beier mouse kidney day 7 Mus musculus CDNA  
DEFINITION clone IMAGE:661585 3', mRNA sequence.

ACCESSION A1465146  
VERSION A1465146.1 GI:4319176

KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota: Metazoa: Chordata: Craniala: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathu: Muridae: Murine; Mus.  
1 (bases 1 to 92)  
Marrta,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
Contact: Marra M/Mashu-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
This clone was previously sequenced on the 5' end only, this new data is from the 3' end  
Seq primer: primer name ambiguous.

## FEATURES

source  
location/Qualifiers

1..92  
/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone\_image="661585"

/clone\_lib="GuayWoodford Beier mouse kidney day 7"

/issue\_type="kidney"

/dev\_stage="juvenile (7 days old)"

/lab\_host="SOLR (kanamycin resistant)"

/note="Organ: kidney; Vector: pBluescript SK-; Site: 1: EcorI; Site 2: XhoI; Cloned unidirectionally. Primer: 01190 dt. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' CTCAGCTTTT TTTT TTTT TTTT 3' Library provided by Lisa Guay-Woodford."

BASE COUNT 15 a 22 c 29 g 26 t

## ORIGIN

## Query Match

Best Local Similarity 100.0%; Score 13; DB 9; Length 92;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCCCTGTGTCCG 19  
|||||  
DB 41 GCCCTGTGTCCG 53

## RESULT 14

CNS012CG 92 bp DNA linear GSS 12-MAY-2000  
Tetradon nigroviridis genome survey sequence, PUC-Orl end of clone  
220109 of library G from Tetradon nigroviridis, genomic survey  
sequence.

ACCESSION AL174121

VERSION AL174121.1 GI:7812178

KEYWORDS GSS: genome survey sequence.

SOURCE Tetradon nigroviridis.

ORGANISM Tetradon nigroviridis

REFERENCE 1 (bases 1 to 92)

AUTHORS Roest-Crollius, H., Jallion, O., Desilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brothier, P., Queller, F., Saurin, W., and Weissenbach, J.

TITLE Human gene number estimate provided by genome wide analysis using  
Tetradon nigroviridis DNA sequence

JOURNAL 2 (bases 1 to 92)

REFERENCE Roest-Crollius, H., Jallion, O., Desilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Queller, F., Saurin, W., Bernot, A., and Weissenbach, J.

AUTHORS Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetradon nigroviridis

JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 92)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000)  
COMMENT This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetradon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/Tetradon>.

## FEATURES

source  
location/Qualifiers

1..92

/organism="Tetradon nigroviridis"

/db\_xref="taxon:99883"

/clone\_image="220109"

/clone\_lib="G"

/note="Genoscope sequence ID : C0AG220AED05SP1-end ;  
PUC-Orl"

BASE COUNT 27 a 21 c 42 g 0 t 2 others

## ORIGIN

Query Match 64.0%; Score 12.8; DB 17; Length 92;  
Best Local Similarity 87.5%; Pred. No. 4.4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGGCGCCCTGTCCG 18  
|||||  
DB 33 TGGCGCCCTGTCCG 18

## RESULT 15

AZ342558 99 bp DNA linear GSS 29-SEP-2000  
1M0075109R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0075109 R, DNA sequence.

ACCESSION AZ342558

VERSION AZ342558.1 GI:10419915

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 99)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beccorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

EMAIL: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0075 row: L column: 09

Seq primer: CACACGAGAACACGATATGACC

Class: plasmid ends

High quality sequence stop: 99.

location/Qualifiers

1..99

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone\_image="UUGC1M0075109"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|pb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 16 a 31 c 23 g 29 t  
ORIGIN

Query Match 64.0%; Score 12.8; DB 17; Length 99;  
Best Local Similarity 87.5%; Pred. No. 4.5e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGGGGCCCTGTGTC 18  
||| ||||| |||  
Db 6 TGGGGCCCTGTGACCC 21

Search completed: November 26, 2002, 04:07:25  
Job time : 766.8 secs

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## SUMMARIES

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2002, 14:46:40 ; Search time 302.2 Seconds

(without alignments)  
1926.063 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20  
Sequence: 1 gtcgccagccagagcagctg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

GenBank: \*  
1: gb\_ba: \*  
2: gb\_ba: \*  
3: gb\_ba: \*  
4: gb\_ba: \*  
5: gb\_ba: \*  
6: gb\_ba: \*  
7: gb\_ba: \*  
8: gb\_ba: \*  
9: gb\_ba: \*  
10: gb\_ba: \*  
11: gb\_ba: \*  
12: gb\_ba: \*  
13: gb\_ba: \*  
14: gb\_ba: \*  
15: gb\_ba: \*  
16: gb\_ba: \*  
17: gb\_ba: \*  
18: gb\_ba: \*  
19: gb\_ba: \*  
20: gb\_ba: \*  
21: gb\_ba: \*  
22: gb\_ba: \*  
23: gb\_ba: \*  
24: gb\_ba: \*  
25: gb\_ba: \*  
26: gb\_ba: \*  
27: gb\_ba: \*  
28: gb\_ba: \*  
29: gb\_ba: \*  
30: gb\_ba: \*  
31: gb\_ba: \*  
32: gb\_ba: \*  
33: gb\_ba: \*  
34: gb\_ba: \*  
35: gb\_ba: \*  
36: gb\_ba: \*  
37: gb\_ba: \*  
38: gb\_ba: \*  
39: gb\_ba: \*  
40: gb\_ba: \*  
41: gb\_ba: \*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match Length	DB ID	Description
1	15.4	77.0	50 6 AX430850	AX430850 Sequence
2	14.2	71.0	42 6 AX231094	AX231094 Sequence
3	14.2	71.0	42 6 AX231098	AX231098 Sequence
4	14.2	71.0	42 6 AX231555	AX231555 Sequence
5	14.2	71.0	42 6 AX232206	AX232206 Sequence
6	14.2	71.0	42 6 AX233340	AX233340 Sequence
7	14.2	71.0	91 9 HSINOSX01	HSINOSX01 Sequence
8	13.4	67.0	51 6 AX157921	AX157921 Sequence
9	13.4	67.0	51 6 AX157922	AX157922 Sequence
10	13.4	67.0	99 11 G34988	G34988 DBX human S
11	13.2	66.0	27 6 AX306740	AX306740 Sequence
12	13.2	66.0	27 6 AX306741	AX306741 Sequence
13	13.2	66.0	28 6 AR130372	AR130372 Sequence
14	13.2	66.0	51 6 AX115349	AX115349 Sequence
15	13.2	66.0	76 6 AR121636	AR121636 Sequence
16	13.2	66.0	76 6 E55383	E55383 Process for
17	13.2	66.0	90 6 AX306734	AX306734 Sequence
18	13.2	66.0	100 11 HSA308722	HSA308722 Homo sapl
19	13.2	65.0	17 6 AR196300	AR196300 Sequence
20	12.8	64.0	27 6 I3657	I3657 Sequence 6
21	12.8	64.0	30 6 I58430	I58430 Sequence 14
22	12.8	64.0	31 6 I58435	I58435 Sequence 19
23	12.8	64.0	55 6 I13710	I13710 Sequence 16
24	12.8	64.0	58 6 AR172735	AR172735 Sequence
25	12.8	64.0	58 6 AR178679	AR178679 Sequence
26	12.8	64.0	58 6 AR181250	AR181250 Sequence
27	12.8	64.0	58 6 AR199931	AR199931 Sequence
28	12.8	64.0	60 6 AX097401	AX097401 Sequence
29	12.8	64.0	60 6 E08036	E08036 DNA encodin
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34	12.8	64.0	63 6 A42422	A42422 Sequence 4
35	12.8	64.0	63 6 A69367	A69367 Sequence 6
36	12.8	64.0	63 6 A72044	A72044 Sequence 6
37	12.8	64.0	63 6 AR080440	AR080440 Sequence
38	12.8	64.0	63 6 AX195143	AX195143 Sequence
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41	12.8	64.0	64 6 I24049	I24049 Sequence 13
42	12.8	64.0	65 6 AX329397	AX329397 Sequence
43	12.8	64.0	66 6 AX430829	AX430829 Sequence
44	12.8	64.0	66 6 AX431269	AX431269 Sequence
45	12.8	64.0	66 6 AX431272	AX431272 Sequence

## ALIGNMENTS

RESULT 1  
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LOCUS AX430850 50 bp mRNA linear PAT 28-JUN-2002  
DEFINITION Sequence 4 from Patent WO0240994.  
ACCESSION AX430850  
VERSION AX430850.1 GI:21655915  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Meshorer, E., Shoham, S., Soreq, H. and Sklan, E.  
AUTHORS  
TITLE System and method for assaying drugs  
JOURNAL Patent: WO 0240994-A 4 23-MAY-2002;

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Db       50 TCCTTCATCATCACGGTGC 34

RESULT 2
LOCUS AX231094                      42 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 490 from Patent WO0162787.
ACCESSION AX231094
VERSION AX231094.1 GI:15592450
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Herath,H.M., Parekh,R.B., Rohlf,C.O., Terrett,J.A. and Tyson,K.L.
TITLE Diagnosis and treatment of bipolar affective disorder
JOURNAL Patent: WO 0162787-A 490 30-Aug-2001;
Oxford Glycosciences (UK) Limited (GB)
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Matches 16; Conservative 0; Mismatches 3;

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RESULT 3
LOCUS AX231098                      42 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 494 from Patent WO0162787.
ACCESSION AX231098
VERSION AX231098.1 GI:15592454
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Herath,H.M., Parekh,R.B., Rohlf,C.O., Terrett,J.A. and Tyson,K.L.
TITLE Diagnosis and treatment of bipolar affective disorder
JOURNAL Patent: WO 0162787-A 494 30-Aug-2001;
Oxford Glycosciences (UK) Limited (GB)
Location/Qualifiers
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DEFINITION	Sequence: 453 from Patent WO0163294.								
ACCESSION	AX231555								
VERSION	AX231555.1	GI:15592461							
KEYWORDS	human.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.								
TITLE	1 (bases 1 to 42)								
JOURNAL	Herath,H.M., Parekh,R.B. and Rohlf,C.O.								
	Diagnosis and treatment of schizophrenia								
	Patent: WO 0163293-A 484 30-AUG-2001;								
	Oxford Glycosciences (UK) Limited (GB)								
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Db	7	GTGGCCATCGAGAGCGACT	25						
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DEFINITION	Sequence 484 from Patent WO0163293.								
ACCESSION	AX232206								
VERSION	AX232206.1	GI:15592539							
KEYWORDS	human.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.								
TITLE	1 (bases 1 to 42)								
JOURNAL	Herath,H.M.A., Parekh,R.B. and Rohlf,C.O.								
	Diagnosis and treatment of schizophrenia								
	Patent: WO 0163293-A 484 30-AUG-2001;								
	Oxford Glycosciences (UK) Limited (GB)								
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Best Local Similarity 84.2%; Pred. No. 2.5e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCAGCCGAGCGACT 19  
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Db 7 GTGCCATCGAGCGACT 25

RESULT 6  
AX233340 42 bp DNA linear PAT 11-SEP-2001  
LOCUS AX233340  
DEFINITION Sequence 664 from Patent WO0162785.  
ACCESSION AX233340  
VERSION AX233340.1 GI:15592679  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 42)  
AUTHORS Herath,H.M., Parekh,R.B., Rohlf,C.C., Terrett,J.A. and Tyson,K.L.  
TITLE Protein and gene and their use for diagnosis and treatment of  
schizophrenia  
JOURNAL Patent: WO 0162785-A 664 30-AUG-2001;  
FEATURES  
source Oxford Glycosciences (UK) Limited (GB)  
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Best Local Similarity 84.2%; Pred. No. 2.5e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 7 GTGCCATCGAGCGACT 25

RESULT 7  
HSINOSX01 91 bp DNA linear PRI 27-JAN-1998  
LOCUS HSINOSX01  
DEFINITION Human inducible nitric oxide synthase (INOS) pseudogene, exon 1.  
ACCESSION U65689  
VERSION U65689.1 GI:1621317  
KEYWORDS  
SEGMENT  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 91)  
AUTHORS Park,C.S., Park,R., Lee,H.S., Lee,H.Y. and Krishna,G.  
TITLE Direct Submission  
JOURNAL Submitted (31-JUL-1996) Section of Chemical Pharmacology, National

INSTITUTES OF HEALTH, Bethesda, MD 20892, USA  
2 (bases 1 to 91)  
AUTHORS Park,C.S., Lee,H.S., Lee,H.Y. and Krishna,G.  
TITLE An unprocessed pseudogene of inducible nitric oxide synthase gene  
JOURNAL In human  
MEDLINE Nitric Oxide 1 (4), 294-300 (1997)  
PUBMED 98368274  
9441901

FEATURES  
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 34 GTGCCAGCCGAGCGACTCT 52

RESULT 8  
AX157921 51 bp DNA linear PAT 22-JUN-2001  
LOCUS AX157921  
DEFINITION Sequence 1249 from Patent WO0140521.  
ACCESSION AX157921  
VERSION AX157921.1 GI:14539252  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 51)  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0140521-A 1249 07-JUN-2001;  
FEATURES  
source Curagen Corporation (US)  
Location/Qualifiers  
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 9 CAGCCAGAGCGACTG 23

RESULT 9  
AX157922 51 bp DNA linear PAT 22-JUN-2001  
LOCUS AX157922  
DEFINITION Sequence 1250 from Patent WO0140521.  
ACCESSION AX157922

VERSION AX157922.1 GI:14539253  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 51)  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0140521-A 1250 07-JUN-2001;  
Curagen Corporation (US)  
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OY 6 CAGCCAGAGCAGCTG 20  
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G34988 99 bp DNA linear STS 06-DEC-1999  
LOCUS G34988  
DEFINITION DBX human STS derived from X-linked gene Homo sapiens STS genomic,  
sequence tagged site.  
ACCESSION G34988  
VERSION G34988.1 GI:2599270  
KEYWORDS STS.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 99)  
AUTHORS Lahn,B.T. and Page,D.C.  
TITLE Functional coherence of the human Y chromosome  
JOURNAL Science 278 (5338), 675-680 (1997)  
MEDLINE 98022381  
PUBMED 9381176  
COMMENT  
Contact: Bruce T. Lahn  
Page Lab  
Whitehead Institute for Biomedical Research  
9 Cambridge Center, Cambridge, MA 02142, USA  
Tel: 6172585164  
Email: blahn@wi.mit.edu  
Primer A: CTACATGCAGATGACATGCTG  
Primer B: GGCCAGGTGATGATGCTG  
STS size: 99  
PCR Profile:  
Denaturation: 94 for 1 min  
Annealing: 60 for 45 sec  
Polymerization: 72 for 45 sec  
PCR Cycles: 30  
Thermal Cycler: MJ Research  
Protocol:  
Template: 50 ng  
Primer: each 1 uM  
dNTPs: 100 uM  
Tag Polymerase: 1 unit  
Total Vol: 20 uL  
Buffer:

MgCl2: 1.5 mM  
KCl: 50 mM  
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AX306740 27 bp DNA linear PAT 11-DEC-2001  
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DEFINITION Sequence 58 from Patent WO0187925.  
ACCESSION AX306740  
VERSION AX306740.1 GI:17645907  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
artificial sequences.  
REFERENCE 1  
AUTHORS Rosendahl,M.S., Cox,G.N. and Doherty,D.H.  
TITLE Methods for refolding proteins containing free cysteine residues  
JOURNAL Patent: WO 0187925-A 58 22-NOV-2001;  
Boulder Biotechnology, Inc. (US)  
FEATURES  
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DEFINITION Sequence 59 from Patent WO0187925.  
ACCESSION AX306741  
VERSION AX306741.1 GI:17645908  
KEYWORDS  
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ORGANISM synthetic construct.  
artificial sequences.  
REFERENCE 1  
AUTHORS Rosendahl,M.S., Cox,G.N. and Doherty,D.H.  
TITLE Methods for refolding proteins containing free cysteine residues  
JOURNAL Patent: WO 0187925-A 59 22-NOV-2001;  
Boulder Biotechnology, Inc. (US)

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Db 26 TGCCAGCCAGCGACT 9

RESULT 13  
ARI30372/c 28 bp DNA linear PAT 16-MAY-2001  
LOCUS  
DEFINITION Sequence 2 from patent US 6190657.  
ACCESSION ARI30372  
VERSION ARI30372.1 GI:14118697  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Pawelek,J.M., Bernudes,D. and Low,K.Brooks.  
TITLE Vectors for the diagnosis and treatment of solid tumors including melanoma  
JOURNAL Patent: US 6190657-A 2 20-FEB-2001;  
FEATURES Location/Qualifiers  
source 1. 28  
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BASE COUNT 6 a 6 c 10 g 6 t  
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RESULT 14  
AX115349 51 bp DNA linear PAT 11-MAY-2001  
LOCUS  
DEFINITION Sequence 472 from Patent WO0129262.  
ACCESSION AX115349  
VERSION AX115349.1 GI:14032291  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 51)  
AUTHORS Picoult-Newburg,L. and Pohl,M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 0129262-A 472 26-APR-2001;  
FEATURES Location/Qualifiers  
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 15  
ARI21636/c 76 bp DNA linear PAT 16-MAY-2001  
LOCUS  
DEFINITION Sequence 31 from patent US 6160089.  
ACCESSION ARI21636  
VERSION ARI21636.1 GI:14105212  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 76)  
AUTHORS Honjo,M., Naitoh,N., Uchida,H., Mochizuki,D. and Matsumoto,K.  
TITLE Method for secretory production of human growth hormone  
JOURNAL Patent: US 6160089-A 31 12-DEC-2000;  
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Job time : 309.2 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:53:51 : Search time 21.55 Seconds  
(Without alignments) 284.619 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20

Sequence: 1 gtccaccagcagcagcactg 20

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Gapop 10.0 , Gapext 1.0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	13.2	66.0	28 4	US-08-658-034-2	Sequence 2, Appl1
2	13.2	66.0	76 4	US-09-348-578-31	Sequence 31, Appl1
3	13.2	66.0	76 4	US-09-699-684-31	Sequence 31, Appl1
4	13.2	66.0	17 4	US-08-679-645-765	Sequence 765, App
5	12.8	64.0	27 1	US-07-749-446-6	Sequence 6, Appl1
6	12.8	64.0	30 1	US-08-360-841-14	Sequence 14, Appl1
7	12.8	64.0	31 1	US-08-360-841-19	Sequence 19, Appl1
8	12.8	64.0	55 1	US-07-826-928A-16	Sequence 16, Appl1
9	12.8	64.0	58 4	US-09-339-913B-54	Sequence 54, Appl1
10	12.8	64.0	58 4	US-09-339-904A-54	Sequence 54, Appl1
11	12.8	64.0	58 4	US-08-769-062B-54	Sequence 54, Appl1
12	12.8	64.0	58 4	US-09-344-002B-54	Sequence 54, Appl1
13	12.8	64.0	58 4	US-09-559-565C-54	Sequence 54, Appl1
14	12.8	64.0	60 1	US-08-325-243A-14	Sequence 14, Appl1
15	12.8	64.0	63 1	US-07-842-089E-5	Sequence 5, Appl1
16	12.8	64.0	63 1	US-08-264-485-5	Sequence 7, Appl1
17	12.8	64.0	63 2	US-09-003-081-7	Sequence 7, Appl1
18	12.8	64.0	63 3	US-08-648-262-7	Sequence 7, Appl1
19	12.8	64.0	63 3	US-08-648-263-7	Sequence 7, Appl1
20	12.8	64.0	64 1	US-08-325-243A-13	Sequence 13, Appl1
21	12.8	64.0	69 1	US-08-215-138-18	Sequence 18, Appl1
22	12.8	64.0	69 1	US-08-215-138-19	Sequence 18, Appl1
23	12.8	64.0	69 1	US-08-407-344-18	Sequence 18, Appl1
24	12.8	64.0	69 1	US-08-407-344-19	Sequence 19, Appl1
25	12.8	64.0	72 1	US-07-826-928A-19	Sequence 19, Appl1
26	12.8	64.0	73 1	US-07-854-845B-2	Sequence 2, Appl1
27	12.8	64.0	77 3	US-08-666-354A-10	Sequence 10, Appl1

C 28	12.8	64.0	78 4	US-08-976-183A-1	Sequence 1, Appl1
C 29	12.8	64.0	78 4	US-08-976-183A-3	Sequence 3, Appl1
C 30	12.8	64.0	87 1	US-07-826-928A-26	Sequence 26, Appl1
C 31	12.8	64.0	87 1	US-07-826-928A-27	Sequence 27, Appl1
C 32	12.8	64.0	87 2	US-08-449-287-18	Sequence 18, Appl1
C 33	12.8	64.0	87 2	US-08-449-287-19	Sequence 19, Appl1
C 34	12.8	64.0	93 1	US-08-458-120-3	Sequence 3, Appl1
C 35	12.8	64.0	93 2	US-08-187-186A-3	Sequence 3, Appl1
C 36	12.8	64.0	93 4	US-08-442-497C-3	Sequence 3, Appl1
C 37	12.8	64.0	93 4	US-09-333-033-3	Sequence 3, Appl1
C 38	12.6	63.0	20 3	US-08-872-855-12	Sequence 12, Appl1
C 39	12.6	63.0	37 3	US-08-862-431-47	Sequence 47, Appl1
C 40	12.6	63.0	63 1	US-08-590-804-31	Sequence 31, Appl1
C 41	12.4	62.0	17 4	US-09-610-155D-3	Sequence 3, Appl1
C 42	12.4	62.0	30 4	US-09-142-334-2	Sequence 2, Appl1
C 43	12.4	62.0	30 4	US-09-142-334-5	Sequence 5, Appl1
C 44	12.4	62.0	60 1	US-08-484-192-154	Sequence 154, App
C 45	12.4	62.0	60 1	US-08-484-192-156	Sequence 156, App

## ALIGNMENTS

RESULT 1  
US-08-658-034-2/c  
Sequence 2, Application US/08658034  
Patent No. 6190657  
GENERAL INFORMATION:  
APPLICANT: Pawelek, John M.  
APPLICANT: Bermudez, David  
APPLICANT: Low, Kenneth Brooks  
TITLE OF INVENTION: VECTORS FOR THE DIAGNOSIS AND TREATMENT  
TITLE OF INVENTION: OF SOLID TUMORS INCLUDING MELANOMA  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pennile & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,034  
FILING DATE: On Even Date Herewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Baldwin, Geraldine F.  
REGISTRATION NUMBER: 31,232  
REFERENCE/DOCKET NUMBER: 8002-036  
TELEPHONE/COMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-658-034-2  
Query Match 66.0%; Score 13.2; DB 4; Length 28;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 GCCCAGCAGAGCAGCTG 20  
||||| ||||| ||||| |||||

Db 28 GCCCTGCATGACCACTG 11

## RESULT 2

US-09-348-578-31/c  
Sequence 31, Application US/09348578  
Patent No. 6160089

## GENERAL INFORMATION:

APPLICANT: HONJO, Masaru  
APPLICANT: NAITOH, Naokazu  
APPLICANT: UCHIDA, Hiroshi  
APPLICANT: MOCHIZUKI, Daisuke

APPLICANT: MATSUMOTO, Kazuya  
TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE  
FILE REFERENCE: 029430-421

CURRENT FILING DATE: 1999-07-07

EARLIER APPLICATION NUMBER: JP 193003/1998

EARLIER FILING DATE: 1998-07-08

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 31

LENGTH: 76

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

LOCATION: (1)..(76)

OTHER INFORMATION: Description of Artificial Sequence: Designed DNA sequence to

OTHER INFORMATION: act as a primer for PCR to produce the latter half of OpA

US-09-348-578-31

Query Match 66.0%; Score 13.2; DB 4; Length 76;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 GCCCAGCCAGAGCGACTG 20

Db 25 GCGCAGCCAGAACGCCCTG 8

## RESULT 3

US-09-699-684-31/c

Sequence 31, Application US/09699684  
Patent No. 6436674

## GENERAL INFORMATION:

APPLICANT: HONJO, Masaru

APPLICANT: NAITOH, Naokazu

APPLICANT: UCHIDA, Hiroshi

APPLICANT: MOCHIZUKI, Daisuke

APPLICANT: MATSUMOTO, Kazuya

TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE

FILE REFERENCE: 029430-421

CURRENT APPLICATION NUMBER: US/09/699,684

PRIOR APPLICATION NUMBER: 2000-10-31

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/348,578

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 31

LENGTH: 76

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

LOCATION: (1)..(76)

OTHER INFORMATION: Description of Artificial Sequence: Designed DNA sequence to

OTHER INFORMATION: act as a primer for PCR to produce the latter half of OpA

US-09-699-684-31

Query Match 66.0%; Score 13.2; DB 4; Length 76;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 GCCCAGCCAGAGCGACTG 20

Db 25 GCGCAGCCAGAACGCCCTG 8

## RESULT 4

US-08-679-645-765/c  
Sequence 765, Application US/08679645  
Patent No. 6350934

## GENERAL INFORMATION:

APPLICANT: Zwick, Michael G.

APPLICANT: Edington, Brent E.

APPLICANT: McSwigen, James A.

APPLICANT: Merlo, Patricia Ann Owens

APPLICANT: Guo, Lining

APPLICANT: Skokut, Thomas A.

APPLICANT: Young, Scott A.

APPLICANT: Folkerts, Otto

TITLE OF INVENTION: COMPOSITION AND METHODS FOR

TITLE OF INVENTION: MODULATION OF GENE EXPRESSION

NUMBER OF SEQUENCES: 1263

CORRESPONDENCE ADDRESS:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/679,645

FILING DATE: July 12, 1996

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/001,135

FILING DATE: July 13, 1995

APPLICATION NUMBER: 08/300,726

FILING DATE: September 2, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 219/247

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 765:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-679-645-765

Query Match 65.0%; Score 13; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 CAGCCAGAGCGAC 18

Db 15 CAGCCAGAGCGAC 3

RESULT 5

US-07-749-446-6/C  
Sequence 6, Application US/07749446  
Patent No. 5593857  
GENERAL INFORMATION:  
APPLICANT: Higaki, Jeffrey N.  
APPLICANT: Tischer, Edmund G.  
APPLICANT: Cordell, Barbara  
APPLICANT: Thompson, Stewart A.  
TITLE OF INVENTION: PRODUCTION OF HOMOGENEOUS CILIARY  
TITLE OF INVENTION: NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: California Biotechnology Inc.  
STREET: 2450 Bayshore Parkway  
CITY: Mountain View  
STATE: California  
COUNTRY: USA  
ZIP: 94043  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/749,446  
FILING DATE: 19911008  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Shearer, Peter R.  
REGISTRATION NUMBER: 28,117  
REFERENCE/DOCKET NUMBER: PC43:US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-962-5860  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-07-749-446-6

Query Match 64.0%; Score 12.8; DB 1; Length 27;  
Best Local Similarity 87.5%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCCAGCCGAGCGACT 19  
DB 27 CCGAGCGAGCGACT 12

RESULT 6  
US-08-360-841-14/C  
Sequence 14, Application US/08360841  
Patent No. 5652120  
GENERAL INFORMATION:  
APPLICANT: PARK, Seung Kook  
APPLICANT: LEE, Kang Moon  
APPLICANT: NHO, Kyo Seung  
APPLICANT: KOH, Yeo Wook  
APPLICANT: KWON, Chang Hyuk  
APPLICANT: CHUNG, Ju Young  
APPLICANT: JEE, Young Su  
APPLICANT: YU, Young Hyo  
TITLE OF INVENTION: A No. 5652120e1 Gene Coding Human Epidermal  
TITLE OF INVENTION: Growth Factor and Process for Preparing the Same  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dady & Dady PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: US

ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,841  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, S. Peter  
REGISTRATION NUMBER: 25,351  
REFERENCE/DOCKET NUMBER: 0136/0A760  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: OMP C2 PRIMER  
US-08-360-841-14

Query Match 64.0%; Score 12.8; DB 1; Length 30;  
Best Local Similarity 87.5%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCAGCCAGCGCGACTG 20  
DB 20 CCAGCCAGTCCGACTG 5

RESULT 7  
US-08-360-841-19  
Sequence 19, Application US/08360841  
Patent No. 5652120  
GENERAL INFORMATION:  
APPLICANT: PARK, Seung Kook  
APPLICANT: LEE, Kang Moon  
APPLICANT: NHO, Kyo Seung  
APPLICANT: KOH, Yeo Wook  
APPLICANT: KWON, Chang Hyuk  
APPLICANT: CHUNG, Ju Young  
APPLICANT: JEE, Young Su  
APPLICANT: YU, Young Hyo  
TITLE OF INVENTION: A No. 5652120e1 Gene Coding Human Epidermal  
TITLE OF INVENTION: Growth Factor and Process for Preparing the Same  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dady & Dady PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: US  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,841  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, S. Peter  
REGISTRATION NUMBER: 25,351  
REFERENCE/DOCKET NUMBER: 0136/0A760  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: OMP N3 PRIMER  
US-08-360-841-19

Query Match 64.0%; Score 12.8; DB 1; Length 31;  
Best Local Similarity 87.5%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCAGCCAGAGCGACTG 20  
DB 15 CCAGCCAGTGCCTG 30

RESULT 8  
US-07-826-928A-16/c  
Sequence 16, Application US/07826928A  
Patent No. 5439829  
GENERAL INFORMATION:  
APPLICANT: Anderson, Leslie D.  
APPLICANT: Cook, James A.  
APPLICANT: David, Gary S.  
APPLICANT: Hochschwender, Susan M.  
APPLICANT: Kasher, Mary S.  
APPLICANT: Smith, Michele C.  
APPLICANT: Stemmer, Willem P.  
TITLE OF INVENTION: METHOD OF IMMOBILIZING AND CROSS LINKING  
TITLE OF INVENTION: PROTEINS AND OTHER MOLECULES AND USES THEREOF  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: IN  
COUNTRY: USA  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/826, 928A  
FILING DATE: 19920124  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, Richard B.  
REGISTRATION NUMBER: 35,296  
REFERENCE/DOCKET NUMBER: X8180A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 317-276-3589  
TELEFAX: 317-276-1294  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 55 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
US-07-826-928A-16

Query Match 64.0%; Score 12.8; DB 1; Length 55;  
Best Local Similarity 87.5%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCAGCCAGAGCGACTG 20  
DB 26 CCAGCCAGTGCCTG 11

RESULT 9  
US-09-339-913B-54  
Sequence 54, Application US/09339913B  
Patent No. 6303344  
GENERAL INFORMATION:  
APPLICANT: Patten, Phillip  
APPLICANT: Stemmer, Willem P.C.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING  
FILE REFERENCE: 02-020503US  
CURRENT APPLICATION NUMBER: US/09/339, 913B  
CURRENT FILING DATE: 1999-06-24  
PRIOR APPLICATION NUMBER: 08/769, 062  
PRIOR FILING DATE: 1996-12-18  
PRIOR APPLICATION NUMBER: 08/198, 431  
PRIOR FILING DATE: 1994-02-17  
PRIOR APPLICATION NUMBER: 08/425, 684  
PRIOR FILING DATE: 1995-04-18  
PRIOR APPLICATION NUMBER: 08/537, 874  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 54  
LENGTH: 58  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: degenerate  
OTHER INFORMATION: oligonucleotide used for codon usage library  
US-09-339-913B-54

Query Match 64.0%; Score 12.8; DB 4; Length 58;  
Best Local Similarity 81.2%; Pred. No. 1.8e+03;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCAGCCAGAGCGACTG 20  
DB 15 CCAGCCAGTGCCTG 30

RESULT 10  
US-09-339-904A-54  
Sequence 54, Application US/09339904A  
Patent No. 6319713  
GENERAL INFORMATION:  
APPLICANT: Patten, Phillip  
APPLICANT: Stemmer, Willem P.C.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING  
FILE REFERENCE: 02-020504US  
CURRENT APPLICATION NUMBER: US/09/339, 904A  
CURRENT FILING DATE: 1999-06-24  
PRIOR APPLICATION NUMBER: 08/769, 062  
PRIOR FILING DATE: 1996-12-18  
PRIOR APPLICATION NUMBER: 08/198, 431  
PRIOR FILING DATE: 1994-02-17  
PRIOR APPLICATION NUMBER: 08/425, 684  
PRIOR FILING DATE: 1995-04-18  
PRIOR APPLICATION NUMBER: 08/537, 874  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 54



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; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: degenerate
US-09-339-904A-54
;
Query Match          64.0%; Score 12.8; DB 4; Length 58;
Best Local Similarity 81.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCAGCCAGAGCGACTG 20
DB 15 CCAGCCAGGCHACHG 30

RESULT 11
US-08-769-062B-54
; Sequence 54, Application US/08769062B
; Patent No. 6335160
; GENERAL INFORMATION:
; APPLICANT: Paten, Phillip
; APPLICANT: Stemmer, William P.C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
; FILE REFERENCE: 02-020500US
; CURRENT APPLICATION NUMBER: US/08/769,062B
; CURRENT FILING DATE: 1996-12-18
; PRIOR APPLICATION NUMBER: 08/198,431
; PRIOR FILING DATE: 1994-02-17
; PRIOR APPLICATION NUMBER: 08/425,684
; PRIOR FILING DATE: 1995-04-18
; PRIOR APPLICATION NUMBER: 08/537,874
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 54
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: degenerate
US-08-769-062B-54
;
Query Match          64.0%; Score 12.8; DB 4; Length 58;
Best Local Similarity 81.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCAGCCAGAGCGACTG 20
DB 15 CCAGCCAGGCHACHG 30

RESULT 12
US-09-344-002B-54
; Sequence 54, Application US/09344002B
; Patent No. 6335484
; GENERAL INFORMATION:
; APPLICANT: Paten, Phillip
; APPLICANT: Stemmer, William P.C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
; FILE REFERENCE: 02-020502US
; CURRENT APPLICATION NUMBER: US/09/344,002B
; CURRENT FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: 08/769,062
; PRIOR FILING DATE: 1996-12-18
; PRIOR APPLICATION NUMBER: 08/198,431
; PRIOR FILING DATE: 1994-02-17
; PRIOR APPLICATION NUMBER: 08/425,684
; PRIOR FILING DATE: 1995-04-18
; PRIOR APPLICATION NUMBER: 08/537,874
; PRIOR FILING DATE: 1995-10-30
```

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; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 54
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: degenerate
US-09-344-002B-54
;
Query Match          64.0%; Score 12.8; DB 4; Length 58;
Best Local Similarity 81.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCAGCCAGAGCGACTG 20
DB 15 CCAGCCAGGCHACHG 30

RESULT 13
US-09-559-565C-54
; Sequence 54, Application US/09559565C
; Patent No. 6455253
; GENERAL INFORMATION:
; APPLICANT: Paten, Phillip
; APPLICANT: Stemmer, William P.C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
; FILE REFERENCE: 02-020506US
; CURRENT APPLICATION NUMBER: US/09/559,565C
; CURRENT FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 54
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: degenerate
US-09-559-565C-54
;
Query Match          64.0%; Score 12.8; DB 4; Length 58;
Best Local Similarity 81.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCAGCCAGAGCGACTG 20
DB 15 CCAGCCAGGCHACHG 30

RESULT 14
US-08-325-243A-14
; Sequence 14, Application US/08325243A
; Patent No. 5541288
; GENERAL INFORMATION:
; APPLICANT: Nakano, Shigeru
; APPLICANT: Mabuchi, Toshiyuki
; APPLICANT: Tada, Miki
; APPLICANT: Tadoda, Yasuo
; APPLICANT: Sugino, Dan
; APPLICANT: Kono, Yoshio
; APPLICANT: Nishimura, Kaoru
; APPLICANT: Okushima, Minoru
; TITLE OF INVENTION: No. 5541288el Peptide Having Elastase Inhibitory
; TITLE OF INVENTION: Activity and Producing Method Thereof
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
```

```

1 ZIP: 60606-6402
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3 COMPUTER READABLE FORM:
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5 MEDIUM TYPE: Floppy disk
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7 COMPUTER: IBM PC compatible
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9 OPERATING SYSTEM: PC-DOS/MS-DOS
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11 SOFTWARE: PatentIn Release #1.0, Version #1.25
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/08/325,243A
16
17 FILING DATE: 16-DEC-94
18
19 CLASSIFICATION: 530
20
21 PRIOR APPLICATION DATA:
22
23 APPLICATION NUMBER: JP 5-31758
24
25 FILING DATE: 22-FEB-1993
26
27 ATTORNEY/AGENT INFORMATION:
28
29 NAME: No. 5541288and, Greta E.
30
31 REGISTRATION NUMBER: 35,302
32
33 REFERENCE/DOCKET NUMBER: 19036/32311
34
35 TELECOMMUNICATION INFORMATION:
36
37 TELEPHONE: 312/474-6300
38
39 TELEFAX: 312/474-0448
40
41 TELE: 25-3856
42
43 INFORMATION FOR SEQ ID NO: 14:
44
45 SEQUENCE CHARACTERISTICS:
46
47 LENGTH: 60 base pairs
48
49 TYPE: nucleic acid
50
51 STRANDEDNESS: single
52
53 TOPOLOGY: linear
54
55 MOLECULE TYPE: Other nucleic acid, synthesized DNA
56
57 FEATURE:
58
59 NAME/KEY: sig peptide
60
61 LOCATION: 1..60
62
63 IDENTIFICATION METHOD: S
64
65 OTHER INFORMATION: Complementary Strand is formed with Sequence
66
67 OTHER INFORMATION: of SEQ. ID. NO.13.
68
69 US-08-325-243A-14

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Query Match				
Best Local Similarity	87.5%;	Pred. No. 1.8e+03;		
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db	23	CCAGGCCAGCGCAACAG	38	

RESULT 15  
 US-07-842-089E-5/C  
 Sequence 5, Application US/07842089E  
 Patent No. 5356875  
 GENERAL INFORMATION:  
 APPLICANT: SARMIENTOS, PAOLO  
 APPLICANT: DE TAXIS DU POET, PHILIPPE  
 APPLICANT: NITTI, GIAMPOLO  
 APPLICANT: SCACHEMI, EMANUELA  
 TITLE OF INVENTION: ANTI-THROMBIN POLYPEPTIDES  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
 ADDRESSEE: P.C.  
 STREET: 1755 Jefferson Davis Highway, Fourth Floor  
 City: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/842,089E  
 FILING DATE: 26-FEB-1992  
 CLASSIFICATION: 435

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ATTORNEY/AGENT INFORMATION:
NAME: O'Brien, No. 5356875man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 769-265-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..63
OTHER INFORMATION: /function="leader peptide"
OTHER INFORMATION: /standard_name="OmpA leader"
OS-07-842-089E-5

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64	Query Match	64.0%	Score 12.8	DB 1	length 63
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					Gaps 0;
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Db	41	CCAGCCAGTGGCCACTG	26		

Search completed: November 23, 2002, 06:36:08  
Job time : 23.55 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:54:41 : Search time 17.25 Seconds  
(without alignments)  
439.108 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20

Sequence: 1 gtgcccagcagcagcagcactg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 195614

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*

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2: /cgn2\_6/ptodata/2/pubpna/PCr\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
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12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	14.2	71.0	42	10	US-09-791-378-664	Sequence 664, App
2	13.4	67.0	100	10	US-09-864-761-18482	Sequence 18482, A
3	12.8	64.0	58	10	US-09-559-671A-54	Sequence 54, Appl
4	12.8	64.0	63	10	US-09-760-008A-4	Sequence 4, Appl1
5	12.8	64.0	65	10	US-09-875-494-20	Sequence 20, Appl
6	12.8	64.0	93	12	US-10-004-832-3	Sequence 3, Appl1
7	12.8	64.0	99	10	US-09-815-343-1484	Sequence 1484, Ap
8	12.6	63.0	79	10	US-09-864-761-26473	Sequence 26473, A
9	12.6	63.0	96	10	US-09-864-761-28720	Sequence 28720, A
10	12.4	62.0	30	10	US-09-875-519A-2	Sequence 2, Appl1
11	12.4	62.0	31	10	US-09-875-519A-5	Sequence 5, Appl1
12	12.4	62.0	31	10	US-09-801-274-1274	Sequence 1274, Ap
13	12	60.0	24	10	US-09-823-936-8	Sequence 8, Appl1
14	12	60.0	24	10	US-09-755-836-7	Sequence 7, Appl1
15	12	60.0	25	10	US-09-877-095-3	Sequence 3, Appl1
16	12	60.0	60	10	US-09-886-900-6	Sequence 6, Appl1
17	12	60.0	87	10	US-09-864-761-22774	Sequence 22774, A
18	12	60.0	100	10	US-09-851-190A-6	Sequence 6, Appl1
19	11.8	59.0	31	10	US-09-801-274-1422	Sequence 1422, Ap

20	11.8	59.0	35	9	US-10-023-096-6	Sequence 6, Appl1
21	11.8	59.0	46	10	US-09-920-171-28	Sequence 28, Appl
22	11.8	59.0	78	10	US-09-864-761-28519	Sequence 28519, A
23	11.8	59.0	84	9	US-10-109-971-7	Sequence 7, Appl1
24	11.8	59.0	88	10	US-09-864-761-30659	Sequence 30659, A
25	11.8	59.0	95	10	US-09-864-761-23346	Sequence 23346, A
26	11.6	58.0	30	10	US-09-875-519A-8	Sequence 8, Appl1
27	11.6	58.0	31	9	US-10-109-971-2	Sequence 2, Appl1
28	11.6	58.0	31	9	US-10-109-971-8	Sequence 8, Appl1
29	11.6	58.0	31	9	US-09-801-274-1045	Sequence 1045, Ap
30	11.6	58.0	72	9	US-09-916-494A-17	Sequence 17, Appl
31	11.6	58.0	75	10	US-09-880-253A-5	Sequence 5, Appl1
32	11.6	58.0	75	10	US-09-880-253A-56	Sequence 56, Appl
33	11.6	58.0	75	10	US-09-880-253A-57	Sequence 57, Appl
34	11.6	58.0	75	10	US-09-880-253A-58	Sequence 58, Appl
35	11.6	58.0	80	10	US-09-864-761-28043	Sequence 28043, A
36	11.4	57.0	17	10	US-09-866-108-9221	Sequence 9221, Ap
37	11.4	57.0	17	10	US-09-866-108-9222	Sequence 9222, Ap
38	11.4	57.0	17	10	US-09-866-108-9223	Sequence 9223, Ap
39	11.4	57.0	17	10	US-09-866-108-9224	Sequence 9224, Ap
40	11.4	57.0	25	10	US-09-866-108-9225	Sequence 9225, Ap
41	11.4	57.0	25	10	US-09-866-108-14113	Sequence 14113, A
42	11.4	57.0	25	10	US-09-866-108-14114	Sequence 14114, A
43	11.4	57.0	25	10	US-09-866-108-14115	Sequence 14115, A
44	11.4	57.0	25	10	US-09-866-108-14116	Sequence 14116, A
45	11.4	57.0	25	10	US-09-866-108-14117	Sequence 14117, A

## ALIGNMENTS

RESULT 1  
US-09-791-378-664  
Sequence 664, Application US/09/91378  
Patent No. US20020142303A1  
GENERAL INFORMATION:  
APPLICANT: Parekh, Rajesh  
TITLE OF INVENTION: SCITZOPHRENIA  
FILE REFERENCE: 9195-061-999  
CURRENT APPLICATION NUMBER: US/09/791,378  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/750,395  
PRIOR FILING DATE: 2000-12-28  
NUMBER OF SEQ ID NOS: 677  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 664  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-791-378-664

Query Match 71.0%; Score 14.2; DB 10; Length 42;  
Best Local Similarity 84.2%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGAGGACT 19  
Db 7 GTGCCATCGAGAGGACT 25

RESULT 2  
US-09-864-761-18482/c  
Sequence 18482, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeomlca-X-1

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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
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PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 18482
LENGTH: 100
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL117694.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN HBLA, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 14
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HEPRT, SIGNAL = 2.5
OTHER INFORMATION: SWISSPROT HIT: P12814, EVALU8 8.00e-12
OTHER INFORMATION: NT HIT: g114435217, EVALU8 1.00e-49
OTHER INFORMATION: EST_HUMAN HIT: BE831655.1, EVALU8 1.00e-49
US-09-864-761-18482

Query Match 67.0%, Score 13.4, DB 10, Length 100;
Best Local Similarity 93.3%, Pred. No. 8.6e+02;
Matches 14, Conservative 0, Mismatches 1, Indels 0, Gaps 0.
3 GCCCAGCCAGAGCGA 17
|||||
89 GCCCAGCCAGAGCGA 75

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RESULT 3  
US-09-559-671A-54  
; Sequence 54, Application US/09559671A

```

Patent No. US20020051976A1
GENERAL INFORMATION:
APPLICANT: Patten, Phillip
APPLICANT: Stemmer, William P.C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
FILE REFERENCE: 02-020503US
CURRENT APPLICATION NUMBER: US/09/559, 671A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 08/769,062
PRIOR FILING DATE: 1996-12-18
PRIOR APPLICATION NUMBER: 08/198,431
PRIOR FILING DATE: 1994-02-17
PRIOR APPLICATION NUMBER: 08/425,684
PRIOR FILING DATE: 1995-04-18
PRIOR APPLICATION NUMBER: 08/537,874
PRIOR FILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54
LENGTH: 58
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: degenerate
OTHER INFORMATION: oligonucleotide used for codon usage library
US-09-559-671A-54

Query Match      64.0%; Score 12.8; DB 10; Length 58;
Best Local Similarity 81.2%; Pred. No. 1.6e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db      15 CCAGCCAGHGHACHG 30

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Query Match	Best Local Similarity	Score	ID	Length
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<p>US-09-760-008A-4/C</p> <p>Sequence 4, Application US/09760008A</p> <p>Patent No. US20020004483A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: NISSEN, TORBEN LADESGAARD</p> <p>APPLICANT: ANDERSEN, KIM VILBOUR</p> <p>APPLICANT: HANSEN, CHRISTIAN KASTEN</p> <p>APPLICANT: MIKKELSEN, JAN MOLLER</p> <p>TITLE OF INVENTION: 6-CSF CONJUGATES</p> <p>FILE REFERENCE: 31-00070005</p> <p>CURRENT APPLICATION NUMBER: US/09/760,008A</p> <p>CURRENT FILING DATE: 2001-05-11</p> <p>PRIOR APPLICATION NUMBER: 60/176,376</p> <p>PRIOR FILING DATE: 2000-01-14</p> <p>PRIOR APPLICATION NUMBER: 60/189,506</p> <p>PRIOR FILING DATE: 2000-03-15</p> <p>PRIOR APPLICATION NUMBER: 60/215,644</p> <p>PRIOR FILING DATE: 2000-06-30</p> <p>PRIOR APPLICATION NUMBER: DK PA 2000 00024</p> <p>PRIOR FILING DATE: 2000-01-10</p> <p>PRIOR APPLICATION NUMBER: DK PA 2000 00341</p> <p>PRIOR FILING DATE: 2000-03-02</p> <p>PRIOR APPLICATION NUMBER: DK PA 2000 00943</p> <p>PRIOR FILING DATE: 2000-06-16</p> <p>NUMBER OF SEQ ID NOS: 15</p> <p>SOFTWARE: PatentIn Ver. 2.1</p> <p>SEQ ID NO 4</p> <p>LENGTH: 63</p> <p>TYPE: DNA</p> <p>ORGANISM: Artificial Sequence</p> <p>FEATURE:</p> <p>OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA</p> <p>US-09-760-008A-4</p>				



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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26473
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006548.19
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9
; OTHER INFORMATION: NT HIT: X83528.1, EVALUE 6.30e-01
; OTHER INFORMATION: EST_HUMAN HIT: A126906.1, EVALUE 9.40e-01
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US-09-864-761-26473
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Query Match          63.0%; Score 12.6; DB 10; Length 79;
Best Local Similarity 78.9%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY      2 TGCCAGCCAGAGCAGCTG 20
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DB      31 TGCGCAGCCAGAGAGCCTG 13
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RESULT 9
US-09-864-761-28720
; Sequence 28720, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28720
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013597.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
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US-09-864-761-28720
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Query Match          63.0%; Score 12.6; DB 10; Length 96;
Best Local Similarity 78.9%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY      2 TGCCAGCCAGAGCAGCTG 20
        |||| || ||||| ||||
DB      51 TGCCGTGTCAGAGCAGCTG 69
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RESULT 10
US-09-875-519A-2
; Sequence 2, Application US/09875519A
; Patent No. US20020068059A1
; GENERAL INFORMATION:
; APPLICANT: Faries, Timothy C.
; APPLICANT: Harrison, Richard A.
; TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
; FILE REFERENCE: 4-30443/A/IMU/PCT
; CURRENT APPLICATION NUMBER: US/09/875,519A
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/GB97/00603
; PRIOR FILING DATE: 1997-03-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: mutagenic
; OTHER INFORMATION: oligodeoxynucleotide GRI1
US-09-875-519A-2
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```

Query Match          62.0%; Score 12.4; DB 10; Length 30;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 TGCCAGCCAGAGC 15
        ||||| ||||| |||
DB      5 TGCCAGCCCAAGC 18
```

RESULT 11  
US-09-875-519A-5/c  
; Sequence 5, Application US/09875519A  
; Patent No. US20020068059A1  
; GENERAL INFORMATION:  
; APPLICANT: Faries, Timothy C.  
; APPLICANT: Harrison, Richard A.  
; TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase  
; FILE REFERENCE: 4-30443/A/IMU/PCT  
; CURRENT APPLICATION NUMBER: US/09/875,519A  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: PCT/GB97/00603  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: antisense  
US-09-875-519A-5

Query Match 62.0%; Score 12.4; DB 10; Length 30;  
Best Local Similarity 92.9%; Pred. No. 2.3e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCCGACGAGCAGC 15  
DB 26 TGCCGACGAGCAGC 13

RESULT 12  
US-09-801-274-1274/c  
; Sequence 1274, Application US/09801274  
; Patent No. US20020032319A1  
; GENERAL INFORMATION:  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Lander, Eric S.  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: 2825.2009-001  
; CURRENT APPLICATION NUMBER: US/09/801,274  
; CURRENT FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: US 60/187,510  
; PRIOR FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: US 60/206,129  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 1802  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1274  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-801-274-1274

Query Match 62.0%; Score 12.4; DB 10; Length 31;  
Best Local Similarity 92.9%; Pred. No. 2.3e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AGCCAGACGAGCTG 20  
DB 30 AGCCAGACGAGCTG 17

RESULT 13  
US-09-823-936-8  
; Sequence 8, Application US/09823936  
; Patent No. US20020061309A1  
; GENERAL INFORMATION:

APPLICANT: GARGER, Stephen J.  
APPLICANT: GROSS, Cynthia  
APPLICANT: LINDBO, John A.  
APPLICANT: FOGUE, Gregory P.  
TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS  
TITLE OF INVENTION: N-TERMINAL VIRAL COAT PROTEIN FUSIONS  
FILE REFERENCE: 008010087CPUS05  
CURRENT APPLICATION NUMBER: US/09/823,936  
CURRENT FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: 09/ 520,967  
PRIOR FILING DATE: 2000-03-08  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Tobacco mosaic virus tobamovirus  
US-09-823-936-8

Query Match 60.0%; Score 12; DB 10; Length 24;  
Best Local Similarity 75.0%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGCCGACGAGCAGCAGCTG 20  
DB 3 GTGCCGACGAGCAGCAGCTG 22

RESULT 14  
US-09-755-836-7  
; Sequence 7, Application US/09755836  
; Patent No. US20020107387A1  
; GENERAL INFORMATION:  
; APPLICANT: Turpen, Thomas H.  
; APPLICANT: Reini, Stephen  
; TITLE OF INVENTION: Production of Peptides in Plants as  
; Viral Coat Protein Fusions  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/755,836  
; FILING DATE: 05-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/324,003  
; FILING DATE: 14-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8129-087  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-755-836-7

Query Match 60.0%; Score 12; DB 10; Length 24;  
Best Local Similarity 75.0%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGAGCGACTG 20  
|| ||||| || |||||  
DB 3 GTACCAGCCGATCGCCTG 22

## RESULT 15

US-09-877-095-3/c  
; Sequence 3, Application US/09877095  
; Patent No. US20020123051A1  
; GENERAL INFORMATION:  
; APPLICANT: Danenberg, K. et al.  
; TITLE OF INVENTION: METHOD OF DETERMINING A CHEMOTHERAPEUTIC  
; TITLE OF INVENTION: REGIMEN BASED ON ERCC1 EXPRESSION  
; FILE REFERENCE: 11220/127  
; CURRENT APPLICATION NUMBER: US/09/877,095  
; CURRENT FILING DATE: 2001-06-11  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide Primer  
US-09-877-095-3

Query Match 60.0%; Score 12; DB 10; Length 25;  
Best Local Similarity 75.0%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGAGCGACTG 20  
||| ||||| |||  
DB 22 GTGCTGGGCCAGACACCTG 3

Search completed: November 23, 2002, 06:42:07  
Job time : 18.25 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 25, 2002, 09:10:06 : Search time 755.55 Seconds  
(Without alignments)  
428.707 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20

Sequence: 1 gtgccagccagcagcagctg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estbda:\*  
2: em\_estbhm:\*  
3: em\_estln:\*  
4: em\_estlmu:\*  
5: em\_estlov:\*  
6: em\_estlpi:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estlom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.8	79.0	64	17	AZ783365 2M0025F03
2	15.2	76.0	83	9	AA797827 vY04b03.r
3	13.8	69.0	64	9	AI037190 u60a09.y
4	13.6	68.0	55	17	AZ487430 IM0317A10
5	13.4	67.0	20	17	AZ946089 2M0207A13
6	13.4	67.0	86	17	AZ475290 IM0293H07

C	7	13.4	67.0	95	14	T80645	T80645 yd92f03.s1
C	8	13.2	66.0	50	9	AU104251	AU104251 AU104251
C	9	13.2	66.0	50	14	H74150	H74150 ysl6c04.r1
C	10	13.2	66.0	58	17	BH635408	BH635408 100800AFO
C	11	13.2	66.0	73	9	AI158821	AI158821 u438a10.r
C	12	13	65.0	76	9	AI18149	AI18149 ml11a12.r
C	13	13	65.0	82	13	BI902359	BI902359 1b86d03.x
C	14	12.8	64.0	42	17	AZ811797	AZ811797 2M0078P06
C	15	12.8	64.0	50	9	AU102538	AU102538 AU102538
C	16	12.8	64.0	51	9	AI833237	AI833237 at76d05.x
C	17	12.8	64.0	52	10	AW059751	AW059751 LEC07.y9
C	18	12.8	64.0	76	9	AA451089	AA451089 v187d06.r
C	19	12.8	64.0	79	9	AI019859	AI019859 ua92h04.r
C	20	12.8	64.0	83	9	AA587260	AA587260 n70f05.s
C	21	12.8	64.0	85	9	AA486861	AA486861 ab16f07.r
C	22	12.8	64.0	94	9	AA571972	AA571972 v118a03.r
C	23	12.8	64.0	97	9	AA837701	AA837701 oe06c02.s
C	24	12.8	64.0	98	14	W99199	W99199 m159f12.r1
C	25	12.8	64.0	100	10	AW601761	AW601761 MR4-BT040
C	26	12.8	64.0	100	10	AW903646	AW903646 CM4-NN103
C	27	12.6	63.0	23	17	AZ605727	AZ605727 2M0127A15
C	28	12.6	63.0	34	17	AZ826457	AZ826457 2M0102P11
C	29	12.6	63.0	48	17	BH808776	BH808776 1008082D0
C	30	12.6	63.0	52	9	AI477512	AI477512 fb57c08.x
C	31	12.6	63.0	62	17	BH849932	BH849932 SALR_0705
C	32	12.6	63.0	65	17	AZ494609	AZ494609 1M0330B03
C	33	12.6	63.0	70	17	AZ389571	AZ389571 1M0150E24
C	34	12.6	63.0	82	9	AA664777	AA664777 nu68f02.s
C	35	12.6	63.0	85	9	AI905106	AI905106 QV-BT077-
C	36	12.6	63.0	88	9	AA926857	AA926857 om07f09.s
C	37	12.6	63.0	89	9	AI905184	AI905184 QV-BT077-
C	38	12.6	63.0	89	9	AI905194	AI905194 QV-BT077-
C	39	12.6	63.0	91	9	AI738408	AI738408 w123e05.x
C	40	12.6	63.0	92	9	AI932967	AI932967 w040f09.x
C	41	12.6	63.0	93	17	BH229029	BH229029 1006149G0
C	42	12.6	63.0	94	9	AI935190	AI935190 w14h06.x
C	43	12.6	63.0	100	12	BF953180	BF953180 CM3-NN118
C	44	12.4	62.0	37	17	BH640631	BH640631 KG05933-5
C	45	12.4	62.0	42	17	BH621959	BH621959 1007115G1

#### ALIGNMENTS

RESULT 1  
AZ783365  
LOCUS  
DEFINITION  
2M0025F03F Mouse 10kb plasmid UNGC1M library Mus musculus genomic  
clone UNGC2M0025F03 F, DNA sequence.  
64 bp DNA linear GSS 16-FEB-2001

ACCESSION  
AZ783365  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus  
house mouse.  
GSS.  
GI:12918022

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0025 row: F column: 03  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 64.  
Location/Qualifiers

## FEATURES

source

1. 64

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="MGC2M0025F03"  
/clone\_lib="Mouse 10kb plasmid UUCGCM library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

14 a 18 c 13 g 19 t

## ORIGIN

Query Match 79.0%; Score 15.8; DB 17; Length 64;  
Best Local Similarity 89.5%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 TGCCACGCCAGCGACTG 20  
||||| ||||| |||||  
Db 31 TGCCACGCCAGCGACTG 49

RESULT 2  
AA797827/c 85 bp mRNA linear EST 10-FEB-1998  
LOCUS  
DEFINITION  
AA797827  
vY04b03.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA  
clone IMAGE:1294445.5' similar to SW:YHNL\_EBV P03181 HYPOTHETICAL  
65.0 KD PROTEIN IN COX14.5 REGION PRECURSOR. ; mRNA sequence.

ACCESSION  
AA797827  
AA797827.1 GI:2860782  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 85)  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

REFERENCE  
AUTHORS  
The WashU-HHMI Mouse EST Project  
Unpublished (1996)  
Contact: Maria M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the

TITLE  
JOURNAL  
COMMENT

Unpublished (1996)  
Contact: Maria M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:675493  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28m13 rev1 ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

## FEATURES

source

1. 85

/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1294445"  
/clone\_lib="Stratagene mouse macrophage (#937306)"  
/tissue\_type="macrophage"  
/dev\_stage="WEHI-3 cell line"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: blood; Vector: pBluescript SK-; Site:1:  
EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer:  
Oligo dr. WEHI-3 cell line. Average insert size: 1.5 kb;  
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG  
3' -3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGT 3'."

## BASE COUNT

13 a 21 c 28 g 23 t

## ORIGIN

Query Match 76.0%; Score 15.2; DB 9; Length 85;  
Best Local Similarity 85.0%; Pred. No. 5.3e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GTCGCCAGCGCGACTG 20  
||||| ||||| |||||  
Db 66 GTCGCCAGCGCGCTGTG 47

RESULT 3  
A1037190/c 64 bp mRNA linear EST 26-JUN-1998  
LOCUS  
DEFINITION  
u60a09.y1 Sugano mouse liver mla Mus musculus cDNA clone  
IMAGE:1450264.5' similar to SW:YHNL\_EBV P03181 HYPOTHETICAL BHLFI  
PROTEIN. ; mRNA sequence.

ACCESSION  
A1037190  
A1037190.1 GI:3260881  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 64)  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

REFERENCE  
AUTHORS  
The WashU-HHMI Mouse EST Project  
Unpublished (1996)  
Contact: Maria M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

TITLE  
JOURNAL  
COMMENT

Unpublished (1996)  
Contact: Maria M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: custom primer used  
High quality sequence stop: 1.  
Location/Qualifiers

## FEATURES

source

1. 64

/organism="Mus musculus"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1450264"

```

/clone_1lb="Sugano mouse liver_mila"
/sex="female"
/dev_strage="adult"
/lab_host="DH10B"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACATGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
(ATGTGGCCCTTTTTTTTTTTTTTTT); double-stranded cDNA was
ligated to a DraIII adaptor (TGTAGGCCCTCATGTG), digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCGCTCTAAAGCCTCG and 3' end
primer CGACCTGCACATCGACACA."

```

Query Match	69.0%	Score 13.8	DB 9	Length 64
Best Local Similarity	88.2%	Pred. No. 2e+04		
Matches	15	Conservative	0	Mismatches 2
				Indels 0
				Gaps 0
QY	1	GTGCCCAGCCAGAGCGA	17	
DB	44	GAGACCAAGCCAGAGCGA	28	

RESULT	4
AZ487430	
LOCUS	
DEFINITION	AZ487430 55 bp DNA linear GSS 05-OCT-2000
ACCESSION	JM031A10F Mouse 10kb plasmid UGNCIM library Mus musculus genomic
VERSION	clone UGNCJM031A10 F, DNA sequence.
KEYWORDS	AZ487430 AZ487430.1 GI:10655167
SOURCE	GSS. house mouse.

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamill, C.,  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.  
1 (bases 1 to 55)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb paired reads

**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0317 row: A column: 10  
 Seq primer: GCGTCTAAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 55.  
 Location/Qualifiers  
 1..55

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UMCJM0317A10"
/clone_lib="Mouse 10kb plasmid UMGCM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
```

note=Vector: pMD4.4. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (911473211419b1AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

Query Match	68.0%	Score 13.6	DB 17	Length 55
Best Local Similarity	80.0%	Pred. NO.2.3e+04		
Matches 16	Conservative	0	Mismatches 4	Indels 0
QY	1	GTGCCAGCCAGAGCGACTG	20	
Db	30	GAGCCAGCCAGCGGTGAGTG	49	

RESULT 5	
AZ946089/c	
LOCUS	AZ946089 20 bp DNA linear GSS 27-APR-2001
DEFINITION	2M0207A13R Mouse 10kb plasmid UUCG2M library Mus musculus genomic
LOCUS	clone UUCG2M0207A13 R, DNA sequence.
ACCESSION	AZ946089
VERSION	AZ946089.1 GI:13812898
KEYWORDS	GSS.
SOURCE	house mouse.

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
1 (pages 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beecorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Petersen, T., Rellly  
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.  
and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

```

FEATURES
source
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: downgenetics.utah.edu
    Insert Length: 10000
    Std Error: 0.00
    Plate: 0207
    row: A
    column: 13
    Seq primer: CACACAGCAAAACACATGAGACC
    Class: plasmid ends
    High quality sequence stop: 20.
    Location/Qualifiers
        1..20

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```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MUC62M207A13"
/clone_11b="Mouse 10kb plasmid MUC62M library"
/sex="female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
note="Vector: PMW42Mv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson

```

Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 4 c 7 g 5 t  
ORIGIN

Query Match 67.0%; Score 13.4; DB 17; Length 20;  
Best Local Similarity 93.3%; Pred. No. 2e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 CCAGCCAGAGCGACT 19  
|||||  
DB 18 CCAGCCAGAGCGACT 4

RESULT 6  
A2475290 86 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0293H07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION  
clone UUGC1M0293H07 F, DNA sequence.

ACCESSION  
A2475290  
VERSION  
A2475290.1 GI:10633415

KEYWORDS  
GSS.

SOURCE  
house mouse.

ORGANISM  
Mus musculus

REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 86)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.

and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts  
Unpublished (2000)

JOURNAL  
Contact: Robert B. Weiss  
University of Utah Genome Center

COMMENT  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA  
Tel: 801 585 5606

Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert length: 1000 Std Error: 0.00  
Plate: 0293 row: H column: 07

Seq primer: CGTGTAAACACACGCCACT  
Class: Plasmid ends

High quality sequence stop: 86.  
Location/Qualifiers

1. 86  
Location/Qualifiers

FEATURES  
source  
/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0293H07"

/clone\_1ib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 17 a 27 c 22 g 20 t  
ORIGIN

Query Match 67.0%; Score 13.4; DB 17; Length 86;  
Best Local Similarity 93.3%; Pred. No. 3.4e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTGCCAGCAGAGC 15  
|||||  
DB 34 GTGCCAGCAGAGC 48

RESULT 7  
T80645 95 bp mRNA linear EST 15-MAR-1995  
LOCUS Y092f03.s1 Soares fetal liver spleen INF15 Homo sapiens CDNA clone

DEFINITION  
IMAGE:115709.3, similar to gb:J04970 CARBOXYPEPTIDASE M PRECURSOR (HUMAN); mRNA sequence.

ACCESSION  
T80645  
VERSION  
T80645.1 GI:703530

KEYWORDS  
EST.

SOURCE  
human.

ORGANISM  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 95)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman

, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washu-Merck EST Project  
Unpublished (1995)

JOURNAL  
Contact: Wilson RK  
Washington University School of Medicine

COMMENT  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@wustl.edu  
Insert Size: 727

High quality sequence starts: 1 High quality sequence stops: 1  
Source: IMAGE Consortium, LNL. This clone is available royalty-free

through LNL; contact the IMAGE Consortium (info@image.llnl.gov)

for further information. Trace considered overall poor quality  
Insert length: 727 Std Error: 0.00

Seq primer: -21m13  
High quality sequence stop: 1.

Location/Qualifiers

1. 95  
Location/Qualifiers

FEATURES  
source  
/organism="Homo sapiens"

/db\_xref="GDB:471326"

/db\_xref="taxon:9606"

/clone="IMAGE:115709"

/clone\_1ib="Soares fetal liver spleen INF15"

/sex="male"

/dev\_stage="20 week-post conception fetus"

/lab\_host="DH10B (ampicillin resistant)"

ACCESSION	H74150
VERSION	H74150.1
KEYWORDS	GI:1047412
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Chisoe,S., Dietrich,N., Dubaque,T., Favello,A., Gish,W., Hawkins,M., Hulman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mards,E., Moore,B., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierly-Meg,J., Treviskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
TITLE	97044478
JOURNAL	Contact: Wilson RK
MEDLINE	Washington University School of Medicine
COMMENT	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu Insert Size: 3344 High quality sequence starts: 1 High quality sequence stops: 1 Source: IMAGE Consortium, LNLN. This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality Insert Length: 3344 Std Error: 0.00 Seq primer: M13RP1 High quality sequence stop: 1. Location/Qualifiers 1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:214950" /clone_lib="Soares Breast 2NBHbst" /sex="Female" /dex_stage="adult" /lab_host="DH10B (ampicillin resistant)" /note="Organ: breast; Vector: pTV73D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCATCTGCAAGCGCAGCGCCGCCCTTTTCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTV73 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	8 a 20 c 18 g 3 t 1 others
ORIGIN	
Query Match	66.0%; Score 13.2; DB 14; Length 50;
Best Local Similarity	83.3%; Pred. No. 3.4e+04;
Matches 15; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
OY	3 GCCCAGCCAGACGACTG 20 
DB	16 GCCCAGCGAGAGACTG 33
RESULT 10	
BH635408/c	BH635408
LOCUS	1008004F07.2EL_x1 1008 - RescueMu GrId I Zea mays genomic, DNA
DEFINITION	sequence.
ACCESSION	BH635408
VERSION	BH635408.1 GI:18657645

KEYWORDS	Zea mays.
SOURCE	GSS.
ORGANISM	Zea mays.
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 58)
TITLE	Walbot.V.
JOURNAL	Maize genomic sequences found using engineered RescuenMu transposon Unpublished (2001)
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 1008004 row: 12 Class: transposon-tagged. Location/Qualifiers
FEATURES	1..58 /organism="Zea mays" /cultivar="mixed background W23/A188/B73" /db_xref="taxon:4577" /clone_lib="1008 - RescuenMu Grid 1" /tissue_type="leaf" /dev_stage="adult" /lab_host="DH10B" /note="Organ: leaf; Vector: RescuenMu (engineered from plasmid backbone); Site_1: BamHI; Site_2: BglII; RescuenMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuenMu, go to the web site www.zmldb.iastate.edu and follow the links for 'RescuenMu'. Grid 1 was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
BASE COUNT	11 a 11 c 19 g 17 t
ORIGIN	
Query Match	66.0%; Score 13.2; DB 17; Length 58;
Best Local Similarity	83.3%; Pred. No. 3.6e+04;
Matches	15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	3 GCCACGCGACGACTG 20
Db	11             32 GCTCAGCTCAGCGACTG 15
RESULT 11	
LOCUS	A1158821 73 bp mRNA linear EST 02-OCT-1998
DEFINITION	IMAGE:1448202.5' similar to SW:RM12_CRICR P5287 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L7/L12 PRECURSOR, mRNA sequence.
ACCESSION	A1158821
VERSION	A1158821.1 GI:3692003
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 73) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE	The WashU-HHMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:921518
FEATURES	Trace considered overall poor quality Possible reversed clone; similarity on wrong strand Seq primer: -28ml3 revZ ET from Amersham High quality sequence stop: 1.
SOURCE	Location/Qualifiers 1..73 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:1448202" /clone_1id="Soares_mammary_gland_NBMNG" /sex="male" /tissue_type="mammary gland" /dev_stage="4 weeks" /lab_host="DH10B" /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(ct) primer [5', TGTTACCAATCTGAGTCGCGAGCGGCCGCAGATGTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	11 a 27 g 11 t
ORIGIN	
Query Match	66.0%; Score 13.2; DB 9; Length 73;
Matches	Similarity 83.3%; Pred. No. 3.9e+04;
Match 15:	Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DY	3 GCCGAGCCGAGCGACTG 20                 Db 33 GCCTTCCGACGAGCGACG 50
RESULT 12	
LOCUS	AAl18149 76 bp mRNA linear EST 15-NOV-1996
DEFINITION	mlnla12.r1 Beddington mouse embryonic region Mus musculus CDNA clone IMAGE:537598 5' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence.
VERSION	AAl18149
KEYWORDS	AAl18149.1 GI:1673180
SOURCE	EST.
ORGANISM	house mouse. Mus musculus.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Mus. 1 (bases 1 to 76)
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellengberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B., Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. The WashU-HHMI Mouse EST Project Unpublished (1996) Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:324534

putative full length read

vector to vector length is 172

Seq primer: -40m13 ET.

#### FEATURES

##### source

Location/Qualifiers

1..76

/organism="Mus musculus"

/strain="C57BL/6 x DBA"

/db\_xref="taxon:10080"

/clone="IMAGE:537598"

/clone\_1ib="Beddington mouse embryonic region"

/sex="pooled"

/tissue\_type="embryo"

/dev\_stage="7.5dpc"

/lab\_host="DH12S"

/note="Organ: whole embryo; Vector: pCMV-SPORT; Site\_1:

Sal1; Site\_2: NotI; Cloned unidirectionally. Primer:

Oligo dT. Gastrulating embryos were collected at 7.5dpc

from C57BL/6 x DBA matings, excluding embryos that had

developed head folds and all extraembryonic tissues.

Average insert size: 1.3 kb (range: 0.5 - 3.0 kb).

Reference in Development 121, 2479-2489 (1995)"

BASE COUNT  
ORIGIN

20 a 26 c 16 g 14 t

#### Query Match

Best Local Similarity 100.0%; Score 13; DB 9; Length 76;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CCAGCCAGAGCGA 17  
Db 1 CCAGCCAGAGCGA 13

RESULT 13  
BI902359/c  
LOCUS

DEFINITION B1902359 82 bp mRNA linear EST 12-MAR-2002  
1b86d03.x4 Amplified Melton Mouse Islets 1 MSL1-A Mus musculus cDNA

clone IMAGE:5653660 3 similar to SM:TRYP\_MOUSE P07146 TRIPSTINOGEN

PRECUSOR ; mRNA sequence.

BI902359.1 GI:16195485

EST.

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 82)

Melton D., Brown J., Kenty G., Pernutt A., Lee C., Kaestner K.,

Lemishke I., Searce M., Brestelli J., Gradwohl G., Clifton S.,

Hillier L., Marra M., Pape D., Wylie T., Martin J., Blistain A.,

Schmitt A., Theising B., Rletter E., Ronko I., Bennett J., Cardenas

M., Gibbons M., McCann R., Cole R., Tsagarisvalli R., Williams T.

, Jackson Y., and Bowers Y.

Endocrine Pancreas Consortium

unpublished (2000)

Other ESTs: 1b86d03.y4

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@bioh.p.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:

Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Juliana Brown

(brown@fas.harvard.edu)

Trace considered overall poor quality

MG1:193986 This sequence now available from the IMAGE consortium,  
for clone orders contact: info@image.llnl.gov

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

#### FEATURES

##### source

Location/Qualifiers

1..82

/organism="Mus musculus"

/strain="ICR"

/db\_xref="taxon:10090"

/clone="IMAGE:5653660"

/clone\_1ib="Amplified Melton Mouse Islets 1 MSL1-A"

/sex="Male"

/tissue\_type="Islets of Langerhans"

/dev\_stage="Adult"

/lab\_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site\_1: Not 1;

Site\_2: Sal 1; Library constructed using Superscript

Plasmid Library kit (Life Technologies). cDNA made by

Oligo-dT priming. Size-selected by column fractionation;

average insert size 0.91 kb. Amplified once on solid

support. cDNA library Preparation: Guolin Chen."

BASE COUNT  
ORIGIN

18 a 21 c 22 g 21 t

#### Query Match

Best Local Similarity 100.0%; Score 13; DB 13; Length 82;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCCAGCCAGA 13  
Db 78 GTGCCAGCCAGA 66

RESULT 14  
AZ811797/c  
LOCUS

DEFINITION AZ811797 42 bp DNA linear GSS 20-FEB-2001  
clone UUGC2M0078P06 F, DNA sequence.

ACCESSION AZ811797  
VERSION AZ811797.1 GI:12980410

KEYWORDS GSS.

SOURCE house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 42)

Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamill C.,

Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T., Reilly

M., Rose M., Rose R., Stokes R., Tingey A., von Niederhausen A.

and Wright D., Weiss R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0078 row: P column: 06

Seq primer: CGTTGTAAACGACGCGCACT

Class: Plasmid ends

High quality sequence stop: 42.

Location/Qualifiers

1..42

/organism="Mus musculus"

```
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0078P06"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/notes/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g1473211419b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
BASE COUNT      8 a      8 c      15 g      11 t
ORIGIN
```

```
Query Match      64.0%; Score 12.8; DB 17; Length 42;
Best Local Similarity 87.5%; Pred. No. 4.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 CCCAGCCAGAGCGACT 19
      1 |||||
DB      29 CTCAGCCAGAGCGATT 14
```

```
RESULT 15
LOCUS      AU102538/c      50 bp      mRNA      linear      EST 30-AUG-2001
DEFINITION      AU102538 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC03012, mRNA sequence.
ACCESSION      AU102538
VERSION      AU102538.1 GI:13552059
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 50)
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL      21270072
MEDLINE
COMMENT      Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
Institute of Medical Science, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
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Job time : 767.8 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2002, 14:46:40 : Search time 302.2 Seconds

(Without alignments)  
1926.063 Million cell updates/sec

Title: US-09-296-264-9

Perfect score: 20  
Sequence: 1 tgaagtcgagtggaagtcg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: gb\_ov:\*

6: gb\_pat:\*

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8: gb\_pl:\*

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10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_da:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_iny:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pln:\*

35: em\_htg\_rtd:\*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	15	75.0	24	6	A57514	A57514 Sequence 6
3	15	75.0	24	6	AR052978	AR052978 Sequence
4	15	75.0	24	6	AR052980	AR052980 Sequence
5	14.8	74.0	48	6	A28016	A28016 PCDA-FVCD3
6	14.8	74.0	48	6	A28017	A28017 PCDA-FVCD3
7	14.4	72.0	100	9	A28144	A1008144 Homo sapi
8	14.2	71.0	30	6	AR106307	AR106307 Sequence
9	14.2	71.0	30	6	AR110116	AR110116 Sequence
10	14.2	71.0	30	6	AR126277	AR126277 Sequence
11	14.2	71.0	51	6	AX161940	AX161940 Sequence
12	14.2	71.0	85	3	AF318496	AF318496 Scutigera
13	14	70.0	24	6	A57510	A57510 Sequence 2
14	14	70.0	24	6	A57516	A57516 Sequence 8
15	14	70.0	24	6	A57518	A57518 Sequence 10
16	14	70.0	24	6	AR052976	AR052976 Sequence
17	14	70.0	24	6	AR052982	AR052982 Sequence
18	14	70.0	24	6	AR052984	AR052984 Sequence
19	13.8	69.0	24	6	AX353651	AX353651 Sequence
20	13.8	69.0	38	6	AX247606	AX247606 Sequence
21	13.8	69.0	48	6	A28937	A28937 Oligonucleo
22	13.8	69.0	48	6	I12699	I12699 Sequence 20
23	13.8	69.0	97	10	AF177699	AF177699 Rattus no
24	13.6	68.0	23	6	AX394046	AX394046 Sequence
25	13.6	68.0	57	6	A09304	A09304 Serratia sp
26	13.6	68.0	57	6	A09305	A09305 Serratia sp
27	13.6	68.0	96	6	A74696	A74696 Sequence 38
28	13.6	68.0	96	6	A77675	A77675 Sequence 38
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31	13.4	67.0	97	6	I40748	I40748 Sequence 79
32	13.2	66.0	25	6	AX174830	AX174830 Sequence
33	13.2	66.0	30	6	AR177831	AR177831 Sequence
34	13.2	66.0	31	6	AX248112	AX248112 Sequence
35	13.2	66.0	51	6	AR022080	AR022080 Sequence
36	13.2	66.0	51	6	AR022081	AR022081 Sequence
37	13.2	66.0	51	6	I92870	I92870 Sequence 44
38	13.2	66.0	51	6	I92871	I92871 Sequence 45
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40	13.2	66.0	65	5	GGIGY1	AF190139 Gallus ga
41	13.2	66.0	65	6	AX485704	AX485704 Sequence
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43	12.8	64.0	33	6	AX395702	AX395702 Sequence
44	12.8	64.0	65	6	AX484981	AX484981 Sequence
45	12.8	64.0	69	6	AR092211	AR092211 Sequence

#### ALIGNMENTS

RESULT 1

LOCUS A57512/c

DEFINITION Sequence 4 from Patent WO9632483.

ACCESSION A57512

VERSION A57512.1 GI:3713370

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1

AUTHORS Masucci,M.G.

TITLE IMMUNE-EVADING PROTEINS

JOURNAL Patent: WO 9632483-A 4 17-OCT-1996;

MASUCCI MARIA GRAZIA (SE)

24 bp DNA linear PAT 03-MAR-1998

COMMENT other publication AU 5284296 961030.  
FEATURES Location/Qualifiers  
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DB 15 GAGGTGCGGGTGAA 1

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LOCUS Sequence 6 from Patent WO9632483.  
DEFINITION A57514  
ACCESSION A57514  
VERSION A57514.1 GI:3713372  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Masucci, M.G.  
TITLE IMMUNE-EVADING PROTEINS  
JOURNAL Patent: WO 9632483-A 6 17-OCT-1996;  
COMMENT MASUCCI MARIA GRAZIA (SE)  
FEATURES Other publication AU 5284296 961030.  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 15 GAGGTGCGGGTGAA 1

RESULT 3  
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DEFINITION AR052978  
ACCESSION AR052978  
VERSION AR052978.1 GI:5977840  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 24)  
TITLE Masucci, M.G.  
JOURNAL Glycine-containing sequences conferring inviability to the immune system  
FEATURES Patent: US 5833991-A 7 10-NOV-1998;  
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DB 15 GAGGTGCGGGTGAA 1

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DEFINITION AR052980  
ACCESSION AR052980  
VERSION AR052980.1 GI:5977842  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 24)  
TITLE Masucci, M.G.  
JOURNAL Glycine-containing sequences conferring inviability to the immune system  
FEATURES Patent: US 5833991-A 10 10-NOV-1998;  
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LOCUS pCD4-FVCD3 construction oligo 2119.  
DEFINITION A28016  
ACCESSION A28016  
VERSION A28016.1 GI:1248563  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Karjalainen, K., Lanzavecchia, A., and Trautnacker, A.  
TITLE Chimeric polypeptides  
JOURNAL Patent: EP 0505908-A 11 30-SEP-1992;  
FEATURES F. HOFFMANN-LA ROCHE AG  
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ACCESSION A28017  
VERSION A28017.1 GI:1248564



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LOCUS	AX161940
DEFINITION	Sequence 5268 from Patent WO0140521.
ACCESSION	AX161940
VERSION	AX161940.1 GI:14543271
KEYWORDS	.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE	1 (bases 1 to 51)
AUTHORS	Shinkels,R.A. and Leach,M.
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL	Patent: WO 0140521-A 5268 07-JUN-2001;
Curagen Corporation (US)	
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LOCUS	AF318496
DEFINITION	Scutigereilla immaculata sex combs reduced protein (Scr) gene,
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ACCESSION	AF318496
VERSION	AF318496.1 GI:12007393
KEYWORDS	.
SOURCE	Scutigereilla immaculata.
ORGANISM	Scutigereilla immaculata
	Eukaryota; Metazoa; Arthropoda; Myriapoda; Symphyla;
	Scutigerellidae; Scutigereilla.
REFERENCE	1 (bases 1 to 85)
AUTHORS	Cook,C.E., Smith,M.L., Telford,M.J., Bastianello,A. and Akam,M.
TITLE	Hox genes and the phylogeny of the arthropods
JOURNAL	Curr. Biol. 11 (10), 759-763 (2001)
MEDLINE	21272202
PUBMED	11378385
REFERENCE	2 (bases 1 to 85)
AUTHORS	Cook,C.E. and Akam,M.E.
TITLE	Direct Submission

JOURNAL	Submitted (03-NOV-2000) Museum of Zoology, University of Cambridge									
	Downing Street, Cambridge CB2 3ET, UK									
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ACCESSION	A57510									
VERSION	A57510.1 GI:3713368									
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ORGANISM	unclassified.									
REFERENCE	1 (bases 1 to 24)									
AUTHORS	Masucci,M.G.									
TITLE	IMMUNE-EVADING PROTEINS									
JOURNAL	Patent: WO 9632483-A 2 17-OCT-1996;									
	MASUCCI MARIA GRAZIA (SE)									
COMMENT	Other publication AU 5284296 961030.									
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ACCESSION	A57516									
VERSION	A57516.1 GI:3713374									
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SOURCE	unidentified.									
ORGANISM	unclassified.									
REFERENCE	1 (bases 1 to 24)									
AUTHORS	Masucci,M.G.									
TITLE	IMMUNE-EVADING PROTEINS									

Wed Dec 4 14:08:35 2002

**JOURNAL** Patent: WO 9632483-A 8 17-OCT-1996;  
MASCOTT MARIA CRISTINA (CSE)

Other publication AU 5284296 961030.

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57518/c 257510 21 Dec

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SEQUENCE 10 FROM PATENT WO9632483.  
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VERSION A57518.1 GI:3713376

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unclassified.

**AUTHORS** MASUCCI, M.G.,  
**TITLE** TIMING-EVADING PROTEINS

**JOURNAL** Patent: WO 9632483-A 10 17-OCT-1996;  
MASUCCI MARIA CROAZIA (SE)

other publication AU 5284296 961030.

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Job time : 309.2 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:52:31 : Search time 98.55 Seconds  
(without alignments)  
457.027 Million cell updates/sec

Title: US-09-296-264-9

Perfect score: 20

Sequence: 1 tggagtcgctggaagtcg 20

Scoring table: IDENTITY\_NUC

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	15	75.0	24	19	AAV55817
5	14.8	74.0	48	13	AAQ28729
6	14.8	74.0	48	13	AAQ28730
7	14.4	72.0	60	24	ABN48299
8	14.2	71.0	21	15	AAQ70342
9	14.2	71.0	30	13	AAQ31897

C	10	14.2	71.0	30	21	AAV52218	G+C rich nucleic a
C	11	14.2	71.0	50	20	AAV52367	Probe used to iso
C	12	14.2	71.0	50	22	AAJ33759	Human SNP oligonuc
C	13	14.2	71.0	50	22	AAJ33771	Human SNP oligonuc
C	14	14.2	71.0	50	22	AAJ33772	Human SNP oligonuc
C	15	14.2	71.0	50	22	AAJ33775	Human SNP oligonuc
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C	18	14.2	71.0	51	22	AAJ33778	Human SNP oligonuc
C	19	14.2	71.0	51	22	AAJ33779	Human SNP oligonuc
C	20	14.2	71.0	51	22	AAJ33780	Human SNP oligonuc
C	21	14.2	71.0	51	22	AAJ33781	Human SNP oligonuc
C	22	14.2	71.0	51	22	AAJ33782	Human SNP oligonuc
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C	25	14.2	71.0	51	22	AAJ33785	Human SNP oligonuc
C	26	14.2	71.0	51	22	AAJ33786	Human SNP oligonuc
C	27	14.2	71.0	51	22	AAJ33787	Human SNP oligonuc
C	28	14.2	71.0	51	22	AAJ33788	Human SNP oligonuc
C	29	14.2	71.0	51	22	AAJ33789	Human SNP oligonuc
C	30	14.2	71.0	51	22	AAJ33790	Human SNP oligonuc
C	31	14.2	71.0	51	22	AAJ33791	Human SNP oligonuc
C	32	14.2	71.0	51	22	AAJ33792	Human SNP oligonuc
C	33	14.2	71.0	51	22	AAJ33793	Human SNP oligonuc
C	34	14.2	71.0	51	22	AAJ33794	Human SNP oligonuc
C	35	14.2	71.0	51	22	AAJ33795	Human SNP oligonuc
C	36	14.2	71.0	51	22	AAJ33796	Human SNP oligonuc
C	37	14.2	71.0	51	22	AAJ33797	Human SNP oligonuc
C	38	14.2	71.0	51	22	AAJ33798	Human SNP oligonuc
C	39	14.2	71.0	51	22	AAJ33799	Human SNP oligonuc
C	40	14.2	71.0	51	22	AAJ33800	Human SNP oligonuc
C	41	14.2	71.0	51	22	AAJ33801	Human SNP oligonuc
C	42	14.2	71.0	51	22	AAJ33802	Human SNP oligonuc
C	43	14.2	71.0	51	22	AAJ33803	Human SNP oligonuc
C	44	14.2	71.0	51	22	AAJ33804	Human SNP oligonuc
C	45	14.2	71.0	51	22	AAJ33805	Human SNP oligonuc

#### ALIGNMENTS

RESULT 1	AAZ31439	standard; DNA; 20 BP.
ID	AAZ31439;	
AC	AAZ31439;	
XX	07-FEB-2000	(first entry)
DT	07-FEB-2000	(first entry)
XX	Human neuropilin mRNA specific antisense oligo GT13609.	
DE	Human neuropilin; growth; metastasis; tumor; neovascularisation;	
XX	Neuropilin; human; growth; metastasis; tumor; neovascularisation;	
KW	cancer; papilloma; diabetic retinopathy; antisense; ss.	
KW		
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
PN	W09955855-A2.	
PD	04-NOV-1999.	
XX		
PF	23-APR-1999;	99WO-CA00324.
XX	23-APR-1999;	98US-0082791.
PR	23-APR-1998;	98US-0082791.
XX		
PA	(GENE-) GENESENSE TECHNOLOGIES INC.	
XX		
PI	Wright JA, Young AH, Lee YS;	
XX		
DR	WPI: 2000-023357/02.	
XX		
PT	Antisense oligonucleotides that inhibit neuropilin expression, useful for treating cancer -	

XX Claim 4; Page 16; 57pp; English.  
PS  
XX  
CC Sequences AA231431-460 represent antisense oligonucleotides which  
CC inhibit human neuropilin expression. The antisense oligonucleotides can  
CC be used to inhibit the growth or metastasis of a mammalian tumor and  
CC inhibit neovascularisation. The oligonucleotides may be used to treat  
CC various forms of cancers or tumors, such as sarcomas, melanomas,  
CC adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell  
CC carcinomas of the mouth, throat, larynx and lung, genitourinary cancers  
CC such as cervical and bladder cancer, hematopoietic cancers, colon cancer,  
CC breast cancer, pancreatic cancer, renal cancer, brain cancer, skin  
CC cancer, liver cancer, head and neck cancers, and nervous system cancers,  
CC as well as benign lesions such as papillomas. The methods may be used to  
CC treat neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration.  
XX  
SQ Sequence 20 BP; 3 A; 2 C; 11 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAGTGGCGGTGGAAGTGC 20  
|||||  
DB 1 TGAGTGGCGGTGGAAGTGC 20

## RESULT 2

ABN49870  
ID ABN49870 standard; DNA; 60 BP.

AC ABN49870;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:22618.

KW Human; mouse; rat; splice transcript; detection; RNA transcript;

KM splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

PN WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-1B01903.

PR 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

PA (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI: 2002-257383/30.

PT New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of  
PT a genome, useful for detecting tissue-, pathology-, and  
PT developmental-specific genes -

PS Example 1; SEQ ID 22618; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the  
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises  
CC several oligonucleotides, each capable of hybridising selectively to a  
CC set of messenger RNAs transcribed from a given transcription unit of  
CC the genome, which encodes one or more messenger RNA splice variants.  
CC The oligonucleotide libraries are useful for detecting mRNAs from a

CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a  
CC particular biological or pathological state, and so allowing the  
CC detection of tissue- and pathology-specific genes such as those genes  
CC only expressed in specific tissue under a specific pathological  
CC condition; to detect developmental specific genes; and to detect RNA  
CC transcripts and splice variants of a transcriptome of a patient suffering  
CC from a particular disorder. ABN27253 to ABN59589 represent  
CC oligonucleotide sequences from rats, humans and mice, which are used in  
CC the exemplification of the present invention.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 60 BP; 17 A; 12 C; 18 G; 13 T; 0 other;

Query Match 76.0%; Score 15.2; DB 24; Length 60;  
Best Local Similarity 85.0%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TGAGTGGCGGTGGAAGTGC 20  
|||||  
DB 25 TGAGTGGCGGTGGAAGTGC 44

## RESULT 3

AAV55815/c  
ID AAV55815 standard; DNA; 24 BP.

AC AAV55815;

DT 18-NOV-1998 (first entry)

DE Multimerisation of minimal motifs using primer ZG52.

KW Fusion protein; stabilising polypeptide; proteolytic degradation;

KM resistance; half-life; autoimmune disease; inflammation; nitro drug;

KW Ikappab regulator protein; inflammatory bowel disease; in vivo imaging;

KW nitroreductase protein; enzyme therapy; prodrug therapy; protease;

OS cancer; pathological condition; minimal motif; PCR primer; ss.

PN Synthetic.

PD Epstein-barr virus.

PN WO9822577-A1.

XX 28-MAY-1998.

PF 17-NOV-1997; 97WO-1B01508.

PR 25-JUN-1997; 97US-0048945.

PR 15-NOV-1996; 96US-0030986.

PA (MASU/) MASUCCI M G.

PI Masucci MG;

DR WPI: 1998-312463/27.

PT New fusion proteins resistant to proteolytic degradation  
PT comprising a core protein with a stabilising polypeptide comprising  
PT a peptide sequence containing glycine repeats

PS Disclosure; Page 72; 120pp; English.

XX Sequences shown in AAV55812 to AAV55827 represent primers used in the  
CC course of the invention for the multimerisation of minimal motifs. The  
CC invention provides a method for increasing the resistance of a core  
CC protein to proteolytic degradation that comprises linking or inserting  
CC onto or into the core protein a stabilising polypeptide of formula



CC ((Glya)X(Glyb)Y(Glyc)Z)n where Glya, Glyb, Glyc are 1-6 sequential Gly  
 CC residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Pnt  
 CC and n can be anything between 1-66. X, Y and Z need not be identical  
 CC from n repeat to n repeat. Alternatively a nucleic acid encoding a  
 CC stabilising polypeptide can be linked onto or inserted into a nucleic  
 CC acid encoding a core protein. The fusion proteins of the invention are  
 CC more resistant to degradation by proteases and, thus, have a longer  
 CC half-life than the unfused core protein. The products can be used for  
 CC treating autoimmune diseases, cancer and inflammation. In particular, the  
 CC core protein may be an IkappaB regulator protein for the treatment of  
 CC inflammatory bowel disease, or a nitroreductase protein which can  
 CC activate nitro drugs in enzyme/prodrug therapy to treat cancer or other  
 CC pathological conditions. The fusion proteins can also be used in  
 CC diagnostic methods such as in vivo imaging.

SQ Sequence 24 BP; 4 A; 14 C; 2 G; 4 T; 0 other;

Query Match 75.0%; Score 15; DB 19; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GAGGTGCGGTGGAA 16  
 |||||||||||||  
 DB 15 GAGGTGCGGTGGAA 1

RESULT 4  
 AAV55817/c  
 ID AAV55817 standard; DNA: 24 BP.  
 XX AAV55817;  
 AC  
 XX  
 DT 18-NOV-1998 (first entry)  
 XX  
 DE Multimerisation of minimal motifs using primer ZGR2.  
 XX  
 KW Fusion protein: stabilising polypeptide; proteolytic degradation;  
 KW resistance; half-life; autoimmune disease; inflammation; nitro drug;  
 KW IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;  
 KW nitroreductase protein; enzyme therapy; prodrug therapy; protease;  
 KW cancer; pathological condition; minimal motif; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Epstein-Barr virus.  
 XX  
 PN MO582577-A1.  
 XX  
 PD 28-MAY-1998.  
 XX  
 PE 17-NOV-1997; 97WO-IB01508.  
 XX  
 PR 25-JUN-1997; 97US-0048945.  
 PR 15-NOV-1996; 96US-0030986.  
 XX  
 PA (MASU/) MASUCCI M G.  
 XX  
 PI Masucci MG;  
 XX  
 DR WPI: 1998-312463/27.  
 XX  
 PT New fusion proteins resistant to proteolytic degradation -  
 PT comprising a core protein with a stabilising polypeptide comprising  
 PT a peptide sequence containing glycine repeats  
 XX  
 PS Disclosure; Page 72; 120pp; English.  
 XX  
 CC Sequences shown in AAV55812 to AAV55827 represent primers used in the  
 CC course of the invention for the multimerisation of minimal motifs. The  
 CC invention provides a method for increasing the resistance of a core  
 CC protein to proteolytic degradation that comprises linking or inserting  
 CC onto or into the core protein a stabilising polypeptide of formula  
 CC ((Glya)X(Glyb)Y(Glyc)Z)n where Glya, Glyb, Glyc are 1-6 sequential Gly  
 CC residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr

CC and n can be anything between 1-66. X, Y and Z need not be identical  
 CC from n repeat to n repeat. Alternatively a nucleic acid encoding a  
 CC stabilising polypeptide can be linked onto or inserted into a nucleic  
 CC acid encoding a core protein. The fusion proteins of the invention are  
 CC more resistant to degradation by proteases and, thus, have a longer  
 CC half-life than the unfused core protein. The products can be used for  
 CC treating autoimmune diseases, cancer and inflammation. In particular, the  
 CC core protein may be an IkappaB regulator protein for the treatment of  
 CC inflammatory bowel disease, or a nitroreductase protein which can  
 CC activate nitro drugs in enzyme/prodrug therapy to treat cancer or other  
 CC pathological conditions. The fusion proteins can also be used in  
 CC diagnostic methods such as in vivo imaging.

SQ Sequence 24 BP; 3 A; 14 C; 2 G; 5 T; 0 other;

Query Match 75.0%; Score 15; DB 19; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GAGGTGCGGTGGAA 16  
 |||||||||||||  
 DB 15 GAGGTGCGGTGGAA 1

RESULT 5  
 AAQ28729  
 ID AAQ28729 standard; DNA: 48 BP.  
 AC  
 XX AAQ28729;  
 AC  
 XX  
 DT 27-FEB-1993 (first entry)  
 XX  
 DE Sequence of oligonucleotide 2119 corresponding to the linking  
 DE peptide between VH and VL domains of plasmid pFvCD3-H-gamma-3.  
 XX  
 KW Chimeric polypeptide; cell surface CD4 molecule; HIV type 1; HIV-1;  
 KW human immunodeficiency virus; antigen binding site; cytotoxic T-;  
 KW cell; CD3 molecule; T-cell receptor complex; PCR; ss.  
 XX  
 OS Synthetic.  
 OS EP505908-A.  
 PN  
 PD 30-SEP-1992.  
 XX  
 PE 18-MAR-1992; 92EP-0104656.  
 XX  
 PR 27-MAR-1991; 91EP-0810220.  
 XX  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 PI Karjalainen K, Lanzavecchia A, Trautnecker A;  
 XX  
 DR WPI: 1992-325228/40.  
 XX  
 PT DNA encoding chimeric bi-specific polypeptide(s) e.g. CD4 and CD3  
 PT binding site - for treating HIV infection, and also cancers e.g.  
 PT ovarian carcinoma(s) or leukaemia(s)  
 XX  
 PS Example; Page 10; 19pp; English.  
 XX  
 CC Plasmid pFvCD3-H-gamma-3 comprises a DNA sequence coding for the  
 CC variable regions of the heavy and the light chain (VH and VL) of  
 CC an anti-human CD3 antibody (FvCD3) derived from hybridoma TR66  
 CC and for all domains except the first of the constant regions of  
 CC the heavy chain of the human immunoglobulin G3. The second strand  
 CC synthesis of the sequences coding for the VL and VH-domains of the  
 CC anti-CD3 hybridoma TR66 was performed by T4 DNA polymerase and 5'  
 CC oligonucleotides 1570 for VH and 1569 for VL sequences. Final  
 CC amplification was then achieved by using the above mentioned  
 CC oligonucleotides and 3' oligonucleotides 1354 and 1239j  
 CC complementary to mouse gamma-HC (immunoglobulin - gamma - heavy  
 CC chain) and C-kappa (constant domain of immunoglobulin kappa-light

CC chain) genes. The L region (initiation codon and leader sequence  
CC for eukaryotic secretion) of the Sp6 HC gene contg. the small  
CC intron was amplified by using 5' oligonucleotides 1609 and 3'  
CC oligonucleotides 1610 which are also complementary (20 bp) to  
CC oligonucleotides 1570 at its 5' end (ie at the beginning of the  
CC amplified VH fragment. Junctional and flanking oligonucleotides  
CC were designed and used to link the L region from Sp6 VH and VL  
CC fragments together in one 35 ppc reaction: the flanking 5' and 3'  
CC oligonucleotides were 1609 and 2768 respectively, the latter having  
CC complementarity to the end for the mouse J-Kappa-5 sequence. The  
CC oligonucleotide 2139 which links VH to VL fragments had 20 bp  
CC complementarity to the end of the JH2-sequence and to  
CC oligonucleotide 1569, ie to the 5' end of the VL sequence. Finally  
CC a synthetic piece of DNA with SalI compatible ends  
CC (oligonucleotides 2119 and 2120) corresponding to a SalI site of  
CC peptide between VH and VL domains, was cloned into a SalI site of  
CC the Intermediate plasmid to give plasmid pFVCD3-H-gamma-3.  
XX

oligonucleotides 1570 for VH and 1569 for VL sequences. Final amplification was then achieved by using the above mentioned oligonucleotides and 3' oligonucleotides 1354 and 1239 complementary to mouse gamma-HC (immunoglobulin - gamma - heavy chain) and C-kappa (constant domain of immunoglobulin kappa-light chain) genes. The L region (initiation codon and leader sequence for eukaryotic secretion) of the Sp6 HC gene cont. The small intron was amplified by using 5' oligonucleotides 1609 and 3' oligonucleotides 1610 which are also complementary (20 bp) to oligonucleotides 1570 at its 5' end (1e at the beginning of the amplified VH fragment. Junctional and flanking oligonucleotides were designed and used to link the L region from Sp6 VH and VL fragments together in one 35 PCR reaction: the flanking 5' and 3' oligonucleotides were 1609 and 2768 respectively, the latter having complementarity to the end for the mouse J-kappa-5 sequence. The oligonucleotide 2139 which links VH to VL fragments had 20 bp complementarity to the end of the JH2-sequence and to oligonucleotide 1569, 1e to the 5' end of the VL sequence. Finally, a synthetic piece of DNA with SalI compatible ends (oligonucleotides 2119 and 2120) corresponding to the linking peptide between VH and VL domains, was cloned into a SalI site of the intermediate plasmid to give plasmid pVPCD3-H-gamma-3.

CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises  
 CC several oligonucleotides, each capable of hybridising selectively to a  
 CC set of messenger RNAs transcribed from a given transcription unit of  
 CC the genome, which encodes one or more messenger RNA splice variants.  
 CC The oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a  
 CC particular biological or pathological state, and so allowing the  
 CC detection of tissue- and pathology-specific genes such as those genes  
 CC only expressed in specific tissue under a specific pathological  
 CC condition; to detect developmental specific genes; and to detect RNA  
 CC transcripts and splice variants of a transcriptome of a patient suffering  
 CC from a particular disorder. ABN27253 to ABN59589 represent  
 CC oligonucleotide sequences from rats, humans and mice, which are used in  
 CC the exemplification of the present invention.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC XX

SO Sequence 60 BP; 16 A; 9 C; 24 G; 11 T; 0 other;

Query Match 72.0%; Score 14.4; DB 24; Length 60;  
 Best Local Similarity 93.8%; Pred. No. 2.7e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 AGGTGCGGGTGAAGT 18  
 |||||  
 Db 6 AGGTGCGGGTGAAGT 21

RESULT 8  
 AAQ70342/c  
 ID AAQ70342 standard; DNA; 21 BP.  
 AC AAQ70342;  
 XX  
 DT 15-FEB-1995 (first entry)  
 XX  
 DE Antisense oligonucleotide for mouse FGF.  
 XX  
 KW Fibroblast growth factor; hybridisation; laser procedures;  
 KW vascular smooth muscle cell; proliferation;  
 KW SMC; vascular stenosis; post angioplasty restenosis;  
 KW atherosclerosis; cardiac hypertrophy; organ transplant; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9415945-A.  
 XX  
 PD 21-JUL-1994.  
 XX  
 PF 28-DEC-1993; 93WO-US12600.  
 XX  
 PR 31-DEC-1992; 92US-0999706.  
 XX  
 PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.  
 XX  
 PI Denner LA, Dixon RAF, Rege AA, Dixon RA;  
 XX  
 DR WPI; 1994-249123/30.  
 XX  
 PT New anti-sense polynucleotide(s) to fibroblast growth factor  
 PT receptor - used for inhibiting vascular smooth muscle cell  
 PT proliferation, partic. for treating restenosis  
 XX  
 PS Claim 3; Page 9; 53pp; English.  
 CC The sequence is an antisense molecule directed against position -3  
 CC to +18, relative to the start codon of the gene for

CC mouse fibroblast growth factor 1. The polynucleotide can be used for  
 CC inhibiting vascular smooth muscle cell proliferation and for treating  
 CC a disease e.g. vascular stenosis, post angioplasty restenosis,  
 CC atherosclerosis, atherosclerosis, atrial venous shunt failure, cardiac  
 CC hypertrophy, vascular surgery and organ transplant.  
 CC See also AAQ70333-60.  
 CC XX

SO Sequence 21 BP; 4 A; 12 C; 2 G; 3 T; 0 other;

Query Match 71.0%; Score 14.2; DB 15; Length 21;  
 Best Local Similarity 84.2%; Pred. No. 3.2e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GAGTGGGGTGAAGTGC 20  
 |||||  
 Db 19 GAGTGGGGTGAAGTGC 1

RESULT 9  
 AAQ31897/c  
 ID AAQ31897 standard; CDNA; 30 BP.  
 AC AAQ31897;  
 XX  
 DT 22-APR-1993 (first entry)  
 XX  
 DE PCR primer #2 for X-linked disease detection by (CGG)n repeat detn.  
 XX  
 KW Fragile X disease; sex chromosome; X chromosome; X linked syndrome;  
 KW X linked retardation; X linked manic depression; TKCR;  
 KW Martin-Bell syndrome; CA polymorphisms; PCR analysis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9220825-A.  
 XX  
 PD 26-NOV-1992.  
 XX  
 PF 22-MAY-1992; 92WO-US04447.  
 XX  
 PR 24-MAY-1991; 91US-0705490.  
 PR 29-AUG-1991; 91US-0751891.  
 XX  
 PA (BATU) BAYLOR COLLEGE MEDICINE.  
 PA (UYEM-) UNIV EMORY SCHOOL MEDICINE.  
 XX  
 PI Caskey CT, Nelson DL, Costra BA, Pleretti M, Warren ST;  
 XX  
 DR WPI; 1992-415801/50.  
 XX  
 PT Gene sequence, related probes and cosmid(s) - useful in  
 PT diagnosing fragile X syndrome, X-linked mental retardation, manic  
 PT depression, and Martin Bell syndrome  
 XX  
 PS Claim 25; Page 54; 75pp; English.  
 XX  
 CC This PCR primer is used together with Q318975 to determine the  
 CC variation of the (CGG)n repeat found at the 5' end of the FMR-1  
 CC gene. n for normal is in the range 16-30 and for X linked diseases,  
 CC n is greater than 30. In the case of fragile X, n is usually twice  
 CC the normal range. Other disease that can be detected include  
 CC X-linked mental retardation (of both fragile X and non-fragile X  
 CC type), X linked manic depressive disease, TKCR syndrome and  
 CC Martin-Bell syndrome.  
 CC XX

SO Sequence 30 BP; 6 A; 17 C; 3 G; 4 T; 0 other;

Query Match 71.0%; Score 14.2; DB 13; Length 30;  
 Best Local Similarity 84.2%; Pred. No. 3.2e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GAGTGGGGTGAAGTGC 20  
 |||||

DB 25 GAGCTGTGTGGAAGTGC 7

RESULT 10  
AAA95218//C  
ID AAA95218 standard; DNA; 30 BP.  
XX  
AC AAA95218;  
XX  
DT 12-JAN-2001 (first entry)  
XX  
DE G+C rich nucleic acid PCR primer f.  
XX  
KW GC rich nucleic acid; DNA amplification; zwitterion;  
KW base pairing disruption; polymerase chain reaction; fragile X syndrome;  
KW spinobulbar muscular atrophy; myotonic dystrophy; Huntington's disease;  
KW Huntington's chorea; spinocerebellar ataxia type 1; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN US6114150-A.  
XX  
PD 05-SEP-2000.  
XX  
PE 02-DEC-1996; 96US-0758662.  
XX  
PR 29-NOV-1995; 95US-0564653.  
XX  
PA (UYVA ) UNIV YALE.  
XX  
PI Weissman SM, Baskaran N;  
XX  
DR WPI; 2000-586478/55.  
XX  
XX WPI; 2000-586478/55.  
PT Uniform amplification of heterogeneous mixture of nucleic acid  
PT templates of varying G+C content, comprises amplifying the reaction  
PT mixture in the presence of betaine and dimethyl sulphoxide -  
XX  
XX  
PS Example 5; column 10; 15pp; English.  
XX  
CC The present sequence is a PCR primer used to demonstrate the method of  
CC the invention, which involves a novel way of amplifying GC rich nucleic  
CC acids. In addition to the normal mixture a zwitterion and a compound  
CC which disrupts base pairing are added to the PCR reaction. The zwitterion  
CC is preferably betaine (trimethyl glycine), D-carnitine, dimethyl glycine  
CC or monomethyl glycine, and the base pair disruption compound may be DMSO,  
CC formamide, sodium perchlorate or glyoxyl, among others. This method is  
CC useful as it allows the uniform and more efficient amplification of  
CC nucleic acids composed of GC rich regions. This is useful in DNA library  
CC construction, as the 5' end of genes are often GC rich, and in the  
CC diagnosis of diseases where GC rich triplets are expanded, for example  
CC fragile X syndrome, spinobulbar muscular atrophy, myotonic dystrophy,  
CC Huntington's disease and spinocerebellar ataxia type 1.  
XX  
SQ Sequence 30 BP; 6 A; 17 C; 3 G; 4 T; 0 other;  
XX  
Query Match 71.0%; Score 14.2; DB 21; Length 30;  
Best Local Similarity 84.2%; Pred. No.3,2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GAGGTGCGGGTGAAGTGC 20  
DB 25 GAGCTGTGTGGAAGTGC 7

RESULT 11  
AAK52367  
ID AAK52367 standard; DNA; 50 BP.  
XX  
AC AAK52367;  
XX  
DT 25-JUN-1999 (first entry)  
XX

DE Probe used to isolate a cDNA clone encoding PRO229.  
XX  
XX Secreted protein; transmembrane protein; human; enterocolitis;  
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;  
KW congenital microvillus atrophy; skin disease; cell growth;  
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;  
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;  
KW fibromodulin; dermal scarring; Usher Syndrome; Atrophila areata;  
KW anti-thrombotic; wound healing; tissue repair; probe; ss.  
XX  
OS Synthetic.  
XX  
PN WO9914328-A2.  
XX  
PD 25-MAR-1999.  
XX  
PE 16-SEP-1998; 98WO-US19330.  
XX  
XX 25-NOV-1997; 97US-0066840.  
PR 17-SEP-1997; 97US-0059113.  
PR 17-SEP-1997; 97US-0059115.  
PR 17-SEP-1997; 97US-0059117.  
PR 17-SEP-1997; 97US-0059119.  
PR 17-SEP-1997; 97US-0059121.  
PR 17-SEP-1997; 97US-0059122.  
PR 17-SEP-1997; 97US-0059184.  
PR 18-SEP-1997; 97US-0059263.  
PR 18-SEP-1997; 97US-0059265.  
PR 15-OCT-1997; 97US-0062126.  
PR 17-OCT-1997; 97US-0062285.  
PR 17-OCT-1997; 97US-0062287.  
PR 21-OCT-1997; 97US-0063486.  
PR 24-OCT-1997; 97US-0062814.  
PR 24-OCT-1997; 97US-0062816.  
PR 24-OCT-1997; 97US-0063045.  
PR 24-OCT-1997; 97US-0063120.  
PR 24-OCT-1997; 97US-0063121.  
PR 24-OCT-1997; 97US-0063127.  
PR 24-OCT-1997; 97US-0063128.  
PR 27-OCT-1997; 97US-0063329.  
PR 27-OCT-1997; 97US-0063327.  
PR 28-OCT-1997; 97US-0063541.  
PR 28-OCT-1997; 97US-0063542.  
PR 28-OCT-1997; 97US-0063544.  
PR 28-OCT-1997; 97US-0063549.  
PR 28-OCT-1997; 97US-0063550.  
PR 28-OCT-1997; 97US-0063564.  
PR 29-OCT-1997; 97US-0063435.  
PR 29-OCT-1997; 97US-0063704.  
PR 29-OCT-1997; 97US-0063732.  
PR 29-OCT-1997; 97US-0063738.  
PR 29-OCT-1997; 97US-0063734.  
PR 29-OCT-1997; 97US-0064215.  
PR 29-OCT-1997; 97US-0063735.  
PR 31-OCT-1997; 97US-0063870.  
PR 31-OCT-1997; 97US-0064103.  
PR 03-NOV-1997; 97US-0064248.  
PR 07-NOV-1997; 97US-0064809.  
PR 12-NOV-1997; 97US-0065186.  
PR 17-NOV-1997; 97US-0065846.  
PR 18-NOV-1997; 97US-0065693.  
PR 21-NOV-1997; 97US-0066120.  
PR 21-NOV-1997; 97US-0066364.  
PR 24-NOV-1997; 97US-0066772.  
PR 24-NOV-1997; 97US-0066466.  
PR 24-NOV-1997; 97US-0066770.  
PR 24-NOV-1997; 97US-0066511.  
PR 24-NOV-1997; 97US-0066453.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;  
PI

DR WPI; 1999-229533/19.  
XX  
XX New isolated human genes and polypeptides used in, e.g. treatment of  
PT gastrointestinal ulceration  
XX  
XX  
PS Example 24; Page 133; 320pp; English.  
CC Oligonucleotides AAX52276-532 represent PCR primers and probes used  
CC to isolate and amplify cDNA encoding secreted and transmembrane  
CC human proteins (see AAX52213-74 and AAY13344-403). The cDNA sequences  
CC are obtained from cDNA libraries, prepared from fetal lung.  
CC fetal kidney, fetal brain, fetal liver and fetal retina. The encoded  
CC polypeptides have specific uses based on their homology to known  
CC polypeptides, e.g. PRO211 and PRO217 can be used for disorders  
CC associated with the preservation and maintenance of gastrointestinal  
CC mucosa and the repair of acute and chronic mucosal lesions (e.g.  
CC enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration  
CC and congenital microvillus atrophy). Skin diseases associated with  
CC abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers  
CC such as lung squamous cell carcinoma of the vulva and gliomas), potent  
CC effects on cell growth and development, diseases related to growth or  
CC survival of nerve cells including Parkinson's disease, Alzheimer's  
CC disease, ALS, neuropathies or cancer. PRO265 can be used as for  
CC fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a  
CC target for anti-tumor drugs. PRO533 may be used in the treatment of usher  
CC syndrome or Atrophla areata. PRO269 can be used as an anti-thrombotic  
CC agent. PRO287 polypeptides and portions may have therapeutic applications  
CC in wound healing and tissue repair. PRO317 can be used for treating  
CC problems of the kidney, uterus, endometrium, blood vessels, or related  
CC tissue, e.g. in the heart of genital tract.  
XX  
SQ Sequence 50 BP; 11 A; 11 C; 22 G; 6 T; 0 other;  
Query Match 71.0%; Score 14.2; DB 20; Length 50;  
Best Local Similarity 84.2%; Pred. No. 3.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 TGAGCTGCGGGTGAAGTC 19  
Db 16 TGAAGGCGGGTGAAGTC 34  
RESULT 12  
AAL33769/c  
ID AAL33769 standard; DNA: 50 BP.  
XX  
AC AAL33769;  
XX  
XX 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #6977.  
XX  
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antitubercular; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; cholestase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200147944-A2.  
XX  
XX 05-JUL-2001.  
XX  
PD 28-DEC-2000; 2000WO-US35498.  
XX  
PF 28-DEC-1999; 99US-0173419.  
XX  
PR 27-DEC-2000; 2000US-0173419.  
XX  
XX (CURA-) CURAGEN CORP.  
PA

XX  
XX Shinkets RA, Leach M;  
PI  
XX  
XX WPI; 2001-465210/50.  
DR  
XX  
XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -  
XX  
XX Claim 1; Page 3381; 4143pp; English.  
PS  
XX  
CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney/  
CC leukemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.  
XX  
SQ Sequence 50 BP; 8 A; 25 C; 8 G; 9 T; 0 other;  
Query Match 71.0%; Score 14.2; DB 22; Length 50;  
Best Local Similarity 84.2%; Pred. No. 3.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 GAGCTGCGGGTGAAGTC 20  
Db 49 GCGGTGAAGCGGTGAAGTC 31  
RESULT 13  
AAL33771/c  
ID AAL33771 standard; DNA: 50 BP.  
XX  
AC AAL33771;  
XX  
XX 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #6979.  
XX  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antitubercular; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; cholestase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200147944-A2.  
XX  
XX 05-JUL-2001.  
XX  
PD 28-DEC-2000; 2000WO-US35498.  
XX  
PF 28-DEC-1999; 99US-0173419.  
XX  
PR 27-DEC-2000; 2000US-0173419.  
XX  
XX (CURA-) CURAGEN CORP.  
PA Shinkets RA, Leach M;  
PI  
XX

DR	WPI: 2001-465210/50.
XX	
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT	oncogenes and histones, useful for diagnosing and treating, e.g.
PT	cancer, autoimmune diseases and infections -
XX	
PS	Claim 1; Page 3382; 4143pp: English.
XX	
CC	The present invention relates to oligonucleotides encoding polymorphic
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC	histones, kinases, colony stimulating factors, complement related
CC	proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC	G-protein coupled receptors and thioesterases. The present sequence is
CC	one such oligonucleotide. The oligonucleotides and the peptides encoded
CC	by them may be used in the prevention, diagnosis and treatment of
CC	diseases associated with inappropriate expression of the proteins listed
CC	above. Disorders that may be prevented, diagnosed and/or treated include
CC	multifactorial diseases with a genetic component, such as autoimmune
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,
CC	leukaemia), diseases of the nervous system and an infection of pathogenic
CC	organisms.
XX	
SO	Sequence 50 BP; 7 A; 26 C; 7 G; 10 T; 0 other;
	Query Match 71.0%; Score 14.2; DB 22; Length 50;
	Best Local Similarity 84.2%; Pred. No. 3.3e+03;
	Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0
OY	2 GAGGTGCGGGTGAAGTGC 20
	1
DB	45 GGGGTGAGGGTGTAGTGC 27
RESURF 14	
AAU33772/c	
ID	AAU33772 standard; DNA; 50 BP.
XX	
XX	AAU33772;
AC	
XX	
DT	24-JAN-2002 (first entry)
XX	
DE	Human SNP oligonucleotide #6980.
XX	
KW	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW	neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW	amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW	complement related protein; cytochrome; kinesin; cytokine; interferon;
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW	multifactorial disease; autoimmune disease; infection;
KW	nervous system disease; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200147944-A2.
XX	
PD	05-JUL-2001.
XX	
PF	28-DEC-2000; 2000WO-US35498.
XX	
PR	28-DEC-1999; 99US-0173419.
XX	
XX	27-DEC-2000; 2000US-0173419.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shinkets RA, Leach M;
XX	
DR	WPI: 2001-465210/50.
XX	
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,

PR	oncogenes and histones, useful for diagnosing and treating, e.g.
PT	cancer, autoimmune diseases and infections -
PS	Claim 1; Page 3382; 4143pp: English.
XX	
XX	
CC	The present invention relates to oligonucleotides encoding polymorphic
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC	histones, kinases, colony stimulating factors, complement related
CC	proteins, cytochromes, kinases, cytokines, interferons, interleukins,
CC	G-protein coupled receptors and thioesterases. The present sequence is
CC	one such oligonucleotide. The oligonucleotides and the peptides encoded
CC	by them may be used in the prevention, diagnosis and treatment of
CC	diseases associated with inappropriate expression of the proteins listed
CC	above. Disorders that may be prevented, diagnosed and/or treated include
CC	multifactorial diseases with a genetic component, such as autoimmune
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,
CC	leukaemia), diseases of the nervous system and an infection of pathogenic
CC	organisms.
XX	
XX	
SO	Sequence 50 BP; 8 A; 26 C; 7 G; 9 T; 0 other;
QY	2 GAGGTCGGGTGAGAGTC 20
DB	43 GGGGTGAGGTGTGTGTGC 25
RESULT 15	
AAAF72525	
ID	AAAF72525 standard; DNA; 50 BP.
AC	AAAF72525;
XX	
XX	24-APR-2001 (first entry)
DE	Human PRO polypeptide gene hybridisation probe SEQ ID NO: 151.
XX	
KM	Human; PRO: dermatological; antipsoriatic; cytostatic; antiinflammatory;
KM	antiparkinsonian nootropic; neuroprotective; pulmonary; cardiac;
KM	antiangiogenic; vasotropic; antistatic; antihematic; cancer;
KM	antiarthritic; antinfertility; antidiabetic; antiviral; diabetes;
KM	ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KM	ischaemia; inflammation; probe; ss.
XX	
OS	Homo sapiens.
XX	
XX	WO200104311-A1.
PN	18-JAN-2001.
PD	
PF	22-FEB-2000; 2000WO-US04414.
XX	
XX	
PR	07-JUL-1999; 99US-0143048.
PR	26-JUL-1999; 99US-0145698.
PR	28-JUL-1999; 99US-0146222.
PR	08-SEP-1999; 99WO-US20594.
PR	13-SEP-1999; 99WO-US20944.
PR	15-SEP-1999; 99WO-US21090.
PR	15-SEP-1999; 99WO-US21547.
PR	05-OCT-1999; 99WO-US23089.
PR	29-NOV-1999; 99WO-US28214.
PR	30-NOV-1999; 99WO-US28313.
PR	16-DEC-1999; 99WO-US30095.
PR	20-DEC-1999; 99WO-US30911.
PR	20-DEC-1999; 99WO-US30999.
PR	05-JAN-2000; 99WO-US00219.
XX	

PA (GETH ) GENENTECH INC.

XX  
PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N,  
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kijavir IJ;  
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
PI Williams PM, Wood WI;

XX  
DR WPI: 2001-081051/09.

XX  
PT Sixty one nucleic acids encoding PRO polypeptides which are useful in  
PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung  
PT squamous cell carcinoma) and neurodegenerative diseases (e.g.  
PT Alzheimer's disease) -

PS  
PS Example 24: Page 170; 393pp; English.

XX  
CC The present sequence is a probe which was used in the isolation of one  
CC of sixty one nucleic acids encoding novel secreted and transmembrane PRO  
CC polypeptides. The PRO polypeptides are useful for treating skin diseases  
CC (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),  
CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative  
CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,  
CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,  
CC ischaemias such as coronary ischaemia, atherosclerosis), inflammatory  
CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),  
CC infertility, AIDS and diabetes and retinal disorders such as retinitis  
CC pigmentosum. The PRO nucleic acids have applications in molecular  
CC biology, including use as hybridization probes, and in chromosome and  
CC gene mapping.

XX  
SQ Sequence 50 BP; 11 A; 11 C; 22 G; 6 T; 0 other;

Query Match 71.0%; Score 14.2; DB 22; Length 50;

Best Local Similarity 84.2%; Pred. NO. 3.3e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TGAGTGGCGGTGAGTGC 19

111 111111111111111

Db 16 TGAAGCGCGGTGAGTGC 34

Search completed: November 23, 2002, 06:28:55  
Job time : 101.6 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:53:51 ; Search time 21.55 Seconds  
(without alignments)  
284.619 Million cell updates/sec

Title: US-09-296-264-9

Perfect score: 20  
Sequence: 1 tgaagtcgagcgagtcgc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 441362 seqs, 1533381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA: \*  
1: /cgn2\_6/prodata/1/lna/5A\_COMB.seq: \*  
2: /cgn2\_6/prodata/1/lna/5A\_COMB.seq: \*  
3: /cgn2\_6/prodata/1/lna/6A\_COMB.seq: \*  
4: /cgn2\_6/prodata/1/lna/5B\_COMB.seq: \*  
5: /cgn2\_6/prodata/1/lna/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/prodata/1/lna/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	75.0	24	2	US-08-529-190B-7
2	15	75.0	24	2	US-08-529-190B-10
3	14.2	71.0	21	5	PCT-US93-12600-10
4	14.2	71.0	30	3	US-07-705-490-11
5	14.2	71.0	30	3	US-08-758-662-7
6	14.2	71.0	30	4	US-07-751-891B-11
7	14	70.0	24	2	US-08-529-190B-4
8	14	70.0	24	2	US-08-529-190B-13
9	14	70.0	24	2	US-08-529-190B-16
10	13.8	69.0	48	1	US-07-917-034A-20
11	13.4	67.0	97	1	US-08-389-412A-79
12	13.2	66.0	18	5	PCT-US93-12600-1
13	13.2	66.0	30	4	US-08-506-296B-34
14	13.2	66.0	51	1	US-08-285-936-44
15	13.2	66.0	51	1	US-08-285-936-45
16	13.2	66.0	51	1	US-08-487-860-44
17	13.2	66.0	51	1	US-08-487-860-45
18	12.8	64.0	33	4	US-09-206-059-70
19	12.8	64.0	60	5	PCT-US93-11985A-4
20	12.8	64.0	69	2	US-08-894-578-149
21	12.6	63.0	20	4	US-08-837-201C-2
22	12.6	63.0	20	4	US-09-364-416-2
23	12.6	63.0	21	5	PCT-US93-12600-25
24	12.6	63.0	23	4	US-09-282-773-203
25	12.6	63.0	24	5	PCT-US93-12600-23
26	12.6	63.0	24	5	PCT-US93-12600-24
27	12.6	63.0	25	4	US-09-009-816-10

28	12.6	63.0	27	5	PCT-US93-12600-22	Sequence 22, App1
29	12.6	63.0	40	3	US-09-277-016-14	Sequence 14, App1
30	12.6	63.0	42	1	US-07-640-029-9	Sequence 9, App1
31	12.6	63.0	42	1	US-07-921-807B-15	Sequence 15, App1
32	12.6	63.0	42	1	US-08-441-944A-15	Sequence 15, App1
33	12.6	63.0	42	4	US-08-439-992A-9	Sequence 9, App1
34	12.6	63.0	45	1	US-08-160-670A-33	Sequence 33, App1
35	12.6	63.0	50	1	US-08-171-389-474	Sequence 47, App1
36	12.6	63.0	50	2	US-08-123-936-474	Sequence 47, App1
37	12.6	63.0	50	2	US-08-475-228A-474	Sequence 47, App1
38	12.6	63.0	50	3	US-08-482-080A-474	Sequence 47, App1
39	12.6	63.0	50	4	US-09-354-947-474	Sequence 47, App1
40	12.6	63.0	50	5	PCT-US93-12388-474	Sequence 47, App1
41	12.6	63.0	61	2	US-08-771-624B-19	Sequence 19, App1
42	12.4	62.0	17	4	US-08-420-211-15	Sequence 15, App1
43	12.4	62.0	21	3	US-08-891-789B-26	Sequence 26, App1
44	12.4	62.0	36	1	US-08-411-795B-414	Sequence 41, App1
45	12.4	62.0	36	1	US-08-411-795B-415	Sequence 41, App1

## ALIGNMENTS

RESULT 1  
US-08-529-190B-7/C  
Sequence 7, Application US/08529190B  
Patent No. 5833991  
GENERAL INFORMATION:  
APPLICANT: Masucci, Maria G.  
TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES  
TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: One Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/529,190B  
FILING DATE: 15-SEP-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE9501324-9  
FILING DATE: 10-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE9501324-9  
FILING DATE: 10-APR-1995  
APPLICATION NUMBER: US08/522,595  
FILING DATE: 01-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Ph.D., Kathleen A  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 3255/53015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-9100  
TELEFAX: 617-345-9111  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-529-190B-7  
Query Match 75.0%; Score 15; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0;



REFERENCE/DOCKET NUMBER: D-5350  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5325  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
US-07-705-490-11

Query Match 71.0%; Score 14.2; DB 3; Length 30;  
Best Local Similarity 84.2%; Pred. No. 4.1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GAGTGGGGTGAAGTC 20  
DB 25 GAGCTGGTGGTGAAGTC 7

RESULT 5  
US-08-758-662-7/c  
Sequence 7, Application US/08758662  
Patent No. 6114150  
GENERAL INFORMATION:  
APPLICANT: Weisman, Sherman  
APPLICANT: Baskaran, Namadev  
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 701 Fifth Avenue, 6300 Columbia Center  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,662  
FILING DATE: 29-NOV-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6114150tenburg, Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 390036.402C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-758-662-7

Query Match 71.0%; Score 14.2; DB 3; Length 30;  
Best Local Similarity 84.2%; Pred. No. 4.1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GAGTGGGGTGAAGTC 20  
DB 25 GAGCTGGTGGTGAAGTC 7

RESULT 6  
US-07-751-891B-11/c  
Sequence 11, Application US/07751891B  
Patent No. 6180337  
GENERAL INFORMATION:  
APPLICANT: Caskey, C. T.  
Nelson, David L.  
Pieretti, Maura  
Warren, Stephen T.  
Oostera, Ben A.  
Fu, Ying-hui  
TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Thomas D. Paul  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/751,891B  
FILING DATE: 29-Aug-1991  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5350  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5325  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-07-751-891B-11

Query Match 71.0%; Score 14.2; DB 4; Length 30;  
Best Local Similarity 84.2%; Pred. No. 4.1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GAGTGGGGTGAAGTC 20  
DB 25 GAGCTGGTGGTGAAGTC 7

RESULT 7  
US-08-529-190B-4/c  
Sequence 4, Application US/08529190B  
Patent No. 5833991  
GENERAL INFORMATION:  
APPLICANT: Masucci, Maria G.  
TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES  
CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: One Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/529,190B  
FILING DATE: 15-SEP-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE9501324-9  
FILING DATE: 10-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US08/522,595  
FILING DATE: 01-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Ph.D., Kathleen A  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 3255/53015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-9100  
TELEFAX: 617-345-9111  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-529-190B-4

Query Match 70.0%; Score 14; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GAGGTGCGGGTGA 15  
|||||  
DB 15 GAGGTGCGGGTGA 2

RESULT 8  
US-08-529-190B-13/c  
Sequence 13, Application US/08529190B  
Patent No. 5833991  
GENERAL INFORMATION:  
APPLICANT: Masucci, Maria G.  
TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES  
TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: One Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/529,190B  
FILING DATE: 15-SEP-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE9501324-9  
FILING DATE: 10-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US08/522,595  
FILING DATE: 01-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Ph.D., Kathleen A

REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 3255/53015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-9100  
TELEFAX: 617-345-9111  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-529-190B-13

Query Match 70.0%; Score 14; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GAGGTGCGGGTGA 15  
|||||  
DB 15 GAGGTGCGGGTGA 2

RESULT 9  
US-08-529-190B-16/c  
Sequence 16, Application US/08529190B  
Patent No. 5833991  
GENERAL INFORMATION:  
APPLICANT: Masucci, Maria G.  
TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES  
TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: One Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/529,190B  
FILING DATE: 15-SEP-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE9501324-9  
FILING DATE: 10-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US08/522,595  
FILING DATE: 01-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Ph.D., Kathleen A  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 3255/53015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-9100  
TELEFAX: 617-345-9111  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-529-190B-16

Query Match 70.0%; Score 14; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GAGTGGCGGTGCA 15  
Db 15 GAGTGGCGGTGCA 2

## RESULT 10

US-07-917-034A-20/C  
Sequence 20, Application US/07917034A  
Patent No. 5427927  
GENERAL INFORMATION:  
APPLICANT: Meyer, Thomas, Pohlner, Johannes, Schumacher,  
APPLICANT: Gnter, Dony, Carola  
TITLE OF INVENTION: Process For The Enzymatic Cleavage  
TITLE OF INVENTION: of Recombinant Proteins Using Iga Proteases  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/917,034A  
FILING DATE: 19920830  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP91/00192  
FILING DATE: 1-Feb-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 40 39 415.8  
FILING DATE: 10-Dec-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 40 15 922.1  
FILING DATE: 17-May-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 40 15 921.3  
FILING DATE: 17-May-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 40 03 149.7  
FILING DATE: 3-Feb-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5427927man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: H0BR 1018  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-917-034A-20

Query Match 69.0%: Score 13.8; DB 1; Length 48;  
Best Local Similarity 88.2%: Pred. No. 6.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGTGGCGGTGCAAGTG 19  
Db 30 AGTGGCGGTGCAAGTG 14

RESULT 11  
US-08-399-412A-79  
Sequence 79, Application US/08399412A  
Patent No. 5622828  
GENERAL INFORMATION:

APPLICANT: Parma, David  
APPLICANT: Gold, Larry  
TITLE OF INVENTION: High-Affinity Oligonucleotide  
TITLE OF INVENTION: Ligands To Secretory Phospholipase  
TITLE OF INVENTION: A2 (sPLA2)  
NUMBER OF SEQUENCES: 122  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/399,412A  
FILING DATE: 6-MARCH-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Julie L. Bernard  
REGISTRATION NUMBER: 36,450  
REFERENCE/DOCKET NUMBER: NEX27  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 97 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: ALL C'S ARE 2'-NH2 cytosine  
FEATURE:  
OTHER INFORMATION: ALL U'S ARE 2'-NH2 uracil  
US-08-399-412A-79

Query Match 67.0%: Score 13.4; DB 1; Length 97;  
Best Local Similarity 73.3%: Pred. No. 1e+03;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 GTGGCGGTGCAAGTG 19  
Db 42 GUGUGGUGGGAAGUG 56

RESULT 12  
PCT-US93-12600-1/C  
Sequence 1, Application PC/TUS9312600  
GENERAL INFORMATION:  
APPLICANT: Denner, Larry A.  
APPLICANT: Rege, Ajay A.  
APPLICANT: Dixon, Richard A.P.  
TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A  
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dressler, Goldsmith, Shore &  
ADDRESSEE: Milnamow, Ltd.

STREET: 180 North Stetson, Suite 4700  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/12600  
FILING DATE: 28-DEC-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/999,706  
FILING DATE: December 31, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Katz, Martin L.  
REGISTRATION NUMBER: 25,011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)616-5400  
TELEFAX: (312)616-5460  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US93-12600-1

Query Match 66.0%; Score 13.2; DB 5; Length 18;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGTGGCGGTGGAAGTGC 20  
DB 18 ATGTGGCGGTGGAAGTGC 1

RESULT 13  
US-08-506-296B-34  
Sequence 34, Application US/08506296B  
GENERAL INFORMATION:  
APPLICANT: Phillips, Greg  
APPLICANT: Cunningham, Bruce A.  
APPLICANT: Crossin, Kathryn L.  
TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES  
TITLE OF INVENTION: CONTAINING FIBROBLAST TYPE III REPEATS AND METHODS OF USE  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESS: The Scripps Research Institute  
STREET: 10550 No. 613325th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: California  
COUNTRY: U.S.  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/506,296B  
FILING DATE: 24-JUL-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 488.0  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-506-296B-34

Query Match 66.0%; Score 13.2; DB 4; Length 30;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGTGGCGGTGGAAGTGC 20  
DB 11 ATGTGGCGGTGGAAGTGC 28

RESULT 14  
US-08-285-936-44  
Sequence 44, Application US/08285936  
GENERAL INFORMATION:  
APPLICANT: Yelton, Dale  
APPLICANT: Glaser, Scott  
APPLICANT: Huse, William  
APPLICANT: Rosok, Mae J.  
TITLE OF INVENTION: No. 5728821e1 Mutant BR96 Antibodies and  
TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESS: Merchant & Gould  
STREET: 11150 Santa Monica Blvd., Suite 400  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90025-3395  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/285,936  
FILING DATE: 04-AUG-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Adriano, Sarah B.  
REGISTRATION NUMBER: 34,470  
REFERENCE/DOCKET NUMBER: 30436.16US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310-445-1140  
TELEFAX: 310-445-9031  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 51 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-285-936-44

Query Match 66.0%; Score 13.2; DB 1; Length 51;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGTGGCGGTGGAAGTGC 19  
DB 13 GAGTGGCGGTGGAAGTGC 30

GenCore version 5.1.3  
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## OM nucleic - nucleic search, using sw model

Run on: December 3, 2002, 14:46:40 ; Search time 302.2 Seconds

(without alignments)  
1926.063 Million cell updates/sec

Title: US-09-296-264-1

Perfect score: 20

Sequence: 1 gagcgagcagccctctcca 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:

1: gb\_da:\*

2: gb\_hlg:\*

3: gb\_in:\*

4: gb\_cm:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_hlg\_hum:\*

31: em\_hlg\_inv:\*

32: em\_hlg\_other:\*

33: em\_hlg\_mus:\*

34: em\_hlg\_pln:\*

35: em\_hlg\_rtd:\*

36: em\_hlg\_mam:\*

37: em\_hlg\_vrt:\*

38: em\_sy:\*

39: em\_hlgc\_hum:\*

40: em\_hlgc\_mus:\*

41: em\_hlgc\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	77.0	57	6	AX286668
2	14.8	74.0	80	5	A00424
3	14.8	74.0	80	5	CHKERSLD
4	14.4	72.0	55	6	AX073623
5	14.4	72.0	55	6	AX359862
6	14.4	72.0	60	6	AX286671
7	14.2	71.0	51	6	AX204378
8	14.2	71.0	51	6	AX481058
9	13.6	68.0	55	6	AR194772
10	13.6	68.0	100	12	P531
11	13.4	67.0	31	6	AX248931
12	13.4	67.0	37	6	AX207259
13	13.4	67.0	42	6	AX207261
14	13.4	67.0	50	6	AX161712
15	13.4	67.0	51	6	AX157115
16	13.4	67.0	51	6	AX157116
17	13.4	67.0	51	6	AX161711
18	13.2	66.0	20	6	AX195334
19	13.2	66.0	33	6	A44871
20	13.2	66.0	42	6	E03621
21	13.2	66.0	50	6	AX165808
22	13.2	66.0	95	6	AX119976
23	13.2	66.0	95	6	AX138025
24	13.2	66.0	99	9	AB011248
25	13.2	66.0	100	1	CE1TN3152
26	12.8	64.0	18	6	AX481122
27	12.8	64.0	20	6	E22417
28	12.8	64.0	26	6	A88149
29	12.8	64.0	26	6	A90116
30	12.8	64.0	42	6	E22401
31	12.8	64.0	48	6	AR193496
32	12.8	64.0	51	6	AX160975
33	12.8	64.0	54	6	AR042317
34	12.8	64.0	55	6	AR194774
35	12.8	64.0	61	6	A89690
36	12.8	64.0	72	1	PRIMERPE
37	12.8	64.0	81	14	AF227771
38	12.8	64.0	81	14	AF227773
39	12.8	64.0	81	14	AF227774
40	12.8	64.0	81	14	AF227775
41	12.8	64.0	81	14	AF227776
42	12.8	64.0	81	14	AF227777
43	12.8	64.0	81	14	AF227778
44	12.8	64.0	81	14	AF227779
45	12.8	64.0	81	14	AF227780

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
AX286668	AX286668	Sequence 9 from Patent WO0181554.	AX286668	AX286668.1	GI:17048736	synthetic construct. synthetic construct artificial sequences.	1	Conzelmann,K.K.	Pneumovirus ns proteins antagonising the interferon (Ifn) response Patent: WO 0181554-A 9 01-NOV-2001; Conzelmann, Karl-Klaus, Prof. Dr. (DE)	

Pred. No. is the number of results predicted by chance to have a





Query Match 72.0%; Score 14.4; DB 6; Length 55;  
Best Local Similarity 93.8%; Pred. No. 5.5e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 GCGGAGCCCCCTCTC 18  
||||| |||||||  
Db 22 GCGGAGCCCCCTCTC 37

RESULT 6  
LOCUS AX286671 60 bp DNA linear PAT 21-NOV-2001  
DEFINITION Sequence 12 from Patent WO0181554.  
ACCESSION AX286671  
VERSION AX286671.1 GI:17048739  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Conzelmann, K.K.  
TITLE Pneumovirus ns proteins antagonising the interferon (1fn) response  
JOURNAL Patent: WO 0181554-A 12 01-NOV-2001;  
Conzelmann, Karl-Klaus, Prof. Dr. (DE)  
FEATURES  
source Location/Qualifiers  
1..60  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Primer mNS1-NotI/ECORV5"

BASE COUNT 13 a 15 c 14 g 18 t

ORIGIN

Query Match 72.0%; Score 14.4; DB 6; Length 60;  
Best Local Similarity 93.8%; Pred. No. 5.5e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 GCGGAGCCCCCTCTC 18  
||||| |||||||  
Db 10 GCGGAGCCCCCTCTC 25

RESULT 7  
LOCUS AX204378 51 bp DNA linear PAT 30-AUG-2001  
DEFINITION Sequence 484 from Patent WO0148245.  
ACCESSION AX204378  
VERSION AX204378.1 GI:15393911  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 51)  
AUTHORS Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE Shinketsu, R.A. and Leach, M.  
JOURNAL Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
Patent: WO 0148245-A 484 05-JUL-2001;  
Curegen Corporation (US)  
FEATURES  
source Location/Qualifiers  
1..51  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
26  
/note="single nucleotide polymorphism  
Accession number cg40310734"

BASE COUNT 3 a 15 c 20 g 13 t

ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 51;  
Best Local Similarity 84.2%; Pred. No. 6.9e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAGCGAGCCCCCTCTCC 19  
||||| ||||||| |||||  
Db 19 GAGCGAGCAGCACCCTCTCC 1

RESULT 8  
LOCUS AX481058 18 bp DNA linear PAT 12-AUG-2002  
DEFINITION Sequence 118 from Patent WO0246412.  
ACCESSION AX481058  
VERSION AX481058.1 GI:22217610  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Rebar, E., Jamieson, A., Liu, Q., Liu, P. Q., Wolffe, A., Eisenberg, S. P.  
TITLE Regulation of angiogenesis with zinc finger proteins  
JOURNAL Patent: WO 0246412-A 118 13-JUN-2002;  
Sangamo Biosciences Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..18  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="target"

BASE COUNT 3 a 2 c 11 g 1 t 1 others

ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 18;  
Best Local Similarity 87.5%; Pred. No. 9.7e+04;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 GCGGAGCCCCCTCTCC 19  
||||| ||||||| |||||  
Db 16 CTGCGAGCCCCCTCTCC 1

RESULT 9  
LOCUS AR194772 55 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 16 from patent US 6348596.  
ACCESSION AR194772  
VERSION AR194772.1 GI:20241364  
KEYWORDS  
SOURCE unknown.  
ORGANISM unknown.  
REFERENCE 1 (bases 1 to 55)  
AUTHORS Lee, L.G., Graham, R.J., Mullah, K.B. and Haxo, F.T.  
TITLE Non-fluorescent asymmetric cyanine dye compounds useful for  
quenching reporter dyes  
Patent: US 6348596-A 16 19-FEB-2002;  
JOURNAL Location/Qualifiers  
1..55  
/organism="unknown"  
FEATURES  
source  
BASE COUNT 5 a 25 c 15 g 10 t

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 55;  
Best Local Similarity 80.0%; Pred. No. 1.3e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GAGCGAGCCCCCTCTCCA 20  
||||| ||||||| |||||  
Db 52 GATGCGAGCCCCCAGTCCA 33

RESULT 10  
LOCUS P531/c 100 bp DNA linear SYN 31-SEP-2001  
DEFINITION Plasmid pMMS-3, with DNA from pMB8, pHS1 and Tn3, pHS1/Tn3 (IR-L)  
junction.

```

ACCESSION      K02977
VERSION         GI:150478
KEYWORDS        Recombination joint; transposon.
SEGMENT         1 of 4
SOURCE          Recombinant plasmid pMW5-3.
ORGANISM        Recombinant plasmid pMW5-3.
REFERENCE       1 (bases 1 to 100)
AUTHORS         McCormick,M., Wishart,W., Ohtsubo,H., Heffron,F. and Ohtsubo,E.
TITLE           Plasmid cotegrates and their resolution mediated by transposon
                Tn3 mutants
                Gene 15 (2-3), 103-118 (1981)
JOURNAL         82051303
MEDLINE         6271635
PUBMED          Recombinant plasmids were generated in vivo, between a
                temperature-sensitive replication mutant of pSC101 (pSC1), which
                codes for tetracycline resistance, and pMB8, carrying the
                ampicillin transposon Tn3. When the repressor gene of Tn3 was
                inactive, all cells examined contained cotegrate recombinations.
                Complete Tn3 mutant #5 DNA was present at both junctions between
                the parental plasmids, in a direct orientation and a 5 bp
                (positions 53-57) PHS1 sequence was directly duplicated at the
                PHS1/Tn3 #5 junctions in pMW5-3.
FEATURES        Location/Qualifiers
SOURCE          1..100
                /organism="Recombinant plasmid pMW5-3"
                /db_xref="taxon:2602"
                /note="Obtained from in vivo recombination of clones pMB8
                (containing Tn3 mutant #5) and PHS1 (temperature-sensitive
                mutant of pSC101)"
BASE COUNT      22 a 21 c 32 g 20 t 5 others
ORIGIN          Query Match 68.0%; Score 13.6; DB 12; Length 100;
                Best Local Similarity 80.0%; Pred. No. 1.2e+05;
                Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY             1 GAGCGGAGCCCCCTCTCCA 20
                ||||| ||||| ||
DB             71 GAGCGTCAAGACCCCTCACCA 52

RESULT 11
LOCUS          AX248931 31 bp DNA linear PAT 28-SEP-2001
DEFINITION     Sequence 1010 from Patent WO0166800.
ACCESSION      AX248931
VERSION        AX248931.1 GI:15863554
KEYWORDS
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 31)
AUTHORS        Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE          Human single nucleotide polymorphisms
                Patent: WO 0166800-A 1010 13-SEP-2001;
JOURNAL        WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES        Location/Qualifiers
SOURCE         1..31
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
BASE COUNT      9 a 12 c 7 g 2 t 1 others
ORIGIN          Query Match 67.0%; Score 13.4; DB 6; Length 31;
                Best Local Similarity 82.4%; Pred. No. 1.7e+05;
                Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY             4 GCGAGCCCCCTCTCCA 20
                1 ||||| ||||| |||||
DB             6 CAGCAGCCCCCTCTGCCA 22

```

```

RESULT 12
LOCUS          AX207259/c 37 bp DNA linear PAT 30-AUG-2001
DEFINITION     Sequence 6 from Patent WO0155366.
ACCESSION      AX207259
VERSION        AX207259.1 GI:15395042
KEYWORDS
SOURCE         synthetic construct.
ORGANISM       synthetic construct.
REFERENCE      1 (bases 1 to 37)
AUTHORS        Schumacher,A.N. and Kessels,H.W.
TITLE          T cell receptor libraries
                Patent: WO 0155366-A 6 02-AUG-2001;
                Vereniging Het Nederlands Kanker Instituut (NL)
JOURNAL        Location/Qualifiers
FEATURES        source
                1..37
                /organism="synthetic construct"
                /db_xref="taxon:32630"
                /note="primer F5 alfa-bottom"
BASE COUNT      8 a 12 c 14 g 3 t
ORIGIN          Query Match 67.0%; Score 13.4; DB 6; Length 37;
                Best Local Similarity 93.3%; Pred. No. 1.6e+05;
                Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY             1 GAGCGGAGCCCCCT 15
                ||||| ||||| ||
DB             18 GAGCGGCGCCCTCT 4

RESULT 13
LOCUS          AX207261/c 42 bp DNA linear PAT 30-AUG-2001
DEFINITION     Sequence 8 from Patent WO0155366.
ACCESSION      AX207261
VERSION        AX207261.1 GI:15395044
KEYWORDS
SOURCE         synthetic construct.
ORGANISM       synthetic construct.
REFERENCE      1 (bases 1 to 42)
AUTHORS        Schumacher,A.N. and Kessels,H.W.
TITLE          T cell receptor libraries
                Patent: WO 0155366-A 8 02-AUG-2001;
                Vereniging Het Nederlands Kanker Instituut (NL)
JOURNAL        Location/Qualifiers
FEATURES        source
                1..42
                /organism="synthetic construct"
                /db_xref="taxon:32630"
                /note="primer F5 beta-bottom"
BASE COUNT      7 a 8 c 15 g 12 t
ORIGIN          Query Match 67.0%; Score 13.4; DB 6; Length 42;
                Best Local Similarity 93.3%; Pred. No. 1.6e+05;
                Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY             1 GAGCGGAGCCCCCT 15
                ||||| ||||| ||
DB             18 GAGCGGCGCCCTCT 4

RESULT 14
LOCUS          AX161712 50 bp DNA linear PAT 22-JUN-2001
DEFINITION     Sequence 5040 from Patent WO0140521.
ACCESSION      AX161712
VERSION        AX161712.1 GI:14543043
KEYWORDS
SOURCE         human.

```

```

ORGANISM      Homo sapiens
REFERENCE      Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        1 (bases 1 to 50)
TITLE          Shimkets,R.A. and Leach,M.
JOURNAL        Nucleic acids containing single nucleotide polymorphisms and
                methods of use thereof
                Patent: WO 0140521-A 5040 07-JUN-2001;
                Curagen Corporation (US)
FEATURES       location/Qualifiers
                source
                1..50
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                misc_feature
                25..26
                /note="Nucleotide deleted between bases 25 and 26
                Accession number cg43981323"
                misc_feature
                26
                /note="2 of 2 allelic variants (5039 is other entry)"
                BASE COUNT      3 a      21 c      18 g      8 t
                ORIGIN
                Query Match      67.0%; Score 13.4; DB 6; Length 50;
                Best Local Similarity 93.3%; Pred. No. 1.6e+05;
                Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      4      CGCGAGCCCCCTCTC 18
Db      34      CGGCATCCCTCTC 48

RESULT 15
AX157115/c
LOCUS      AX157115      51 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 443 from Patent WO0140521.
ACCESSION  AX157115
VERSION     AX157115.1 GI:14538446
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 51)
AUTHORS     Shimkets,R.A. and Leach,M.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
            Patent: WO 0140521-A 443 07-JUN-2001;
            Curagen Corporation (US)
JOURNAL     location/Qualifiers
FEATURES    source
            1..51
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            misc_feature
            26
            /note="1 of 2 allelic variants (444 is other entry)
            Accession number cg44925402"
            BASE COUNT      11 a      11 c      17 g      12 t
            ORIGIN

Query Match      67.0%; Score 13.4; DB 6; Length 51;
Best Local Similarity 93.3%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1      GAGGCGAGCCCCCT 15
Db      43      GAGCGGAGCCCCCT 29

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Search completed: December 3, 2002, 18:11:52  
 Job time : 310.2 secs

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XX Claim 4; Page 16; 57pp; English.  
PS  
XX  
CC Sequences AA3131-460 represent antisense oligonucleotides which  
CC inhibit human neuropilin expression. The antisense oligonucleotides can  
CC be used to inhibit the growth or metastasis of a mammalian tumor and  
CC inhibit neovascularisation. The oligonucleotides may be used to treat  
CC various forms of cancers or tumors, such as sarcomas, melanomas,  
CC adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell  
CC carcinomas of the mouth, throat, larynx and lung, genitourinary cancers,  
CC such as cervical and bladder cancer, hematopoietic cancers, colon cancer,  
CC breast cancer, pancreatic cancer, renal cancer, brain cancer, skin  
CC cancer, liver cancer, head and neck cancers, and nervous system cancers,  
CC as well as benign lesions such as papillomas. The methods may be used to  
CC treat neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration.  
XX  
SQ Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 other;  
  
Query Match 100.0%; Score 20; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 GAGCGCAGCCCTCTCCA 20  
Db 1 GAGCGCAGCCCTCTCCA 20  
|||||  
  
RESULT 2  
AAL33643  
ID AAL33643 standard; DNA; 50 BP.  
XX  
AC AAL33643;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #6851.  
XX  
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;  
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
XX complement related protein; cytochrome; thiosin; cytokine; interferon;  
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;  
XX multifactorial disease; autoimmune disease; infection;  
XX nervous system disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-US35498.  
XX  
PR 28-DEC-1999; 99US-0173419.  
XX  
PR 27-DEC-2000; 2000US-0173419.  
XX  
PA (CUPRA-) CUPRAGEN CORP.  
XX  
PI Shinkets RA, leach M;  
XX  
DR WPI: 2001-465210/50.  
XX  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
XX oncogenes and histones, useful for diagnosing and treating, e.g.  
XX cancer, autoimmune diseases and infections -  
PS Claim 1; Page 3341; 4143pp; English.  
XX  
CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,

CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, thioesterases. Interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.  
XX  
SQ Sequence 50 BP; 10 A; 16 C; 18 G; 6 T; 0 other;  
  
Query Match 72.0%; Score 14.4; DB 22; Length 50;  
Best Local Similarity 93.8%; Pred. No. 5.2e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
OY 5 GGCAGCCCCCTCTCCA 20  
Db 17 GGCAGCCCCCTCTCCA 32  
|||||  
  
RESULT 3  
AAF25148  
ID AAF25148 standard; DNA; 55 BP.  
XX  
AC AAF25148;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of a recombinant Respiratory syncytial virus.  
XX  
XX Respiratory syncytial virus; RSV; attenuated vaccine; RSV A; RSV B;  
XX BRSV; HSRV; SS.  
XX  
OS Respiratory syncytial virus.  
XX  
PN WO200104335-A2.  
XX  
PD 18-JAN-2001.  
XX  
PF 24-JUN-2000; 2000WO-US17755.  
XX  
PR 09-JUL-1999; 99US-0143132.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Buchholz U, Collins PL, Murphy BR, Whitehead SS, Krempf CD;  
XX  
DR WPI: 2001-103088/11.  
XX  
XX Isolated chimeric human-bovine respiratory syncytial virus (RSV),  
XX useful in an attenuated vaccine to elicits an immune response against  
XX either or both human RSV A or RSV B -  
PS Disclosure: Page 145; 148pp; English.  
XX  
XX The specification describes a chimeric human-bovine respiratory syncytial  
XX virus (RSV) that is infectious and attenuated in humans. The virus  
XX comprises a major nucleocapsid protein, a nucleocapsid phosphoprotein,  
XX a large polymerase protein, a RNA polymerase elongation factor, and a  
XX partial or complete RSV background genome, or antigenome of a human RSV  
XX or bovine RSV combined with one or more heterologous genes or genome  
XX segment of a different RSV to form a human-bovine chimeric RSV genome  
XX or antigenome. The chimeric RSV is useful in an attenuated vaccine to  
XX elicits an immune response against either or both human RSV A or RSV B.  
XX  
SQ Sequence 55 BP; 14 A; 16 C; 11 G; 14 T; 0 other;

Query Match 72.0%; Score 14.4; DB 22; Length 55;  
 Best Local Similarity 93.8%; Pred. No. 5.2e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 GCGGACGCCCCCTCTC 18  
 ||||| |||||  
 Db 22 GCGGCGCGCCCCCTCTC 37

RESULT 4  
 ABK13065  
 ID ABK13065 standard; DNA: 55 BP.

XX AC ABK13065.

DT 23-APR-2002 (first entry)

DE Recombinant BRSV genome construct rBRSV/A2-GIF2 leader sequence.

XX Respiratory syncytial virus; RSV; vaccine; immunostimulatory;

KW antiviral; gene therapy; rBRSV/A2-GIF2; GS.

XX Bovine respiratory syncytial virus.

OS Synthetic.

XX PN WO200200693-A2.

XX PD 03-JAN-2002.

XX PF 22-JUN-2001; 2001WO-US20107.

XX PR 23-JUN-2000; 2000US-213708P.

XX PA (USGO ) US GOVERNMENT.

XX PI Krempf CD, Collins PL, Murphy BR, Buchholz U, Whitehead SS;

XX DR WPI; 2002-090518/12.

XX PT An isolated infectious recombinant respiratory syncytial virus (RSV)  
 PT having one or more shifted RSV gene(s) or genome segment(s) within the  
 PT recombinant genome or antigenome, useful as an attenuated vaccine  
 PT against RSV strains -

XX PS Example 3; Fig 6; 168pp; English.

XX CC The invention relates to an isolated infectious recombinant respiratory  
 CC syncytial virus (RSV) having one or more shifted RSV gene(s) or genome  
 CC segment(s) within the recombinant genome or antigenome that is/are  
 CC positionally shifted to a more promoter-proximal or promoter-distal  
 CC position relative to a position of the RSV gene(s) or genome segment(s)  
 CC within a wild type RSV genome or antigenome. Also described is (1) a  
 CC method for stimulating the immune system of an individual to induce  
 CC protection against RSV which comprises administering to the individual an  
 CC immunologically sufficient amount of the recombinant RSV combined with a  
 CC physiologically acceptable carrier; and (2) an isolated infectious  
 CC chimeric RSV comprising a major nucleocapsid protein, a nucleocapsid  
 CC phosphoprotein, a large polymerase protein, a RNA polymerase elongation  
 CC factor, and a partial or complete bovine RSV background genome or  
 CC antigenome combined with heterologous gene(s) and/or genome segment(s)  
 CC of a human RSV selected from heterologous gene(s) and/or genome  
 CC segment(s) of RSV NS1, NS2, M, SH, G, and/or F, to form a human-bovine  
 CC chimeric RSV genome or antigenome. The recombinant RSV is useful in an  
 CC attenuated vaccine to elicit an immune response against either human  
 CC RSV A or RSV B or both human RSV A and RSV B. The present sequence  
 CC represents recombinant BRSV genome construct rBRSV/A2-GIF2 leader  
 CC sequence as described in the method of the invention.

XX SO Sequence 55 BP; 14 A; 16 C; 11 G; 14 T; 0 other;

Query Match 72.0%; Score 14.4; DB 24; Length 55;  
 Best Local Similarity 93.8%; Pred. No. 5.2e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 GCGGACGCCCCCTCTC 18  
 ||||| |||||  
 Db 22 GCGGCGCGCCCCCTCTC 37

RESULT 5  
 AAQ97261  
 ID AAQ97261 standard; cDNA: 30 BP.

XX AC AAQ97261;

DT 28-DEC-1995 (first entry)

DE Not-dc oligo primer.

XX Astrocyte-type 1; ATL; neuron; ss.

XX OS Synthetic.

XX PN WO9517203-A1.

XX PD 29-JUN-1995.

XX PF 22-DEC-1994; 94WO-US14771.

XX PR 20-DEC-1994; 94US-0359480.

XX PR 22-DEC-1993; 93US-0172327.

XX PR 18-JUL-1994; 94US-0275709.

XX PA (UYNE-) UNIV NEW JERSEY.

XX PI Black IB, Dreyfuss CF, Schaar DG;

XX DR WPI; 1995-240472/31.

XX PT New astrocyte-derived neurotrophic factor proteins - related nucleic  
 PT acid, vectors and transformed cells, useful for stimulating neuronal  
 PT cell survival and growth

XX PS Example 2; Page 43; 107pp; English.

XX CC cDNA was synthesized from astrocyte total RNA using reverse  
 CC transcriptase primed by a Not-dc oligo (given in AAQ97260).  
 CC Products were used for non-sequence specific cDNA amplification,  
 CC using Not-dt (AAQ97260) and Not-dc, asymmetric PCR and subtractive  
 CC hybridization to isolate novel astrocyte type 1 cDNA clones  
 CC (AAQ97243-46).

XX SO Sequence 30 BP; 1 A; 21 C; 7 G; 1 T; 0 other;

Query Match 71.0%; Score 14.2; DB 16; Length 30;  
 Best Local Similarity 84.2%; Pred. No. 6.4e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAGGCGACGCCCCCTCTCC 19  
 ||||| |||||  
 Db 8 GAGGCGCGCCCCCCCCC 26

RESULT 6  
 AAH79869/C  
 ID AAH79869 standard; DNA: 51 BP.

XX AC AAH79869;

DT 19-SEP-2001 (first entry)

DE Human DNA containing single nucleotide polymorphism SEQ ID NO. 484.

XX Human; single nucleotide polymorphism; SNP; angiotensin;  
 KW 4-hydroxybutyrate; dehydrogenase; protein therapy;  
 KW adenosine triphosphate-dependent RNA helicase;

KW major histocompatibility complex Class I histocompatibility antigen; MHC;  
 KW phosphoglycerate kinase; immunosuppressive; immunostimulatory;  
 KW antineumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;  
 KW antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; ds.  
 XX  
 OS Homo sapiens.  
 PN WO200148245-A2.  
 PD 05-JUL-2001.  
 PF 27-DEC-2000; 2000WO-US35346.  
 PF 27-DEC-1999; 99US-0472688.  
 PR 27-DEC-1999; 99US-0472688.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 PA Shinkets RA, Leach M;  
 PI WPI; 2001-418297/44.  
 DR  
 XX Polymorphic nucleic acids encoding e.g. angiotensin, dehydrogenase,  
 PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate  
 PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune  
 PT diseases and infections -  
 XX  
 XS Claim 1; Page 195; 484pp; English.

The invention relates to nucleic acids (AAH79386-AAH80336) encoding polymorphic variants of proteins (AAC98010-AA98328) related to angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major histocompatibility complex (MHC) Class I histocompatibility antigen and/or phospholipase kinase. These nucleic acid single nucleotide polymorphisms (SNPs) and the encoded proteins have potential immunosuppressive, immunostimulatory, antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic, antileukemic, neuroprotective and antimicrobial activity and may be useful in gene/protein therapy, vaccines, modulation of the expression and activity of proteins related to angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major histocompatibility complex (MHC) Class I histocompatibility antigen and/or phospholipase kinase. Disorders that may be prevented, diagnosed and/or treated by the above methods include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia), diseases of the nervous system, an infection of pathogenic organisms. They may also be used to alter phenotypic traits such as longevity, appearance, strength, speed and endurance.

Sequence 51 BP; 3 A; 15 C; 20 G; 13 T; 0 other;

Query Match	71.08%	Score 14.2	DB 22	Length 51
Best Local Similarity	84.28%	Pred. No. 6.3e+03		
Matches 16	Conservative 0	Mismatches 3	Indels 0	Gaps 0

```

2Y      1 GAGCGGACGCCCTCTCC 19
          ||| ||| ||| |||
Db      19 GAGCAGCAGCACCCACTCC 1

```

## RESULT 7

ABT04101/c  
ID ABT04101 standard; DNA; 18 BP.

AC ABT04101;

DT 25-SEP-2002 (first entry)

DE Human VEGF zinc finger target site SEQ ID NO: 118

KW Zinc finger protein; angiogenesis; vasculogenesis; ischaemia;

KW diabetic retinopathy; psoriasis; arthropathy; cancer; tumor growth;  
KW gene therapy; antiatherosclerotic; vasotropic; antiatheritic; vulnary;  
KW antineur; cytostatic; antiproliferative; antidiabetic; ophthalmological;  
KW osteopathic; antifertility; ds.

OS Homo sapiens

PN WO200246412-A2.

PD 13-JUN-2002.

PF 06-DEC-2001; 2001WO-US468861.

PR	07-DEC-2000; 2000US-0733604.
PR	12-DEC-2000; 2000US-0736083

PR 30-APR-2001; 2001US-0846033.  
yy

PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX

PI Rebar E, Jamieson A, Liu Q, Liu P, Wolffe A, Eisenberg SP,  
PI Jarvis F.

XX  
DB WPT: 2002-527918/56

PT New zinc finger protein that binds to target site in vascular  
PT endothelial growth factor gene, useful for modulating expression of the  
PT gene and for treating atherosclerosis, ischemia, arthritis, wound or  
PT ulcer -

PS Claim 1; Page 103; 195pp; English.

CC The present invention relates to a zinc finger protein that binds to a  
CC target site in one or more vascular endothelial growth factor (VEGF)  
CC genes. The protein is useful for modulating expression of a VEGF gene  
CC thereby regulating angiogenesis and vasculogenesis. This can be used to  
CC treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, target  
CC diabetic retinopathy or psoriasis. The present sequence is a target DNA  
CC sequence for a zinc finger protein shown in the invention.

**SQ** Sequence 18 BP; 3 A; 2 C; 11 G; 1 T; 1 other;

Query Match	70.08;	Score 14;	DB 24;	Length 18;
Best Local Similarity	87.58;	Pred. No. 7.8e+03;		
Matches 14; Conservative	1;	Mismatches	0;	Gaps 0;

QY	4	CGGACGCCCTCTCC	19
Db	16	CTGCRGCCCTCTCC	1

## RESULT 8

ID ABN52872 standard; DNA; 65 BP.

AC ABN52872;

DT 15-JUL-2002 (first entry)

Mouse spliced transcript detection oligonucleotide SEQ ID NO:25620.

KW Human, mouse; rat; splice transcript; detection; RNA transcript, splice variant; transcriptome; oligonucleotide library; ss.

OS Mus musculus.

PN WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB01903.

PR 28-JUL-2000; 2000US-221607P.  
03-MAY-2001; 2001US-287724P

PR 02-MAY-2001; 2001US-287724P.



XX (COMP-) COMPUGEN INC.  
 XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX WPI: 2002-257383/30.  
 DR  
 XX  
 PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of  
 PT a genome, useful for detecting tissue-, pathology-, and  
 PT developmental-specific genes  
 PS Example 1; SEQ ID 25620; 47pp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the  
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises  
 CC several oligonucleotides, each capable of hybridizing selectively to a  
 CC set of messenger RNAs transcribed from a given transcription unit of  
 CC the genome, which encodes one or more messenger RNA splice variants.  
 CC The oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a  
 CC particular biological or pathological state, and so allowing the  
 CC detection of tissue- and pathology-specific genes such as those genes  
 CC only expressed in specific tissue under a specific pathological  
 CC condition; to detect developmental specific genes; and to detect RNA  
 CC transcripts and splice variants of a transcriptome of a patient suffering  
 CC from a particular disorder. ABN27253 to ABN59589 represent  
 CC oligonucleotide sequences from rats, humans and mice, which are used in  
 CC the exemplification of the present invention.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WRO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 65 BP; 11 A; 20 C; 22 G; 12 T; 0 other;  
 Query Match 69.0%; Score 13.8; DB 24; Length 65;  
 Best Local Similarity 88.2%; Pred. No. 9.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 AGCGGACGCCCTCTC 18  
 DB 18 AGCGGACGCCCTCTCC 2  
 RESULT 9  
 AAQ49420  
 ID AAQ49420 standard; cDNA: 90 BP.  
 XX  
 XX AAQ49420:  
 XX  
 DT 27-APR-1994 (first entry)  
 XX  
 DE Cytochrome P450 homologue cDNA insert pCGP163 start.  
 XX  
 XX Transgenic plants; altered petal colour; partial sequence; ss.  
 OS  
 OS Petunia cv. OGB (Old Glory Blue).  
 XX  
 PN WO9320206-A.  
 XX  
 PD 14-OCT-1993.  
 XX  
 PF 25-MAR-1993; 93WO-AU00127.  
 XX  
 PR 27-MAR-1992; 92AU-0001538.  
 PR 07-JAN-1993; 93AU-0006698.  
 XX

PA (ITFL-) INT FLOWER DEV PTY LTD.  
 XX  
 XX Cornish EC, Holton TA, Tanaka Y;  
 PI  
 DR WPI: 1993-336914/42.  
 XX  
 XX  
 PT Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to  
 PT create transgenic plants with altered petal colour  
 PS  
 XX Disclosure; Fig 4A; 86pp; English.  
 XX  
 CC The sequence is that of the start of a partial nucleotide sequence  
 CC of a cytochrome P450 homologue cDNA insert isolated from pCGP163.  
 CC The end of this sequence is given in AA058357.  
 XX  
 SQ Sequence 90 BP; 28 A; 22 C; 14 G; 26 T; 0 other;  
 Query Match 69.0%; Score 13.8; DB 14; Length 90;  
 Best Local Similarity 88.2%; Pred. No. 9.1e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 GCGGACGCCCTCTCC 19  
 DB 36 GCGGACGCCCTCTCC 52  
 RESULT 10  
 ABA91984/c  
 ID ABA91984 standard; DNA; 55 BP.  
 XX  
 XX ABA91984:  
 AC  
 DT 23-MAY-2002 (first entry)  
 XX  
 DE Single nucleotide polymorphism BAK target oligonucleotide F2662T.  
 XX  
 XX Single nucleotide polymorphism: SNP; detection: Tagman; assay;  
 KW quencher: hybridisation; human; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6348596-B1.  
 PD 19-FEB-2002.  
 XX  
 PF 20-JUL-1999; 99US-0357740.  
 XX  
 PR 23-JAN-1998; 98US-0012525.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 XX Lee LG, Graham RJ, Mullah KB, Haxo FT;  
 PI  
 DR WPI: 2002-225175/28.  
 XX  
 XX  
 PT New non-fluorescent asymmetric cyanide dye compounds, useful for  
 PT quenching reporter dyes in nucleic acid hybridisation assays employing  
 PT fluorescence energy transfer as means of detection -  
 PS  
 PS Example 4; Column 66; 62pp; English.  
 XX  
 CC The present sequence is that of single nucleotide polymorphism  
 CC (SNP) BAK target oligonucleotide F2622T. This target sequence was  
 CC used in a multiplex endpoint single nucleotide polymorphism (SNP)  
 CC analysis designed to demonstrate the use of a novel non-fluorescent  
 CC asymmetric cyanide dye, nitrothiazole blue (NTB), as an quenching  
 CC reporter dye. A 7-colour homogeneous detection of multiple PCR  
 CC products was performed. The test system was a set of 3 SNPs,  
 CC denoted MPO, BAK and IIG. For each SNP system there were 2  
 CC primers (see ABA91969-74) and 2 sequence-specific probes (see  
 CC ABA91975-80), each with NTB at the 3' end, and a different reporter  
 CC dye (6-FAM, DR10, DR66, dTMR, DROX and JAZ) at the 5' end. The 7th  
 CC colour was from aluminium phthalocyanine tetrasulfonate, used as a

CC passive reference. Following PCR, the reactions were measured on a  
 CC luminescence spectrometer in synchronous scanning mode. The  
 CC spectral overlap in the set was evaluated by calculation of the  
 CC conditioning number of the 7x7 matrix (dye fluorescence versus  
 CC wavelength). The small value of the condition number (1.5) proved  
 CC that crosstalk between the dyes was minimal. SNP analyses of  
 CC known, synthetic target DNA sequences (see ABA91981-90) and genomic  
 CC DNA (from human blood samples and Raji (ATCC CCL-86) cells) were  
 CC plotted as normalised, subtracted spectra and as data points in dot  
 CC plots. The synthetic targets, containing priming sites and both  
 CC possible alleles, were constructed by synthesising the forward and  
 CC reverse 5' ends of the target with a 10 bp complementary region at  
 CC the 3' terminus. The oligonucleotides were combined and the ends  
 CC filled in. The BAK target utilised a separate pair of primers for  
 CC each allele (see also ABA91985-87). The multiplex PCR system  
 CC provides increased sample throughput and potential cost savings.  
 CC  
 SQ Sequence 55 BP; 5 A; 25 C; 15 G; 10 T; 0 other;

Query Match 68.0%; Score 13.6; DB 24; Length 55;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GAGCGGACGCCCTCTCCA 20  
 || ||||| ||||| |||||  
 Db 52 GATGGGACGCCCTCTCCA 33

## RESULT 11

ABA96211/C  
 ID ABA96211 standard; DNA: 57 BP.

AC ABA96211;

DX 12-MAR-2002 (first entry)

DE Extracellular signal-regulated PK-1 related oligonucleotide 5.

KW Extracellular signal-related protein kinase-1; ss.

OS Unidentified.

PN KR98031184-A.

PD 25-JUL-1998.

PF 31-OCT-1996; 96KR-0050731.

PR 31-OCT-1996; 96KR-0050731.

PA (GLDS ) LG CHEM LTD.

PI Kim CH, Cho JM, Chung HH, Lee JH;

DR WPI; 1999-369099/31.

PT Process for preparing extracellular signal-regulated protein kinase-1

PS from E. coli -

XX Disclosure: fig 5, 10pp; Korean.

CC The invention relates to preparing extracellular signal-regulated

CC protein kinase-1. The present sequence is that of an oligonucleotide,

CC useful to the invention.

CC  
 SQ Sequence 57 BP; 9 A; 13 C; 27 G; 8 T; 0 other;

Query Match 68.0%; Score 13.6; DB 20; Length 57;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 OY 1 GAGCGGACGCCCTCTCCA 20  
 || ||||| ||||| || |||||

Db 39 GAACGGCTGCCCTTCACCA 20

## RESULT 12

ABN57612  
 ID ABN57612 standard; DNA: 65 BP.

AC ABN57612;

DX 15-JUL-2002 (first entry)

DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:30360.

KW Human: mouse; rat; splice transcript; detection; RNA transcript;

XX splice variant; transcriptome; oligonucleotide library; ss.

OS Mus musculus.

PN WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-1B01903.

PR 28-JUL-2000; 2000US-221607P.

PA 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI; 2002-257383/30.

PT New oligonucleotide libraries comprising oligonucleotides which

PT selectively hybridize to mRNAs transcribed from a transcription unit of

PT a genome, useful for detecting tissue-, pathology-, and

PT developmental-specific genes

PS Example 1; SEQ ID 30360; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting

CC messenger RNAs that populate a (sub-)transcriptome, where the

CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple

CC transcription units that populate a genome. The library comprises

CC several oligonucleotides, each capable of hybridising selectively to a

CC set of messenger RNAs transcribed from a given transcription unit of

CC the genome, which encodes one or more messenger RNA splice variants.

CC The oligonucleotide libraries are useful for detecting mRNAs from a

CC biological sample, in expression profiling studies, in qualitatively or

CC quantitatively characterising the corresponding transcriptome, and in

CC detecting RNA transcripts and splice variants of human or animal

CC transcriptomes. The libraries may also be used as specialised mini

CC libraries to detect transcripts of a sub-transcriptome under a

CC particular biological or pathological state, and so allowing the

CC detection of tissue- and pathology-specific genes such as those genes

CC only expressed in specific tissue under a specific pathological

CC condition; to detect developmental specific genes; and to detect RNA

CC transcripts and splice variants of a transcriptome of a patient suffering

CC from a particular disorder. ABN27253 to ABN59569 represent

CC oligonucleotide sequences from rats, humans and mice, which are used in

CC the exemplification of the present invention.

CC N.B. The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences.

CC  
 SQ Sequence 65 BP; 19 A; 18 C; 14 G; 14 T; 0 other;

Query Match 68.0%; Score 13.6; DB 24; Length 65;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 OY 1 GAGCGGACGCCCTCTCCA 20  
 ||||| || || ||||| |||||

DB 32 GAGCAGCCGCTCTCTCA 51

RESULT 13  
AAx87463/c  
ID AAx87463 standard; DNA; 84 BP.  
XX  
XX  
AC AAx87463;  
XX  
XX  
DT 08-OCT-1999 (first entry)  
XX  
XX  
DE plasmid pmtrix PCR primer right.  
XX  
XX  
KM ET cloning, recE; recT; Escherichia coli; PCR; primer; pmtrix;  
KM mouse; trichorax; homologous recombination; ss.  
XX  
OS Synthetic.  
XX  
XX  
PN MO9929837-A2.  
XX  
XX  
PD 17-JUN-1999.  
XX  
XX  
PF 07-DEC-1998; 98MO-EP07945.  
XX  
XX  
PR 05-OCT-1998; 98EP-0118756.  
XX  
XX  
PR 05-DEC-1997; 97EP-0121462.  
XX  
XX  
PA (EMBL-) EMBL EURO LAB MOLEKULARBIOLOGIE.  
XX  
XX  
PI Buchholz F, Stewart F, Zhang Y;  
XX  
XX  
DR WPI; 1999-457893/38.  
XX  
XX  
PT A method for cloning DNA using a recE and recT homologous  
XX  
XX  
PS recombination system  
XX  
XX  
PS Disclosure: Page 138; 139pp; English.  
XX  
XX  
CC This is the nucleotide sequence of a primer used in the PCR  
XX  
XX  
CC amplification of a linear DNA fragment used in a method of the  
XX  
XX  
CC invention. The template was pmtrix, a pluescript vector carrying  
XX  
XX  
CC mouse trichorax cDNA, and the targeting vector was pZero2.1. Host  
XX  
XX  
CC cells and/or vectors expressing Escherichia coli recE and recT  
XX  
XX  
CC genes (or functionally related genes) are useful in a novel cloning  
XX  
XX  
CC method, designated ET cloning, which involves homologous  
XX  
XX  
CC recombination via the recET mechanism (see also AAx87427-29). The  
XX  
XX  
CC method covalently combines one preferably linear, extrachromosomal  
XX  
XX  
CC DNA fragment (the fragment to be cloned) with a second preferably  
XX  
XX  
CC circular DNA vector. The method is particularly applicable to  
XX  
XX  
CC complex or difficult DNA constructs, such as those intended for  
XX  
XX  
CC homologous recombination in eukaryotic cells.  
XX  
XX  
SQ Sequence 84 BP; 12 A; 22 C; 30 G; 20 T; 0 other;

Query Match 68.0%; Score 13.6; DB 20; Length 84;  
Best Local Similarity 80.0%; Pred. No. 1.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GAGCGGAGCCGCTCTCA 20  
DB 81 GAGCGGAGCCGCTCTCA 62

RESULT 14  
AAC07582/c  
ID AAC07582 standard; cDNA; 92 BP.  
XX  
XX  
AC AAC07582;  
XX  
XX  
DT 06-OCT-2000 (first entry)  
XX  
XX  
DE Human secreted protein 5' EST, SEQ ID NO: 11657.

XX  
XX  
KM Human: 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KM gene therapy; chromosome mapping; ss.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN EP1033401-A2.  
XX  
XX  
PD 06-SEP-2000.  
XX  
XX  
PF 21-FEB-2000; 2000EP-0200610.  
XX  
XX  
PR 26-FEB-1999; 99US-0122487.  
XX  
XX  
PA (GENEST) GENSET.  
XX  
XX  
PI Dumas Milne Edwards J, Duclert A, Giordano J;  
XX  
XX  
DR WPI; 2000-500381/45.  
XX  
XX  
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
XX  
XX  
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
XX  
XX  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX  
XX  
PS Claim 1; SEQ ID 11657; 71pp + CD-ROM; English.

The present sequence is one of a large number of 5' ESTs derived from  
CC  
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
CC  
CC identified within the present sequence. The 5' ESTs were prepared from  
CC  
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
CC  
CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
CC  
CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
CC  
CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
CC  
CC derived from the 5' ends of mRNAs and even in those cases where longer  
CC  
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
CC  
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
CC  
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
CC  
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
CC  
CC They are used to obtain upstream regulatory sequences and to design  
CC  
XX  
XX  
SQ Sequence 92 BP; 17 A; 21 C; 37 G; 17 T; 0 other;

Query Match 68.0%; Score 13.6; DB 21; Length 92;  
Best Local Similarity 80.0%; Pred. No. 1.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GAGCGGAGCCGCTCTCA 20  
DB 34 GAGCGGAGCCGCTCTCA 15

RESULT 15  
AAH43131/c  
ID AAH43131 standard; cDNA; 37 BP.  
XX  
XX  
AC AAH43131;  
XX  
XX  
DT 17-OCT-2001 (first entry)  
XX  
XX  
DE Primer: F5-alpha-bottom.  
XX  
XX  
XX T cell receptor; TCR; Influenza A; ligand; functional processing;  
XX  
XX  
KM affinity; polymerase chain reaction; primer; amplification; PCR; ss.  
XX  
XX  
OS Synthetic.  
XX  
XX  
PN EP1118661-A1.  
XX  
XX  
PD 25-JUL-2001.  
XX  
XX  
PF 13-JAN-2000; 2000EP-0200110.

PR 13-JAN-2000; 2000EP-0200110.  
XX  
XX (HETN-) HET NEDERLANDS KANKER INST.  
PA  
XX  
XX Schumacher ANM, Kessels HWHG;  
PI  
XX  
XX WPI; 2001-459002/50.  
DR  
XX  
XX Generating receptors with desired specificities for ligands, which upon  
PT binding to the ligand under-goes functional processing in order to  
PT provide a biological response after ligand-binding -  
XX  
XX  
XX Disclosure; Page 6; 21pp; English.  
PS  
XX  
XX The sequences given in AAH43128-34 are primers which were used in the  
CC amplification and cloning of the complementarily determining regions  
CC (CDR3) of a T cell receptor which was generated by the method of the  
CC invention. The method of the invention allows generation of receptors  
CC with desired specificities for ligands, which upon binding to the  
CC ligand under-go functional processing in order to provide a biological  
CC response after ligand-binding. The method is used for generating  
CC libraries of cells with receptors of differing affinities.  
XX  
SQ Sequence 37 BP; 8 A; 12 C; 14 G; 3 T; 0 other;  
  
Query Match 67.0%; Score 13.4; DB 22; Length 37;  
Best Local Similarity 93.3%; Pred.No.1.4e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GAGCGGCAGCCCCCT 15  
XXXXXXXXXXXXXXXXXXXX  
DB 18 GAGCGGCAGCCCCCT 4

Search completed: November 23, 2002, 06:28:25  
Job time : 102.6 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:53:51 : Search time 21.55 seconds  
(without alignments)  
284.619 Million cell updates/sec

Title: US-09-296-264-1

Perfect score: 20

Sequence: 1 gagcgagagccccctcca 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

687286

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents NA:\*

- 1: /cgn2\_6/pdata/1/lna/5A\_COMB.seq:\*
- 2: /cgn2\_6/pdata/1/lna/5B\_COMB.seq:\*
- 3: /cgn2\_6/pdata/1/lna/6A\_COMB.seq:\*
- 4: /cgn2\_6/pdata/1/lna/6B\_COMB.seq:\*
- 5: /cgn2\_6/pdata/1/lna/PCFUS\_COMB.seq:\*
- 6: /cgn2\_6/pdata/1/lna/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	14.8	74.0	60	Patent No. 5252465
2	13.6	68.0	55	Sequence 16, Appl
3	13.2	66.0	30	Sequence 3, Appl
4	12.8	64.0	20	Sequence 19, Appl
5	12.8	64.0	42	Sequence 3, Appl
6	12.8	64.0	48	Sequence 49, Appl
7	12.8	64.0	54	Sequence 1107, Ap
8	12.8	64.0	55	Sequence 18, Appl
9	12.8	64.0	91	Sequence 53, Appl
10	12.8	64.0	93	Sequence 420, App
11	12.6	63.0	21	Sequence 136, App
12	12.6	63.0	21	Sequence 136, App
13	12.6	63.0	21	Sequence 42, App
14	12.6	63.0	21	Sequence 136, App
15	12.6	63.0	25	Sequence 18, Appl
16	12.6	63.0	25	Sequence 18, Appl
17	12.6	63.0	26	Patent No. 5504194
18	12.6	63.0	35	Sequence 1, Appl
19	12.6	63.0	35	Sequence 48, Appl
20	12.6	63.0	35	Sequence 48, Appl
21	12.6	63.0	39	Sequence 9, Appl
22	12.6	63.0	41	Sequence 5, Appl
23	12.6	63.0	42	Sequence 47, Appl
24	12.6	63.0	44	Sequence 47, Appl
25	12.6	63.0	44	Sequence 29, Appl
26	12.6	63.0	69	Sequence 27, Appl
27	12.6	63.0	69	Sequence 62, Appl

28	12.6	63.0	69	US-08-482-085B-62	Sequence 62, Appl
29	12.6	63.0	69	US-08-475-411A-29	Sequence 29, Appl
30	12.6	63.0	69	US-08-478-029A-29	Sequence 29, Appl
31	12.6	63.0	93	US-08-592-383-8	Sequence 8, Appl
32	12.4	62.0	27	US-08-233-030-44	Sequence 44, Appl
33	12.4	62.0	65	5174993-17	Patent No. 5174993
34	12.4	62.0	65	5505941-17	Patent No. 5505941
35	12.4	62.0	69	US-08-488-161-102	Sequence 102, App
36	12.4	62.0	69	US-09-273-685-102	Sequence 102, App
37	12.4	62.0	69	US-09-273-685-102	Sequence 102, App
38	12.2	61.0	21	US-09-689-291A-8	Sequence 8, Appl
39	12.2	61.0	25	US-08-641-627A-17	Sequence 17, Appl
40	12.2	61.0	25	US-08-641-627A-18	Sequence 18, Appl
41	12.2	61.0	25	US-08-641-627A-19	Sequence 19, Appl
42	12.2	61.0	27	US-09-263-023-10	Sequence 10, Appl
43	12.2	61.0	27	US-09-471-867-10	Sequence 10, Appl
44	12.2	61.0	33	US-08-750-134A-1	Sequence 1, Appl
45	12.2	61.0	33	US-09-363-745-1	Sequence 1, Appl

#### ALIGNMENTS

```
RESULT 1
5252465-13/C
; Patent No. 5252465
; APPLICANT: NIGON, VICTOR-MARC;VERDIER, GERARD;CHEBLLOUNE,
; YAHIA;COSSET, FRANCOIS-LOIC;LEGRAS, CATHERINE;REYS-BRION,
;ASTRID;BELAKEBI, MUSTAPHA;MALLET, FRANCOIS;SAVATIER, PIERE;
;THORVAL, PIERICK;SAMARUT, JACQUES;PONCET, DIDIER;BAGNIS,
; CLAUDE;BENCHAIRI, MILOUD
; TITLE OF INVENTION: AVIAN ERYTHROBLASTOSIS VIRUS VECTORS FOR
; INTEGRATION AND EXPRESSION OF HETEROLOGOUS GENES IN AVIAN CELLS
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/477, 833
; FILING DATE: 03-OCT-1988
; SEQ ID NO:13:
; LENGTH:60
5252465-13
Query Match          74.0%; Score 14.8; DB 6; Length 60;
Best Local Similarity 88.9%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2  AGCGGAGCCCCCTCTCC 19
Db      22  AGCGGAGCCCCCTCTAC 5
RESULT 2
US-09-357-740-16/C
; Sequence 16, Application US/09357740
; Patent No. 6348596
; GENERAL INFORMATION:
; APPLICANT: Lee, Linda G.
; APPLICANT: Graham, Ronald J.
; APPLICANT: Mullah, Khaluzzaman B.
; APPLICANT: Haxo, Francis T.
; TITLE OF INVENTION: ASYMMETRIC CYANINE DYE QUENCHERS
; FILE REFERENCE: 9584-007
; CURRENT APPLICATION NUMBER: US/09/357,740
; CURRENT FILING DATE: 1999-07-20
; EARLIER APPLICATION NUMBER: 09/012,525
; EARLIER FILING DATE: 1998-01-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
```

OTHER INFORMATION: Oligonucleotide  
US-09-357-740-16

Query Match 68.0%; Score 13.6; DB 4; Length 55;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTCTCC 20  
|| ||||| |||||  
DB 52 GATGGGAGCCCCCAGTCCA 33

RESULT 3  
PCT-US95-07372-3

Sequence 3, Application PC/TUS9507372

GENERAL INFORMATION:

APPLICANT: Oklahoma Medical Research Foundation

TITLE OF INVENTION: Calcium Binding Recombinant

TITLE OF INVENTION: Antibody Against Protein C

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst

STREET: 2800 One Atlantic Center

STREET: 1201 West Peachtree Street

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07372

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31.284

REFERENCE/DOCKET NUMBER: OKRF106CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 873-8794

TELEFAX: (404) 873-8795

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

HYPOTHEICAL: NO

ANTI-SENSE: NO

PCT-US95-07372-3

Query Match

Best Local Similarity 66.0%; Score 13.2; DB 5; Length 30;

Best Local Similarity 83.3%; Pred. No. 2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCCCTCTCC 19  
||||| ||||| ||  
DB 2 AGCGGAGCCCCCTCTCC 19

RESULT 4  
US-09-120-853-19/c

Sequence 19, Application US/09120853

Patent No. 6057437

GENERAL INFORMATION:

APPLICANT: Kamiya, Kiya

APPLICANT: Matsuda, Yoko

APPLICANT: Uchida, Kiyoshi

TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID COMPOUND

TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID COMPOUND

FILE REFERENCE: 07898/030001

CURRENT APPLICATION NUMBER: US/09/120.853

CURRENT FILING DATE: 1998-07-21

EARLIER APPLICATION NUMBER: JP 213838/1997

EARLIER FILING DATE: 1997-07-25

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 19

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Artificial

OTHER INFORMATION: nucleic acid sequence

US-09-120-853-19

Query Match 64.0%; Score 12.8; DB 3; Length 20;  
Best Local Similarity 87.5%; Pred. No. 3e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGGAGCCCCCTCTCC 19  
||| ||||| |||||  
DB 20 CTGCGGCCCCCTCTCC 5

RESULT 5  
US-09-120-853-3/c

Sequence 3, Application US/09120853

Patent No. 6057437

GENERAL INFORMATION:

APPLICANT: Kamiya, Kiya

APPLICANT: Matsuda, Yoko

APPLICANT: Uchida, Kiyoshi

TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID COMPOUND

FILE REFERENCE: 07898/030001

CURRENT APPLICATION NUMBER: US/09/120.853

CURRENT FILING DATE: 1998-07-21

EARLIER APPLICATION NUMBER: JP 213838/1997

EARLIER FILING DATE: 1997-07-25

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 42

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Artificial

OTHER INFORMATION: nucleic acid sequence

US-09-120-853-3

Query Match 64.0%; Score 12.8; DB 3; Length 42;  
Best Local Similarity 87.5%; Pred. No. 3e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGGAGCCCCCTCTCC 19  
||| ||||| |||||  
DB 42 CTGCGGCCCCCTCTCC 27

RESULT 6  
US-09-400-653A-49

Sequence 49, Application US/09400653A

Patent No. 6348311

GENERAL INFORMATION:

APPLICANT: Kastan, Michael

APPLICANT: Camman, Christine

APPLICANT: Kim, Seong-Tae

APPLICANT: Lim, Dae-Sik

TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies

FILE REFERENCE: 2427/1P142

CURRENT APPLICATION NUMBER: US/09/400,653A

CURRENT FILING DATE: 1999-09-21

PRIOR APPLICATION NUMBER: 09/248,061  
PRIOR FILING DATE: 1998-02-10  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 49  
LENGTH: 48  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR primer  
US-09-400-653A-49

Query Match  
Best Local Similarity 87.5%; Score 12.8; DB 4; Length 48;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAGCGCGACCCCTC 16  
|||||  
DB 7 GAGCGCGCGACCTC 22

RESULT 7  
US-08-311-486C-1107/C  
Sequence 1107, Application US/08311486C  
Patent No. 5811300

GENERAL INFORMATION:  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth Draper  
APPLICANT: Kevin Kisich  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwigen  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
NUMBER OF SEQUENCES: 1157  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,486C  
FILING DATE: September 23, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Waldburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/166  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1107:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 54 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-311-486C-1107

Query Match  
Best Local Similarity 87.5%; Score 12.8; DB 1; Length 54;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 GGCAGCCCCCTCTCCA 20  
|||||  
DB 21 GGTAGCCCTCTCTCCA 6

RESULT 8  
US-09-357-740-18/C  
Sequence 18, Application US/09357740  
Patent No. 6348596

GENERAL INFORMATION:  
APPLICANT: Lee, Linda G.  
APPLICANT: Graham, Ronald J.  
APPLICANT: Mullah, Khairuzzaman B.  
APPLICANT: Haxo, Francis T.  
TITLE OF INVENTION: ASYMMETRIC CYANINE DYE QUENCHERS  
FILE REFERENCE: 9584-007  
CURRENT APPLICATION NUMBER: US/09/357,740  
CURRENT FILING DATE: 1999-07-20  
EARLIER APPLICATION NUMBER: 09/012,525  
EARLIER FILING DATE: 1998-01-23  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 18  
LENGTH: 55  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
US-09-357-740-18

Query Match  
Best Local Similarity 87.5%; Score 12.8; DB 4; Length 55;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 GGCAGCCCCCTCTCCA 20  
|||||  
DB 48 GGCAGCCCCCAGTCCA 33

RESULT 9  
US-07-752-101A-53  
Sequence 53, Application US/07752101A  
Patent No. 5326857

GENERAL INFORMATION:  
APPLICANT: Yamamoto, Fumi-Ichiro  
APPLICANT: White, Thayer  
APPLICANT: Hakomori, Sen-Itiroh  
APPLICANT: Clausen, Henrik  
TITLE OF INVENTION: ABO GENOTYPING  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: U.S.  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/752,101A

FILING DATE: 19910829  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 150036.406C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
TELEFAX: 206-682-6031  
TELEX: 3723836  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-07-752-101A-53

Query Match 64.0%; Score 12.8; DB 1; Length 91;  
Best Local Similarity 87.5%; Pred. No. 3e+03; 2; Mismatches 0; Gaps 0;  
Matches 14; Conservative 0; Indels 0;

OY 4 CGGAGCCCCCTCTCC 19  
||||||| 11 11  
Db 57 CGGAGCCCCCTCTCC 72

RESULT 10  
US-08-976-413A-420  
Sequence 420, Application US/08976413A  
Patent No. 6127119  
GENERAL INFORMATION:  
APPLICANT: STEPHENS, ANDREW  
APPLICANT: GOLD, LARRY  
APPLICANT: SPECK, ULRIKH  
TITLE OF INVENTION: NUCLEIC ACID LIGANDS OF TISSUE TARGET  
NUMBER OF SEQUENCES: 440  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 8.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/976,413A  
FILING DATE: 21-NOVEMBER-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/433,124  
FILING DATE: 03-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX31/CIP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 420:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: All C's are 2'-F cytosine  
FEATURE:  
OTHER INFORMATION: All U's are 2'-F uracil  
US-08-976-413A-420

Query Match 64.0%; Score 12.8; DB 3; Length 93;  
Best Local Similarity 75.0%; Pred. No. 3e+03;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 CGGAGCCCCCTCTCC 19  
||||||| 11 11  
Db 37 CGAGAGCCCCCTCTCC 52

RESULT 11  
US-08-465-590-136  
Sequence 136, Application US/08465590  
Patent No. 5824770  
GENERAL INFORMATION:  
APPLICANT: Georgopoulos, Katia A.  
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE  
NUMBER OF SEQUENCES: 164  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 STATE STREET, Suite 510  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Ascii (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,590  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/238,212  
FILING DATE: 02-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/121,438  
FILING DATE: 14-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/946,233  
FILING DATE: 14-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Paul L.  
REGISTRATION NUMBER: 35,695  
REFERENCE/DOCKET NUMBER: MPG-006C2DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 136:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-465-590-136

Query Match 63.0%; Score 12.6; DB 1; Length 21;



Best Local Similarity 78.9%; Pred. No. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCCCTCTCCA 20  
Db 2 AGGGGAATCTCCCTCTCCA 20

## RESULT 12

US-08-711-417C-136  
; Sequence 136, Application US/08711417C  
; Patent No. 6228611

GENERAL INFORMATION:

APPLICANT: Georgopoulos, Katia A.

TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

NUMBER OF SEQUENCES: 202

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/711.417C

FILING DATE: 05-Sep-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/238,212

FILING DATE: 02-May-1994

APPLICATION NUMBER: 08/121,438

FILING DATE: 14-Sep-1993

APPLICATION NUMBER: 07/946,233

FILING DATE: 14-Sep-1992

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis P.

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10287/007001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 136:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 136:

US-08-711-417C-136

Query Match 63.0%; Score 12.6; DB 4; Length 21;

Best Local Similarity 78.9%; Pred. No. 3.6e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCCCTCTCCA 20  
Db 2 AGGGGAATCTCCCTCTCCA 20

## RESULT 13

US-09-177-650-42

; Sequence 42, Application US/09177650

Patent No. 6413719

GENERAL INFORMATION:

APPLICANT: Leppert, Mark F.

APPLICANT: Singh, Nanda

APPLICANT: Charlier, Carole

TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE

TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)

TITLE OF INVENTION: AND OTHER EPILEPSIES

FILE REFERENCE: 2323-134

CURRENT APPLICATION NUMBER: US/09/177,650

CURRENT FILING DATE: 1998-10-23

EARLIER APPLICATION NUMBER: 60/063,147

EARLIER FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 129

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 42

LENGTH: 21

TYPE: DNA

ORGANISM: Homo sapiens

US-09-177-650-42

Query Match 63.0%; Score 12.6; DB 4; Length 21;

Best Local Similarity 78.9%; Pred. No. 3.6e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCCCTCTCCA 20  
Db 1 AGCGGAGCCCCCTCTCCA 19

## RESULT 14

PCT-US93-08743-136

; Sequence 136, Application PC/TUS9308743

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

NUMBER OF SEQUENCES: 152

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08743

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 946,233

FILING DATE: 14-SEP-1992

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 136:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

PCT-US93-08743-136

Query Match 63.0%; Score 12.6; DB 5; Length 21;

Best Local Similarity 78.9%; Pred. No. 3.6e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCCCTCTCCA 20  
Db 2 AGGGGAATCTCCCTCTCCA 20

## RESULT 15

US-08-772-512A-18

; Sequence 18, Application US/08772512A

Patent No. 6023705

GENERAL INFORMATION:

APPLICANT: Soderlund, David M.

APPLICANT: Knipfle, Douglas C.

APPLICANT: Ingles, Patricia J.

TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM

TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE

TITLE OF INVENTION: FLIES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
STREET: P.O. Box 1051, Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/772,512A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/608,618  
FILING DATE: 01-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Braman, Susan J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/601(CRFD-1657)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1636  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-772-512A-18

Query Match 63.0%; Score 12.6; DB 3; Length 25;  
Best Local Similarity 78.9%; Pred. NO. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GAGCGGAGCCCCCTCTCC 19  
||||| |||||  
Db 2 GAGCGGCGGCCCCGGCCCC 20

Search completed: November 23, 2002, 06:35:55  
Job time : 23.35 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:54:41 : Search time 17.25 Seconds  
(without alignments)  
439.108 Million cell updates/sec

Title: US-09-296-264-1  
Perfect score: 20  
Sequence: 1 gagcgagcagccctctca 20

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 195614

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published\_Applications\_NA:\*  
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2: /cgn2\_6/ptodata/2/pubpna/PCr\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
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9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	72.0	55	10	US-09-887-469-13 Sequence 13, Appl
2	13.4	67.0	31	10	US-09-801-274-1010 Sequence 1010, Ap
3	13.2	66.0	69	10	US-09-818-063-35 Sequence 35, Appl
4	13.2	66.0	69	10	US-09-918-063-37 Sequence 37, Appl
5	12.8	64.0	27	10	US-09-783-708-7 Sequence 7, Appl
6	12.8	64.0	61	10	US-09-359-672-3 Sequence 3, Appl
7	12.8	64.0	100	10	US-09-861-893-41 Sequence 41, Appl
8	12.6	63.0	27	10	US-09-895-141-40 Sequence 40, Appl
9	12.6	63.0	41	10	US-09-808-660-5 Sequence 5, Appl
10	12.4	62.0	31	10	US-09-801-274-1263 Sequence 1263, Ap
11	12.4	62.0	87	10	US-09-920-118-1 Sequence 1, Appl
12	12.4	62.0	87	10	US-09-920-118-2 Sequence 2, Appl
13	12.2	61.0	18	12	US-10-037-616-17 Sequence 17, Appl
14	12.2	61.0	35	10	US-09-732-348-8 Sequence 8, Appl
15	12.2	61.0	38	10	US-09-732-348-20 Sequence 20, Appl
16	12.2	61.0	44	10	US-09-916-230-25 Sequence 25, Appl
17	12.2	61.0	48	9	US-09-905-291A-355 Sequence 355, App
18	12.2	61.0	48	10	US-09-909-320-355 Sequence 355, App
19	12.2	61.0	48	10	US-09-909-088B-355 Sequence 355, App

20	12.2	61.0	56	10	US-09-983-965-4006 Sequence 4006, Ap
21	12.2	61.0	83	10	US-09-864-761-26469 Sequence 26469, A
22	12.2	61.0	84	10	US-09-864-761-23396 Sequence 23396, A
23	12	60.0	35	12	US-10-011-125-7 Sequence 7, Appl
24	12	60.0	36	10	US-09-740-668A-57 Sequence 57, Appl
25	12	60.0	43	12	US-10-011-125-6 Sequence 6, Appl
26	12	60.0	46	10	US-09-859-773A-6 Sequence 6, Appl
27	12	60.0	56	10	US-09-294-093B-19 Sequence 19, Appl
28	12	60.0	61	9	US-09-946-807-1302 Sequence 1302, Ap
29	12	60.0	61	10	US-09-795-668-1302 Sequence 1302, Ap
30	12	60.0	61	10	US-09-795-668-1302 Sequence 1302, Ap
31	12	60.0	75	10	US-09-864-761-28813 Sequence 28813, A
32	12	60.0	78	10	US-09-864-761-24773 Sequence 24773, A
33	12	60.0	97	10	US-09-864-761-32467 Sequence 32467, A
34	11.8	59.0	31	10	US-09-801-274-353 Sequence 353, App
35	11.8	59.0	31	10	US-09-801-274-958 Sequence 958, App
36	11.8	59.0	31	10	US-09-091-134-1 Sequence 1, Appl
37	11.8	59.0	35	10	US-09-006-298-12 Sequence 12, Appl
38	11.8	59.0	78	10	US-09-919-580-702 Sequence 702, App
39	11.8	59.0	85	10	US-09-919-580-702 Sequence 702, App
40	11.8	59.0	88	10	US-09-815-343-316 Sequence 316, App
41	11.8	59.0	88	10	US-09-919-580-574 Sequence 574, App
42	11.8	59.0	93	10	US-09-764-887-545 Sequence 545, App
43	11.6	58.0	20	10	US-09-791-406-71 Sequence 71, Appl
44	11.6	58.0	21	10	US-09-837-235-11 Sequence 11, Appl
45	11.6	58.0	21	10	US-09-837-235-13 Sequence 13, Appl

#### ALIGNMENTS

RESULT 1  
US-09-887-469-13  
; Sequence 13, Application US/09887469  
; Patent No. US20020146433A1  
; GENERAL INFORMATION:  
; APPLICANT: Krempf, Christine D.  
; APPLICANT: Collins, Peter L.  
; APPLICANT: Murphy, Brian R.  
; APPLICANT: Buchholz, Ursula  
; APPLICANT: Whitehead, Stephen S.  
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING  
; TITLE OF INVENTION: PROTECTIVE ANTIGENS FROM PROMOTOR-PROXIMAL-GENES  
; FILE REFERENCE: 15280-424-IUS  
; CURRENT APPLICATION NUMBER: US/09/887,469  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/213,708  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 55  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Artificial  
; OTHER INFORMATION: Respiratory Syncytial Virus  
US-09-887-469-13  
Query Match 72.0% Score 14.4; DB 10; Length 55;  
Best Local Similarity 93.8%; Pred. No. 7.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 GCGGACGCCCTCTC 18  
Db 22 GCGGACGCCCTCTC 37  
RESULT 2  
US-09-801-274-1010  
; Sequence 1010, Application US/09801274  
; Patent No. US20020032319A1  
; GENERAL INFORMATION:



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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 61
; TYPE: DNA
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(60)
US-09-359-672-3

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 10; Length 61;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTC 16
Db 59 GCGGCGAGCTCCCTC 44

RESULT 7
US-09-861-893-41
; Sequence 41, Application US/09861893
; Patent No. US20020045257A1
; GENERAL INFORMATION:
; APPLICANT: Feinberg, Andrew
; APPLICANT: Strichman-Almashanu, Liora
; APPLICANT: Jiang, Shan
; TITLE OF INVENTION: METHODS FOR ASSAYING GENE IMPRINTING AND
; TITLE OF INVENTION: METHYLATED CPG ISLANDS
; FILE REFERENCE: 01107.00128
; CURRENT APPLICATION NUMBER: US/09/861,893
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/206,158
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/206,161
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-861-893-41

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 10; Length 100;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTC 16
Db 71 GCGGCGAGCCCTC 86

RESULT 8
US-09-895-141-40/C
; Sequence 40, Application US/09895141
; Patent No. US2002012008A1
; GENERAL INFORMATION:
; APPLICANT: Benzer, Seymour
; APPLICANT: Min, Kyung-Tai
; TITLE OF INVENTION: LIFE EXTENSION OF DROSOPHILA BY A DRUG TREATMENT
; FILE REFERENCE: 30431.3US01
; CURRENT APPLICATION NUMBER: US/09/895,141
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215401
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 40
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 3'RT-PCR
; OTHER INFORMATION: Primer Sequence for Hexokinase
US-09-895-141-40

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 10; Length 27;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCTTCCA 20
Db 27 AGCTCCAGCTCCATCCA 9

RESULT 9
US-09-908-660-5
; Sequence 5, Application US/09908660
; Patent No. US20020081709A1
; GENERAL INFORMATION:
; APPLICANT: Bogedain, Christoph
; APPLICANT: Maass, Gerd
; APPLICANT: Hallek, Michael
; TITLE OF INVENTION: SYSTEM FOR THE PRODUCTION OF AAV VECTORS
; FILE REFERENCE: 8484-0057-999
; CURRENT APPLICATION NUMBER: US/09/908,660
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/214,151
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-908-660-5

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 10; Length 41;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTTCC 19
Db 7 GAGCGGCGCCCGGTCC 25

RESULT 10
US-09-801-274-1263/C
; Sequence 1263, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1263
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1263

Query Match
Best Local Similarity 62.0%; Score 12.4; DB 10; Length 31;
Best Local Similarity 81.2%; Pred. No. 5.3e+03;
```

```
Matches 13: Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 5 GGCAGCCCTCTCCA 20
   ||| ||| ||| ||| |||
Db 30 GGCAGCCCTCTCYA 15

RESULT 11
US-09-920-118-1/c
; Sequence 1, Application US/09920118
; Patent No. US20020102734A1
; GENERAL INFORMATION:
; APPLICANT: Menzel, Rolf
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIRECTED GENE ASSEMBLY
; FILE REFERENCE: 10424-003
; CURRENT APPLICATION NUMBER: US/09/920,118
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/222,134
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Primer
US-09-920-118-1

Query Match
Best Local Similarity 92.0%; Score 12.4; DB 10: Length 87;
Best Local Similarity 92.9%; Pred. No. 5.3e+03;
Matches 13: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGCGCCGCC 14
   ||| ||| ||| |||
Db 72 GAGCGGCGCCGCC 59

RESULT 12
US-09-920-118-2
; Sequence 2, Application US/09920118
; Patent No. US20020102734A1
; GENERAL INFORMATION:
; APPLICANT: Menzel, Rolf
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIRECTED GENE ASSEMBLY
; FILE REFERENCE: 10424-003
; CURRENT APPLICATION NUMBER: US/09/920,118
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/222,134
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Primer
US-09-920-118-2

Query Match
Best Local Similarity 62.0%; Score 12.4; DB 10: Length 87;
Best Local Similarity 92.9%; Pred. No. 5.3e+03;
Matches 13: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGCGCCGCC 14
   ||| ||| ||| |||
Db 20 GAGCGGCGCCGCC 33

RESULT 13
US-10-037-616-17
; Sequence 17, Application US/10037616
; Patent No. US20020123148A1
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```
; GENERAL INFORMATION:
; APPLICANT: English, Denis
; APPLICANT: Kovacs, Richard J.
; APPLICANT: Rizzo, Maria T.
; APPLICANT: Silva, Daniel T.
; TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic Use
; FILE REFERENCE: 7042-119
; CURRENT APPLICATION NUMBER: US/10/037,616
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/243,887
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-037-616-17

Query Match
Best Local Similarity 61.0%; Score 12.2; DB 12: Length 18;
Best Local Similarity 82.4%; Pred. No. 6.4e+03;
Matches 14: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CGGAGCCCTCTCCA 20
   | ||| ||| ||| |||
Db 1 CAGAGCCCTCTCCA 17

RESULT 14
US-09-732-348-8/c
; Sequence 8, Application US/09732348
; Patent No. US20020046419A1
; GENERAL INFORMATION:
; APPLICANT: Yen Choo, et al.
; TITLE OF INVENTION: Regulated Gene Expression in Plants
; FILE REFERENCE: 674538-2001
; CURRENT APPLICATION NUMBER: US/09/732,348
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc-feature
; LOCATION: (1)..(35)
; OTHER INFORMATION: forward primer
US-09-732-348-8

Query Match
Best Local Similarity 61.0%; Score 12.2; DB 10: Length 35;
Best Local Similarity 82.4%; Pred. No. 6.4e+03;
Matches 14: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCTCTC 18
   | ||| ||| ||| |||
Db 33 ACCGGAGCGCCTCTC 17

RESULT 15
US-09-732-348-20/c
; Sequence 20, Application US/09732348
; Patent No. US20020046419A1
; GENERAL INFORMATION:
; APPLICANT: Yen Choo, et al.
; TITLE OF INVENTION: Regulated Gene Expression in Plants
; FILE REFERENCE: 674538-2001
; CURRENT APPLICATION NUMBER: US/09/732,348
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
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Query Match	61.0%	Score 12.2	DB 10	Length 38
Best Local Similarity	82.4%	Pred. No. 6.4e+03		
Matches 14, Conservative	0	Mismatches 3	Indels 0	Gaps 0

Query Match	61.0%	Score 12.2	DB 10	Length 38
Best Local Similarity	82.4%	Pred. 6.4e+03		
Matches 14	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Oy	2	AGCGCAGCCCTCTC	18	
db	36	ACCGGCAGCGCCTCTC	20	

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nuclele - nuclele search, using sw model

Run on: November 25, 2002, 09:10:06 ; Search time 755.55 Seconds

(without alignments)  
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Title: US-09-296-264-1

Perfect score: 20

Sequence: 1 gagcgagcagccctctcca 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 357874

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
EST :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
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16: em\_estlom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
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26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.2	76.0	98	10	BE425297 WHE0311.D
2	14.8	74.0	65	9	AI270452 qu88c06.x
3	14.2	71.0	50	9	AU107434 AU107434
4	14.2	71.0	58	9	AI123506 qa01909.x
5	14.2	71.0	59	17	BH855612 SALK_0848
6	14.2	71.0	85	14	BQ808288 1030003A0

Result No.	Score	Query Match	Length	DB ID	Description
7	14.2	71.0	87	17	TA2H03P
8	13.8	69.0	74	12	BC315169
9	13.8	69.0	84	13	BM090905
10	13.8	69.0	86	10	AM593901
11	13.8	69.0	95	9	AI051259
12	13.8	69.0	96	9	AA835222
13	13.8	69.0	97	17	AA356019
14	13.8	69.0	100	10	AA605663
15	13.6	68.0	57	17	AA962155
16	13.6	68.0	66	17	TA391A11P
17	13.6	68.0	67	13	BI908580
18	13.6	68.0	82	9	AA870618
19	13.6	68.0	89	9	AA579142
20	13.4	67.0	75	17	AA339132
21	13.4	67.0	93	17	TA358C080
22	13.2	66.0	43	17	BH855596
23	13.2	66.0	50	9	AU103490
24	13.2	66.0	61	17	AZ791343
25	13.2	66.0	79	9	A1799649
26	13.2	66.0	79	12	BE880374
27	13.2	66.0	82	9	A1915454
28	13.2	66.0	82	12	BF168237
29	13.2	66.0	90	9	AA680840
30	13.2	66.0	93	10	BE287079
31	13.2	66.0	60	17	BH891314
32	12.8	64.0	37	9	AA897070
33	12.8	64.0	50	9	AU102552
34	12.8	64.0	50	9	AU102553
35	12.8	64.0	53	9	AU102554
36	12.8	64.0	53	12	BF013395
37	12.8	64.0	61	12	BE740294
38	12.8	64.0	70	13	BJ084169
39	12.8	64.0	86	17	BH413188
40	12.8	64.0	87	14	BQ821696
41	12.8	64.0	87	17	FR0023597
42	12.8	64.0	91	9	AA865904
43	12.8	64.0	91	12	BF436210
44	12.8	64.0	93	12	BF506824
45	12.8	64.0	94	14	BQ808815

## ALIGNMENTS

RESULT 1  
BE425297/c  
LOCUS  
DEFINITION  
WHE0311.D02.D02S Wheat unstressed seedling shoot cDNA library  
Triticum aestivum cDNA clone WHE0311.D02.D02, mRNA sequence.  
ACCESSION  
BE425297.1 GI:9423056  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
broad wheat.  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;  
Triticeae; Triticum.  
REFERENCE  
1 (bases 1 to 98)  
Anderson,O.D., Cho,S., Choi,D.W., Close,T.J., Fenton,R.D., Han  
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,  
Seaton,C.L. and Tong,J.C.  
The structure and function of the expressed portion of the wheat  
genomes  
Unpublished (2000)  
Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific  
West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818  
Email: oanderson@pw.usda.gov  
Sequence have been trimmed to remove vector sequence and low  
quality sequence with phred score less than 20

FEATURES Seq primer: Stratagene SK primer.  
Location/Qualifiers  
source 1..98

/organism="Ptilium aestivum"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="WHE0311\_D02\_D02"  
/clone\_lib="Wheat unstressed seedling shoot cDNA library"  
/tissue\_type="Etiolated shoot"  
/dev\_stage="Five day old seedling"  
/lab\_host="E. coli SOLR"  
/note="Vector: lambda uni-ZAP XR, excised phagemid;  
Site\_1: EcoRI; Site\_2: XhoI; Seeds were surface-sterilized,  
germinated and grown aseptically in the dark at room  
temperature on filter paper with water, mystatin and  
cefotaxime in covered crystallization dishes. Shoots were  
harvested. The tissue, total RNA, and poly(A) RNA were  
prepared, a cDNA library was made, and the cDNA clones  
were in vivo excised to give plus-script phagemids in the  
17 Close lab (Choi, Close, Fenton) at the University of  
California, Riverside. Plasmid DNA preparations and DNA  
sequencing were performed in the OD Anderson lab (all  
other authors)."

BASE COUNT 17 a 30 c 36 g 15 t  
ORIGIN

Query Match 76.0%; Score 15.2; DB 10; Length 98;  
Best Local Similarity 85.0%; Pred. No. 2.3e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAGCGGACGCCCTCTCCA 20  
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Db 94 GAGCGGACGCCCTCGACCA 75

RESULT 2  
LOCUS AI270452 65 bp mRNA linear EST 17-NOV-1998  
DEFINITION qu88c06.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:1979146 3',  
mRNA sequence.  
ACCESSION AI270452  
VERSION AI270452.1 GI:3889619  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 65)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/dbp/image/image.html](http://www.bio.llnl.gov/dbp/image/image.html)  
Seq primer: -40UP from Gibco.

FEATURES  
source

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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1979146"  
/clone\_lib="NCI\_CGAP\_Gas4"  
/tissue\_type="poorly differentiated adenocarcinoma with  
signet ring cell features"  
/lab\_host="DH10B"  
/note="Organ: stomach; Vector: pCMV-SPORT6; Site\_1: SalI;

Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.69 kb. Life Technologies catalog #:  
11549-011"  
BASE COUNT 10 a 27 c 18 g 10 t  
ORIGIN

Query Match 74.0%; Score 14.8; DB 9; Length 65;  
Best Local Similarity 88.9%; Pred. No. 3.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AGCGGACGCCCTCTGCC 19  
|||||  
Db 1 AGCGGACGCCCTCTGCC 18

RESULT 3  
LOCUS AU107434 50 bp mRNA linear EST 30-AUG-2001  
DEFINITION AU107434 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
LNG15774, mRNA sequence.  
ACCESSION AU107434  
VERSION AU107434.1 GI:13556955  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata  
,H., Oca,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL MEDLINE  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: [ysuzuki@ims.u-tokyo.ac.jp](mailto:ysuzuki@ims.u-tokyo.ac.jp)  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
,S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
source 1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="LNG15774"  
/clone\_lib="Sugano Homo sapiens cDNA library"  
/note="Differential display comparison of untreated and  
dimethylfumarate treated u937 cells"

BASE COUNT 10 a 23 c 14 g 3 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 9; Length 50;  
Best Local Similarity 84.2%; Pred. No. 5.5e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAGCGGACGCCCTCTCC 19  
|||||  
Db 13 GAGCGGACGCCCTCTCC 31

RESULT 4  
LOCUS AI123506 58 bp mRNA linear EST 01-OCT-1998  
DEFINITION q401909.x1 Soares\_Parathyroid\_tumor\_NbHPA Homo sapiens cDNA clone  
IMAGE:1683616 3' similar to SW:DNA\_DROME P48608 DIAPHANOUS PROTEIN.  
;contains element MSRI repetitive element ;, mRNA sequence.  
ACCESSION AI123506  
VERSION AI123506.1 GI:3539272  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 58)  
AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/dbcrp/image/image.html](http://www-bio.llnl.gov/dbcrp/image/image.html)

FEATURES  
source  
Trace considered overall poor quality  
Insert Length: 953 Std Error: 0.00  
Seq primer: -40m3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..58  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="1683616"  
/clone\_lib="Soares\_parathyroid\_tumor\_NBHPA"  
/tissue\_type="parathyroid tumor"  
/dev\_stage="adult"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: parathyroid gland; Vector: pT773D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer  
15'-TGTACCAATCTGAGTGGAGCGCCGACACATTTTTTTTTTTTTTTTTTTT  
TTTTT-3'); double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot - 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

BASE COUNT 18 a 24 c 13 g 3 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 9; Length 58;  
Best Local Similarity 84.2%; Pred. No. 5.5e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AGCGGACGCCCCCTCTCA 20  
|||||  
Db 10 AGCGGACGCCCCCCCCCA 28

RESULT 5  
BH855612 59 bp DNA linear GSS 08-JUL-2002  
LOCUS BH855612  
DEFINITION SALK\_084890.49.05.x Arabidopsis thaliana TMA insertion lines  
Arabidopsis thaliana genomic clone SALK\_084890.49.05.x, DNA sequence.  
ACCESSION BH855612  
VERSION BH855612.1 GI:21705202  
KEYWORDS GSS.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 59)  
AUTHORS Alonso,J.M., Leishe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

TITLE 'C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednits,L., Shin,P., Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished (2001)  
JOURNAL Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: [eckersalk.edu](mailto:eckersalk.edu)  
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of Atg31410.  
Class: TDNA tagged.

FEATURES  
source  
Location/Qualifiers  
1..59  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone\_image="SALK\_084890.49.05.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 21 a 7 c 20 g 11 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 17; Length 59;  
Best Local Similarity 84.2%; Pred. No. 5.5e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAGCGGACGCCCCCTCTC 19  
|||||  
Db 45 GAGCGGACGCTCTCTCC 27

RESULT 6  
BO808288 85 bp mRNA linear EST 01-AUG-2002  
LOCUS BO808288  
DEFINITION 1030003A09.x2 C. reinhardtii CC-1690, Deflagellation (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.  
ACCESSION BO808288  
VERSION BO808288.1 GI:22048620  
KEYWORDS EST.  
SOURCE Chlamydomonas reinhardtii.  
ORGANISM Chlamydomonas reinhardtii.  
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.  
REFERENCE 1 (bases 1 to 85)  
AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.  
Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1030  
Unpublished (2002)  
JOURNAL Contact: Charles Hauser  
DCMB Box 91000  
Duke University  
Durham, NC 27708-1000  
Tel: 919 613 8159  
Fax: 919 613 8177  
Email: [chauser@duke.edu](mailto:chauser@duke.edu)

FEATURES  
source  
Location/Qualifiers  
1..85  
/organism="Chlamydomonas reinhardtii"  
/strain="CC-1690 wild type mt+ 21gr"  
/db\_xref="taxon:3055"  
/clone\_lib="C. reinhardtii CC-1690, Deflagellation (normalized), Lambda Zap II"

/note="Vector: Bluescript II SK-; Site\_1: EcoRI; Site\_2: XhoI; Deflagellation library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells which had been re-synthesizing flagella for 15, 30 and 60 min after being deflagellated by pH shock. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. Bluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with Exsist (Stratagene) phage. The library was normalized using method 4 described in Bonaldi et al., (1996) Genome Research 6: 791-806."

BASE COUNT 16 a 39 c 30 g 0 t

ORIGIN

Query Match 71.0%; Score 14.2; DB 14; Length 85;  
Best Local Similarity 84.2%; Pred. No. 5.7e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCGCAGCCCCCTCTCC 19  
||||| 11111 11111

Db 35 GAGCGCAGCCCCCTCTCC 53

RESULT 7  
TA2H03P 87 bp DNA linear GSS 16-SEP-2000  
LOCUS T. brucei sheared genomic DNA clone 2h03, forward sequence, genomic  
DEFINITION survey sequence.  
ACCESSION AL441676  
VERSION AL441676.1 GI:10185383  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei.  
ORGANISM Trypanosoma brucei.  
Eukaryota; Euzoenzoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
REFERENCE 1 (bases 1 to 87)  
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
TITLE Direct Submission  
JOURNAL Submitted (15-SEP-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Camps, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v+1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).  
Location/Qualifiers  
1. 87  
/organism="Trypanosoma brucei"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="2h03"

BASE COUNT 17 a 12 c 41 g 17 t

ORIGIN

Query Match 71.0%; Score 14.2; DB 17; Length 87;  
Best Local Similarity 84.2%; Pred. No. 5.7e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGCAGCCCCCTCTCCA 20  
||||| 11111 11111

Db 53 ATCGCATCTCTCTCCA 35

RESULT 8  
BG315169 74 bp mRNA linear EST 28-FEB-2002  
LOCUS P01.0.136 Human THP1 cell line library Homo sapiens CDNA, mRNA  
DEFINITION sequence.  
ACCESSION BG315169  
VERSION BG315169.1 GI:18998041  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 74)  
AUTHORS Andersson, T., Borang, S., Larsson, M., Thelin, A., Ekstrand-Hammarstrom, B., Wirta, V., Wembo, A., Lundberg, J. and Odeberg, J.  
TITLE Identification of candidate genes in atherosclerosis - Virtual chip analysis in RDA based transcript profiling of monocyte/macrophage response to oxidised LDL  
JOURNAL Unpublished (2001)  
COMMENT Contact: Andersson Tove  
Department of Biotechnology  
KTH  
Teknikringen 34, plan 6, 100 44 Stockholm, Sweden  
Tel: +46 8 790 71 29  
Fax: +46 8 245452  
Email: tove@biochem.kth.se  
POLYA="No".  
Location/Qualifiers  
1. 74  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Human THP1 cell line library"  
/cell\_line="THP1"  
/note="Vector: pRIT28, Site\_1: BamHI; Site\_2: BamHI; Shotgun cloning of RDA difference products. Macrophage and foamcell libraries were submitted to successive rounds of subtractive hybridisations generating populations of gene fragments that are differentially expressed in macrophage to foam cell formation."

BASE COUNT 15 a 25 c 21 g 12 t 1 others

ORIGIN

Query Match 69.0%; Score 13.8; DB 12; Length 74;  
Best Local Similarity 88.2%; Pred. No. 8.1e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCGCAGCCCCCTCTC 18  
||||| 11111 11111

Db 21 AGCGCAGCCCCCTCTC 37

RESULT 9  
BM090905 84 bp mRNA linear EST 20-NOV-2001  
LOCUS 191706.x1 Human Fetal Pancreas 1A Homo sapiens CDNA 3' similar to  
DEFINITION TR:029269 Q29269 UNKNOWN PROTEIN ; mRNA sequence.  
ACCESSION BM090905  
VERSION BM090905.1 GI:17019871  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 84)  
AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Seace, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blustein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R., Williams, T., Jackson, Y. and Bowers, Y.  
TITLE Endocrine Pancreas Consortium

JOURNAL  
COMMENT

Unpublished (2000)  
Other ESTs: 1g17d06.y1  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@biolhp.harvard.edu  
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Dr. Hiroshi Inoue  
(hino@imgate.wustl.edu).

## FEATURES

## source

Location/Qualifiers

1. 84

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_1lb="Human Fetal Pancreas 1A"

/tissue\_type="Fetal Pancreas (4 Pooled Donors, 18 - 20 weeks, Stratagene #738023)"

/dev\_stage="Fetal Pancreas"

/note="Vector: Bluescript SK(-); Site\_1: NotI; Site\_2: XhoI; cDNA made by oligo-dT priming. Size-selected by CHROMA SPIN-1000 (Clontech). Average insert size ~1kb. 5'

XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permut Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110 E-mail: hino@imgate.wustl.edu Tel: 314-362-1916, Fax: 314-747-2692."

## BASE COUNT

## ORIGIN

12 a 32 c 25 g 15 t

## Query Match

Best Local Similarity 69.0%; Score 13.8; DB 13; Length 84;  
Matches 15; Conservative 0; Pred. No. 8.2e+04;

Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTCC 19  
Db 2 GCGGCGCGCCCTCGCC 18

RESULT 10  
AM593901

## LOCUS

h928h03.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2946965 3',  
mRNA sequence.

## ACCESSION

AM593901.1 GI:7281159

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

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## FEATURES

## source

Seq primer: -40UP from Gdbco.  
Location/Qualifiers

1. 86

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_1lb="NCI\_CGAP\_GC6"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA from the normalized library NCI\_CGAP\_G4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

## BASE COUNT

12 a 32 c 25 g 17 t

Query Match 69.0%; Score 13.8; DB 10; Length 86;  
Best Local Similarity 88.2%; Pred. No. 8.2e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTCC 19  
Db 1 GCGGCGCGCCCTCGCC 17

## RESULT 11

## LOCUS

AI051259 95 bp mRNA linear EST 24-SEP-1998  
OY49102.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:1669179 3',  
mRNA sequence.

AI051259  
AI051259.1 GI:3306793

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## COMMENT

## COMMENT

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## COMMENT

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 95)  
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BRGAP), Tumor Gene Index  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Email: rgabs-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
www.bio.linn.gov/bbrp/image/image.html  
Insert length: 843 Std Error: 0.00  
Seq primer: -40m13 fwd. ER from Amersham.  
Location/Qualifiers

## FEATURES

1. 95

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_1lb="NCI\_CGAP\_Brn23"

/tissue\_type="gliblastoma (pooled)"

/lab\_host="DH10B"

/note="Organ: brain; Vector: p773D-Pac (Pharmacia) with a  
modified polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTTT

Possible reversed clone: polyT not found



```

Db      59 GCGGCGAGTCCCTCGCC 43

RESULT 14
LOCUS    AM605663              100 bp    mRNA    linear    EST 23-MAR-2000
DEFINITION QV2-DT0075-190100-027-a12 DT0075 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM605663
VERSION   AM605663.1 GI:7310404
KEYWORDS EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 100)
AUTHORS   HGCP http://www.ludwig.org.br/ORESTES.
TITLE     The FAPESP/LICR Human Cancer Genome Project
JOURNAL   Unpublished (1999)
COMMENT   Contact: Simpson A.J.G.
           Laboratory of Cancer Genetics
           Ludwig Institute for Cancer Research
           Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
           Brazil
           Tel: +55-11-2704922
           Fax: +55-11-2707001
           Email: asimpson@ludwig.org.br
           This sequence was derived from the FAPESP/LICR Human Cancer Genome
           Project. This entry can be seen in the following URL
           (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV2&cl2=QV2-DT0075-
           190100-027-a12&cl3=2000-01-19&cl4=1)
           Seq primer: puc 18 forward
           High quality sequence start: 12
           High quality sequence stop: 100.
FEATURES
   source
       1..100
           /organism="Homo sapiens"
           /db_xref="taxon:9606"
           /clone.lib="DT0075"
           /dev_stage="Adult"
           /note="Organ: denis_dash: Vector: puc18; Site_1: SmaI;
           Site_2: SmaI; A mini-library was made by cloning products
           derived from ORESTES PCR (U.S. Letters Patent application
           No. 196,716 - Ludwig Institute for Cancer Research)
           profiles into the pUC 18 vector. Reverse transcription of
           tissue mRNA and cDNA amplification were performed under
           low stringency conditions."
BASE COUNT      16 a      35 c      32 g      17 t
ORIGIN
Query Match      69.0%; Score 13.8; DB 10; Length 100;
Best Local Similarity 88.2%; Pred. No. 8.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 GCGGCGAGTCCCTCTCC 19
        ||||| ||||| ||
Db      40 GCGGCGAGTCCCTCTCC 56

RESULT 15
LOCUS    AZ962155              57 bp    DNA    linear    GSS 27-APR-2001
DEFINITION 2M0230D24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
ACCESSION AZ962155
VERSION   AZ962155.1 GI:13833382
KEYWORDS GSS.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 57)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
           Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

```

```

TITLE     'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
           and Wright,D., Weiss,R.
           Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
           University of Utah Genome Center
           University of Utah
           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
           84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: dduun@genetics.utah.edu
           Insert Length: 10000 Std Error: 0.00
           Plate: 0230 row: D column: 24
           Seq primer: CACACAGCAACAGCTATGACC
           Class: plasmid ends
           High quality sequence stop: 57.
FEATURES
   source
       1..57
           /organism="Mus musculus"
           /strain="C57BL/6J"
           /db_xref="taxon:10090"
           /clone.lib="UUGC2M0230D24"
           /clone.lib="Mouse 10kb plasmid UUGC2M library"
           /sex="Female"
           /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
           /note="Vector: PMD42nv; Purified genomic DNA from M.
           musculus C57BL/6J (female) was obtained from the Jackson
           Laboratory Mouse DNA Resource
           (http://www.jax.org/resources/documents/dnares/). The DNA
           was hydrodynamically sheared by repeated passage through a
           0.005 inch orifice at constant velocity. The sheared DNA
           was blunt end-repaired with T4 DNA polymerase and T4
           polynucleotide kinase. Adaptor oligonucleotides were
           ligated to the blunt ends in high molar excess. The
           adaptor DNA was purified and size-selected for a 9.5 to
           10.5 kb range using preparative agarose gel
           electrophoresis. Vector DNA was prepared from a derivative
           of PMD42 (g11473211419b1AF129072.1), a copy-number
           inducible derivative of plasmid R1. The vector was ligated
           with adaptors complementary to the insert adaptors and
           purified. The sheared, adaptor mouse DNA was annealed to
           adaptor vector DNA, and transformed into
           chemically-competent E. coli XL10-Gold (Stratagene) cells
           and selected for ampicillin resistance."
BASE COUNT      9 a      10 c      23 g      15 t
ORIGIN
Query Match      68.0%; Score 13.6; DB 17; Length 57;
Best Local Similarity 80.0%; Pred. No. 9.5e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 GAGCGGCGAGTCCCTCTCCA 20
        || ||||| || |||||
Db      37 GAGGCGAGGACCATCTCCA 18

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Search completed: November 26, 2002, 04:06:14  
 Job time : 774.8 secs

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FEATURES
  source
    1. .99
      /organism="Bacillus licheniformis"
      /db_xref="taxon:1402"
BASE COUNT      32 a      26 c      20 g      20 t      1 others
ORIGIN
Query Match      77.0%; Score 15.4; DB 6; Length 99;
Best Local Similarity 94.1%; Pred. No. 2.6e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GCACGGCGCAGAGGAGC 20
Db      31 GCACGGCGCAGAGGAGC 47

RESULT 2
LOCUS      AX356224      27 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION      Sequence 18 from Patent WO0200905.
ACCESSION      AX356224
VERSION      AX356224.1 GI:18620731
KEYWORDS
SOURCE      synthetic construct.
            synthetic construct
            artificial sequences.
REFERENCE      1
AUTHORS      Conner,T.W., Dubois,P., Malven,M. and Maseucci,J.D.
TITLE      Plant regulatory sequences for selective control of gene expression
JOURNAL      Patent: WO 0200905-A 18 03-JAN-2002;
            Monsanto Technology LLC (US)
FEATURES
  source
    1. .27
      /organism="synthetic construct"
      /db_xref="taxon:32630"
      /note="Synthetic"
BASE COUNT      8 a      6 c      11 g      2 t
ORIGIN
Query Match      76.0%; Score 15.2; DB 6; Length 27;
Best Local Similarity 85.0%; Pred. No. 3.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CGAGCAGCGCGCAGAGGAGC 20
Db      7 CGAGCAGCGCGCAGAGGAGC 26

RESULT 3
LOCUS      E27048/c      87 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION      Novel receptor protein and utilization of the same.
ACCESSION      E27048
VERSION      E27048.1 GI:13026378
KEYWORDS      JP 1999152300-A/3.
SOURCE      unidentified.
            unidentified.
            unclassified.
REFERENCE      1 (bases 1 to 87)
AUTHORS      Kazunori,N., Yasushi,A. and Takashi,H.
TITLE      Novel receptor protein and utilization of the same
JOURNAL      Patent: JP 1999152300-A 3 08-JUN-1999;
            TAKEDA CHEM IND LTD
            OS Unidentified
            PN JP 1999152300-A/3
            PD 08-JUN-1999
            PE 24-APR-1998 JP 1998114450
            PR
PI      KAZUNORI NISHI, YASUSHI ARAI, TAKASHI HORIGUCHI PC
C07K14/715,A61K45/00,C07K16/28,C12N15/09,C12P21/02, PC
C12N15/10,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,
PC      C12N5/00,

```

```

PC      (C12N15/00,C12R1:91)
CC      Strandedness: Double;
CC      Topology: Linear;
FH      Key
FT      source
      1. .87
      /organism="Unidentified".
FEATURES
  source
    1. .87
      /organism="unidentified"
      /db_xref="taxon:32644"
BASE COUNT      3 a      36 c      32 g      16 t
ORIGIN
Query Match      76.0%; Score 15.2; DB 6; Length 87;
Best Local Similarity 85.0%; Pred. No. 3.2e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CGACGAGCGCGCAGAGGAGC 20
Db      64 CGACGAGCGCGCAGAGGAGC 45

RESULT 4
LOCUS      A91560      21 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION      Sequence 87 from Patent WO9824928.
ACCESSION      A91560
VERSION      A91560.1 GI:6740515
KEYWORDS
SOURCE      unidentified.
            unidentified
            unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS      Pallsgaard,N. and Hokland,P.
TITLE      DETECTION OF CHROMOSOMAL ABNORMALITIES
JOURNAL      Patent: WO 9824928-A 87 11-JUN-1998;
            PALLSGAARD NIELS (DK); HOKLAND PETER (DK)
FEATURES
  source
    1. .21
      /organism="unidentified"
      /db_xref="taxon:32644"
BASE COUNT      7 a      3 c      9 g      2 t
ORIGIN
Query Match      72.0%; Score 14.4; DB 6; Length 21;
Best Local Similarity 93.8%; Pred. No. 8.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 AGCAGCGCGCAGAGGA 18
Db      1 AGCAGCGCGCAGAGGA 16

RESULT 5
LOCUS      AX454812/c      21 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION      Sequence 14 from Patent WO0206535.
ACCESSION      AX454812
VERSION      AX454812.1 GI:21714041
KEYWORDS
SOURCE      synthetic construct.
            synthetic construct
            artificial sequences.
REFERENCE      1
AUTHORS      Miller,M.M., Afanassieff,M. and Bries,W.E.
TITLE      Method for breeding disease resistant domesticated fowl
JOURNAL      Patent: WO 0206535-A 14 24-JAN-2002;
            City of Hope (US)
FEATURES
  source
    1. .21
      /organism="synthetic construct"
      /db_xref="taxon:32630"
      /note="Primer for SSCP analysis of Mhc B class II-beta

```

```
BASE COUNT      4 a      7 c      6 g      4 t
ORIGIN

Query Match
Best Local Similarity 72.0%; Score 14.4; DB 6; Length 21;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CACGCGCAGAGAGC 20
Db      16 CACGCTGACAGAGC 1

RESULT 6
AX156996      50 bp      DNA      linear      PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 324 from Patent WO0140521.
ACCESSION AX156996
VERSION AX156996.1 GI:14538327
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Shinkels,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS methods of use thereof
PATENT: WO 0140521-A 324 07-JUN-2001;
JOURNAL Curegen Corporation (US)
FEATURES
source 1..50
location/Qualifiers
misc_feature
/organism="Homo sapiens"
/db_xref="taxon:9606"
25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg20436198"
26
misc_feature
/note="2 of 2 allelic variants (323 is other entry)"
BASE COUNT 5 a      14 c      28 g      3 t
ORIGIN

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 6; Length 50;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CGAGCAGCGCGCAGAGAGC 19
Db      30 CGAGGACGCGCGGACGAGC 48

RESULT 7
AX156995      51 bp      DNA      linear      PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 323 from Patent WO0140521.
ACCESSION AX156995
VERSION AX156995.1 GI:14538326
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Shinkels,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS methods of use thereof
PATENT: WO 0140521-A 323 07-JUN-2001;
JOURNAL Curegen Corporation (US)
FEATURES
source 1..51
location/Qualifiers
misc_feature
/organism="Homo sapiens"
/db_xref="taxon:9606"
26

BASE COUNT 26 a      11 c      11 g      7 t

BASE COUNT      5 a      14 c      29 g      3 t
ORIGIN

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 6; Length 51;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CGAGCAGCGCGCAGAGAGC 19
Db      31 CGAGCAGCGCGCGAGAGC 49

RESULT 8
RATMAP/c      100 bp      mRNA      linear      ROD 27-APR-1993
LOCUS
DEFINITION Rat major acute phase protein mRNA (alpha1-MAP gene), partial cds.
ACCESSION M26758
VERSION M26758.1 GI:205301
KEYWORDS major acute phase protein.
SOURCE Rat (strain Sprague-Dawley) liver cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS Anderson,K.P., Martin,A.D. and Heath,E.C.
TITLE Rat major acute-phase protein: biosynthesis and characterization of
METHODS cDNA clone
JOURNAL Arch Biochem Biophys. 233 (2), 624-635 (1984)
58021400
MEDLINE
PUBMED 6207775
FEATURES
source 1..100
location/Qualifiers
CDS
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
<1..>100
/note="major acute phase protein"
/codon_start=2
/protein_id="AAA41567.1"
/db_xref="GI:205302"
/translation="TILLTCSKLPSLAQEBGAQEMDRNDETVPQAV"
BASE COUNT 26 a      28 c      24 g      22 t
ORIGIN

Query Match
Best Local Similarity 84.2%; Pred. No. 8.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GAGCAGCGCGCAGAGAGC 20
Db      28 GAGCTTGAGCAGAGAGAGC 10

RESULT 9
AR170305/c      37 bp      DNA      linear      PAT 17-DEC-2001
LOCUS
DEFINITION Sequence 19 from patent US 6291245.
ACCESSION AR170305
VERSION AR170305.1 GI:17908264
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Kopetzki,E. and Schantz,C.
TITLE Host-vector system
PATENT: US 6291245-A 19 18-SEP-2001;
JOURNAL
FEATURES
source 1..37
location/Qualifiers
BASE COUNT 8 a      11 c      11 g      7 t
```

ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 37;  
Best Local Similarity 88.2%; Pred. No. 1.4e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAG 17  
|||||  
Db 28 CGAGCAGCGCGCAGCGG 12

RESULT 10

AX007133/c 37 bp DNA linear PAT 06-SEP-2000  
LOCUS Sequence 19 from Patent EP0972838.  
ACCESSION AX007133  
VERSION AX007133.1 GI:9995024  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 37)  
AUTHORS Schantz,C. and Kopetzki,E.  
TITLE Escherichia coli host/vector system based on antibiotic-free  
JOURNAL Selection by complementation of an auxotrophy  
PATENT: EP 0972838-A 19 19-JAN-2000;  
ROCHE DIAGNOSTICS GMBH (DE)  
FEATURES Location/Qualifiers  
source 1..37  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="primer"  
BASE COUNT 8 a 11 c 11 g 7 t  
ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 37;  
Best Local Similarity 88.2%; Pred. No. 1.4e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAG 17  
|||||  
Db 28 CGAGCAGCGCGCAGCGG 12

RESULT 11

E51079/c 37 bp DNA linear PAT 18-JUN-2001  
LOCUS Novel Escherichia coli/host vector system based on selection not  
DEFINITION relying on antibiotic by complementing auxotrophy.  
ACCESSION E51079  
VERSION E51079.1 GI:13023276  
KEYWORDS JP 2000050888-A/19.  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 37)  
AUTHORS Erhard,K. and Chritiane,S.  
TITLE Novel Escherichia coli/host vector system based on selection not  
JOURNAL Patent: JP 2000050888-A 19 22-FEB-2000;  
ROCHE DIAGNOSTICS GMBH  
COMMENT OS Artificial Sequence  
PN JP 2000050888-A/19  
PD 22-FEB-2000  
PF 15-JUL-1999 JP 1999202303  
PR 15-JUL-1998 EP 98113156.8,09-OCT-1998 EP 98119078.8 PI  
ERHARD KOPETSUKI,CHRITITIANE SCHANZ  
PC C12N15/09,C12N1/21,C12P21/02//((C12N1/21,C12P1:19),(C12P21/02,  
PC C12P1:19)  
CC C12N15/00  
FH key Location/Qualifiers  
FT source 1..37

FT /organism='Artificial Sequence',  
FEATURES Location/Qualifiers  
source 1..37  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
BASE COUNT 8 a 11 c 11 g 7 t  
ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 37;  
Best Local Similarity 88.2%; Pred. No. 1.4e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAG 17  
|||||  
Db 28 CGAGCAGCGCGCAGCGG 12

RESULT 12

AR112201 23 bp DNA linear PAT 16-MAY-2001  
LOCUS Sequence 90 from patent US 6130041.  
ACCESSION AR112201  
VERSION AR112201.1 GI:14092101  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Acton,S.Laurene.  
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses  
JOURNAL Patent: US 6130041-A 90 10-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..23  
/organism="unknown"  
BASE COUNT 6 a 10 c 6 g 1 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 23;  
Best Local Similarity 80.0%; Pred. No. 1.8e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGG 20  
|||||  
Db 4 CCAGCAGCGCGCAGGTAGC 23

RESULT 13

AR149243 23 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 90 from patent US 6228581.  
ACCESSION AR149243  
VERSION AR149243.1 GI:15113834  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Acton,S.L. and Ordovas,J.M.  
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses  
JOURNAL Patent: US 6228581-A 90 08-MAY-2001;  
FEATURES Location/Qualifiers  
source 1..23  
/organism="unknown"  
BASE COUNT 6 a 10 c 6 g 1 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 23;  
Best Local Similarity 80.0%; Pred. No. 1.8e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGG 20

Db 4 CCAGCAGCGCCAGAGTAGC 23

## RESULT 14

127230

LOCUS 127230 Sequence 36 from patent US 5563254. DNA 1 linear PAT 06-FEB-1997

DEFINITION Sequence 36 from patent US 5563254.

ACCESSION 127230

VERSION 127230.1 GI:1818006

KEYWORDS

SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 27)

AUTHORS Hoffman, S.J. and Nagai, K.

TITLE Polynucleotides encoding genetically engineered mutant hemoglobins

JOURNAL Patent: US 5563254-A 36 08-OCT-1996;

FEATURES 1. 27 Location/Qualifiers

SOURCE /organism="unknown"

BASE COUNT 7 a 11 c 7 g 2 t

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 27;

Best Local Similarity 80.0%; Pred. No. 1.8e+05; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 4;

OY 1 CGAGCAGCGCCAGAGAGC 20

Db 6 CCAGCAGCGCCAGAGAGC 25

## RESULT 15

A07810/c

LOCUS A07810 35 bp DNA 1 linear PAT 26-AUG-1993

DEFINITION Oligonucleotide.

ACCESSION A07810

VERSION A07810.1 GI:413246

KEYWORDS

SOURCE

ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 35)

AUTHORS Paques, E.P.

TITLE Mutants of urinary plasminogen activator, their production and use

JOURNAL Patent: EP 0387380-A 1 19-SEP-1990;

BEHRINGWERKE Aktiengesellschaft

FEATURES 1. 35 Location/Qualifiers

SOURCE /organism="synthetic construct"

BASE COUNT 2 a 13 c 11 g 9 t

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 35;

Best Local Similarity 80.0%; Pred. No. 1.7e+05; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 4;

OY 1 CGAGCAGCGCCAGAGAGC 20

Db 27 CGAGCAGCGCCAGAGAGC 8

Search completed: December 3, 2002, 18:12:02  
Job time : 312.2 secs

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XX Claim 4; Page 16; 57pp; English.  
PS  
XX  
CC Sequences AA21431-460 represent antisense oligonucleotides which  
CC inhibit human neuropilin expression. The antisense oligonucleotides can  
CC be used to inhibit the growth or metastasis of a mammalian tumor and  
CC inhibit neovascularisation. The oligonucleotides may be used to treat  
CC various forms of cancers or tumors, such as sarcomas, melanomas,  
CC adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell  
CC carcinomas of the mouth, throat, larynx and lung, genitourinary cancers  
CC such as cervical and bladder cancer, hematopoietic cancers, colon cancer,  
CC breast cancer, pancreatic cancer, renal cancer, brain cancer, skin  
CC cancer, liver cancer, head and neck cancers, and nervous system cancers,  
CC as well as benign lesions such as papillomas. The methods may be used to  
CC treat neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration.  
XX  
SQ Sequence 20 BP; 5 A; 6 C; 9 G; 0 U; 0 other;  
  
Query Match 100.0%; Score 20; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CGAGCAGCGCGCAGAGAGC 20  
DB 1 CGAGCAGCGCGCAGAGAGC 20  
|||||  
  
RESULT 2  
ABK76729  
ID ABK76729 standard; DNA; 99 BP.  
XX  
AC ABK76729;  
XX  
XX 13-AUG-2002 (first entry)  
DT  
DE Bacillus licheniformis genomic sequence tag (GST) #4020.  
XX  
XX Differential gene expression; genomic sequenced tag; GST;  
KW altered culture condition; environmental stress;  
KW physiological provocation; ds.  
XX  
XX Bacillus licheniformis.  
OS  
XX  
XX WO200229113-A2.  
PN  
PD 11-APR-2002.  
XX  
XX 05-OCT-2001; 2001WO-US31437.  
PF  
XX 06-OCT-2000; 2000US-0680598.  
PR 27-MAR-2001; 2001US-279526P.  
XX  
XX (NOVO ) NOVOZYMES BIOTECH INC.  
PA (NOVO ) NOVOZYMES AS.  
XX  
XX Berka R, Clausen IG;  
PI  
XX WPI: 2002-416684/44.  
DR  
XX Monitoring differential expression of several genes in first Bacillus  
PT cell relative to expression of same genes in one or more second  
PT Bacillus cells, by using substrate containing Bacillus genomic  
PT sequenced tag array -  
XX  
XX Claim 4; SEQ ID NO 4020; 200pp; English.  
PS  
XX The invention describes a method of monitoring differential expression of  
CC genes in a first Bacillus cell relative to expression of the genes in  
CC other Bacillus cells, comprising hybridising labelled nucleic acid probes  
CC isolated from Bacillus cells to a substrate containing array of Bacillus  
CC genomic sequenced tags (GST), examining the array, and determining  
CC relative gene expression by an observed hybridisation reporter signal of

CC a spot in the array. The method is useful for measuring the expression of  
CC genes in a first Bacillus cell relative to expression of the same genes  
CC in one or more second Bacillus cells. The method is useful for monitoring  
CC global expression of several genes from a Bacillus cell, discovering new  
CC genes, identifying possible functions of unknown open reading frames and  
CC monitoring gene copy number variation and stability. Monitoring changes  
CC in expression of genes may be used to provide a representation of the way  
CC in which Bacillus cells adapt to changes in culture conditions,  
CC environmental stress or other physiological provocation. Extensive  
CC follow-up characterisation is unnecessary, when one spot on an array  
CC equals one gene or one open reading frame, since sequence information is  
CC available. This sequence represents a genomic sequence tag (GST) used in  
CC the method of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 99 BP; 32 A; 26 C; 20 G; 20 T; 1 other;  
  
Query Match 77.0%; Score 15.4; DB 24; Length 99;  
Best Local Similarity 94.1%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 GCACGCGCGCAGAGAGC 20  
DB 31 GCACGCGCGCAGAGAGC 47  
|||||  
  
RESULT 3  
ABK27825  
ID ABK27825 standard; DNA; 27 BP.  
XX  
XX ABK27825;  
XX  
XX 09-APR-2002 (first entry)  
DT  
DE Corn male reproductive tissue promoter, PCR primer #15.  
XX  
XX Corn; male reproductive tissue; promoter; plant; gene stacking;  
KW fertility; insect; pathogen; herbicide tolerance; primer; ss.  
XX  
XX Zea mays.  
OS  
XX  
XX WO200200905-A2.  
PN  
PD 03-JAN-2002.  
XX  
XX 26-JUN-2001; 2001WO-US20658.  
PF  
XX 28-JUN-2000; 2000US-214357P.  
PR  
XX (MONS ) MONSANTO TECHNOLOGY LLC.  
PA  
XX Conner TW, Dubois P, Malven M, Masucci JD;  
PI  
XX WPI: 2002-147890/19.  
DR  
XX New plant regulatory sequences or promoters and nucleic acids encoding  
PT them, useful for regulating gene expression, especially in male  
PT reproductive tissues -  
XX  
XX Example 3; Page 96; 131pp; English.  
PS  
XX The invention relates to an isolated nucleic acid (I) promoter capable of  
CC regulating transcription of an operably linked DNA sequence. The promoter  
CC sequences may be used for selectively modulating expression of any  
CC operatively linked gene and provide additional regulatory element  
CC diversity in a plant expression vector in gene stacking approaches, and  
CC for regulating gene expression in male reproductive tissues or gene  
CC transcriptions of any target gene (e.g. for controlling fertility, insect,  
CC pathogen or herbicide tolerance). The nucleic acids are useful as  
CC hybridisation probes or primers in hybridisation assays of other plant



CC tissues to identify closely related or homologous genes and associated  
 CC regulatory sequences. ABR27808-ABK27918 represent corn male  
 CC reproductive tissue promoter sequences and PCR primers of the invention.  
 XX  
 SQ Sequence 27 BP; 8 A; 6 C; 11 G; 2 T; 0 other;

Query Match 76.0%; Score 15.2; DB 24; Length 27;  
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGGAGC 20  
 ||||| ||||| ||||| ||||| |||||  
 Db 7 CGAGCAGCGCGCAGAGGAGC 26

RESULT 4  
 AAN80520  
 ID AAN80520 standard; DNA; 48 BP.

AC AAN80520;  
 XX  
 DT 03-OCT-2002 (updated)  
 DT 11-DEC-1990 (first entry)

DE Synthetic oligonucleotide used in prodn. of hybrid gene.

KW Synthetic oligonucleotide; hybrid gene; RESA 3'repeat;  
 KM Plasmodium falciparum; malaria; vaccine.

OS Synthetic.

XX Key Location/Qualifiers  
 FT CDS 1..24  
 FT /\*tag= a  
 FT /note="claimed peptide"

PN W08802757-A.

PD 21-APR-1988.

PF 16-OCT-1987; 87WO-A000352.

PR 17-OCT-1986; 86AU-0008551.

PA (SARA-) SARAMANE PTY. LTD.

PI Langford CJ, Edwards SJ;

DR WPI: 1988-119462/17.

DR P-PSDB: AAP80519.

XX New hybrid protein or polypeptide - contg. epitope(s) or mlmotope(s) of

PT Disclosure; : pp: English.

XX several antigens esp. useful as antimalarial antigens.

CC The oligonucleotide encodes an epitope of a P.falciparum antigen.

CC (Updated on 03-OCT-2002 to add missing OS field.)

XX Sequence 48 BP; 14 A; 12 C; 20 G; 2 T; 0 other;

Query Match 74.0%; Score 14.8; DB 9; Length 48;  
 Best Local Similarity 88.9%; Pred. No. 2.6e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAGCAGCGCGCAGAGGAG 19  
 ||||| ||||| ||||| ||||| |||||  
 Db 13 GAGCAGCGCGCAGAGGAG 30

RESULT 5  
 AAV40985

ID AAV40985 standard; DNA; 21 BP.

XX  
 AC AAV40985;

DT 25-SEP-1998 (first entry)

DE Primer TELAML1:1216L21 for abnormality detection.

KW PCR primer; chromosomal abnormality; abnormality detection; leukaemia;  
 KW lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma;  
 KW medullablastoma; malignant melanoma; malignant neoplastic condition; ss.

OS Synthetic.  
 OS Homo sapiens.

FN W09824928-A2.

PD 11-JUN-1998.

PF 08-DEC-1997; 97WO-DK0556.

PR 06-DEC-1996; 96DK-0001401.

PA (PALL/) PALLISGAARD N.

PI Hokland P, Pallisgaard N;

DR WPI: 1998-333344/29.

PT Detection of chromosomal abnormalities - by subjecting patient  
 PT sample nucleic acids to a multiplex molecular amplification  
 PT procedure using primers specific for characteristic nucleic acid  
 PT sequence

PS Claim 73; Page 85; 126pp; English.

XX This sequence represents a primer used in the method of the invention for  
 CC the detection of the presence or absence of chromosomal abnormalities,  
 CC each abnormality being associated with a condition in a subject and each  
 CC being defined by at least one characteristic nucleic acid sequence. The  
 CC method comprises: (a) obtaining a sample of nucleic acids derived from a  
 CC subject which may harbour one of the chromosomal abnormalities;  
 CC (b) subjecting the sample to a multiplex molecular amplification (MMA)  
 CC procedure, where a number of the characteristic sequences, if present in  
 CC a sufficient amount, will be amplified; (c) retrieving the product(s)  
 CC from step (b), and detecting the presence and/or absence of an amplicon  
 CC characteristic of the abnormal sequences to detect the presence or  
 CC absence of corresponding chromosomal abnormalities; where the MMA  
 CC procedure comprises the use of at least 7 mutually distinct primers (MDP)  
 CC in one single reaction mixture, each of the primers defining an end of at  
 CC least one characteristic nucleic acid sequence, and where at least one of  
 CC the primers defines the first end of at least two characteristic nucleic  
 CC acid sequences, the characteristic nucleic acid sequences each being  
 CC determined in their opposite ends by MDP selected from the remainder of  
 CC the MDP. The methods can be used for detecting chromosomal abnormalities  
 CC associated with diseases including numerous leukaemia's, lymphoma's,  
 CC carcinoma's, adenocarcinoma's, sarcoma's, glioma's, neuroblastoma's,  
 CC medullablastoma, malignant melanoma, and malignant neoplastic conditions.  
 XX

SQ Sequence 21 BP; 7 A; 3 C; 9 G; 2 T; 0 other;

Query Match 72.0%; Score 14.4; DB 19; Length 21;  
 Best Local Similarity 93.8%; Pred. No. 4e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 AGCAGCGCGCAGAGGA 18  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 AGCAGCGCGCAGAGGA 16

RESULT 6  
 ABR88264/C  
 ID ABR88264 standard; DNA; 21 BP.

```
XX ABK88264;
AC
XX
DT 07-OCT-2002 (first entry)
DE Exon 2 (alpha1 domain) of chicken class I gene PCR primer RV69BL.
XX
XX Chicken; exon 2; alpha1 domain; class I gene; Rf-Y; B-F; B-L; B-G;
KW major histocompatibility complex; MHC; domesticated fowl;
KM Marek's disease; genetic disease resistance; PCR; primer; ss.
XX
OS Gallus sp.
PN US2002083482-A1.
XX
XX 27-JUN-2002.
XX
XX 22-JUN-2001; 2001US-0886607.
XX
XX 19-JUL-2000; 2000US-0619758.
XX
XX (MILL/) MILLER M M.
PA (BRIL/) BRILES W E.
PA (AFAN/) AFANASSIEFF M.
XX
XX MILLER MM, Briles WE, Afanassieff M;
PI
XX
XX WPI; 2002-557335/59.
XX
XX Determining the major histocompatibility complex genotypes of a
PT domesticated fowl useful for selecting fowl, particularly chickens,
PT genetically resistant to a variety of diseases, particularly Marek's
PT disease -
XX
XX
XX Claim 14; Page 7; 22pp; English.
XX
XX The present invention relates to a new method for determining the major
CC histocompatibility complex (MHC) genotypes of a domesticated fowl. The
CC method of the invention involves amplifying and denaturing nucleic acid
CC from the fowl which contains a region with a sequence corresponding to an
CC Rf-Y, B-F, B-L or B-G region of the genome and separating the denatured
CC products electrophoretically to produce a pattern characteristic to the
CC genotypes of the fowl. The method is useful for determining the MHC
CC genotypes of domestic fowl. The method may be used to select for domestic
CC fowl, particularly chickens, genetically resistant to a variety of
CC diseases, particularly Marek's disease. The methods of the invention are
CC useful for producing offspring that carry genetic resistance to disease.
CC The present nucleic acid sequence represents an exon 2 (alpha1 domain) of
CC chicken class I gene PCR primer that was used in the methods of the
CC invention for MHC genotyping.
XX
XX
SQ Sequence 21 BP; 4 A; 7 C; 6 G; 4 T; 0 other;
Query Match 72.0%; Score 14.4; DB 24; Length 21;
Best Local Similarity 93.8%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 5 CACGGCGCAGAGGAGC 20
DB 16 CACGGTGCAGAGGAGC 1
RESULT 7
AAD29196/c
ID AAD29196 standard; DNA; 21 BP.
XX
XX AAD29196;
XX
XX 07-MAY-2002 (first entry)
DT
XX Fowl MHC B class II-beta genotype analysing PCR primer, RV69BL.
XX Fowl; haplotyping; breeding; domesticated fowl; disease resistance;
```

```
KW major histocompatibility; MHC; Marek's disease; PCR primer; ss.
XX
XX Gallus sp.
OS
XX WO200206535-A2.
XX
XX 24-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US22519.
XX
XX 19-JUL-2000; 2000US-0619758.
XX
XX (CITY ) CITY OF HOPE.
XX
XX MILLER MM, Afanassieff M, Briles WE;
PI
XX
XX WPI; 2002-171822/22.
XX
XX Determining major histocompatibility complex genotypes of domesticated
PT fowl for breeding disease resistant fowl by comparing B and Rf-Y
PT systems of genome from the fowl to corresponding known genotypes -
XX
XX Claim 14; Page 16; 37pp; English.
XX
XX The invention relates to a method for haplotyping and breeding
CC domesticated fowl for increased disease resistance. Disease
CC resistance in domesticated fowl has been associated with the B and
CC Rf-Y systems of major histocompatibility (MHC) genes. The method
CC is useful for determining the Mhc genotypes of a domesticated fowl.
CC The method is useful in selecting domesticated fowl which are
CC resistant to a preselected disease preferably Marek's disease by
CC determining a genotype of Rf-Y, B-F, B-L or B-G genes of the
CC domesticated fowl, correlating the determined genotypes with
CC resistance to the preselected disease and selecting a domesticated
CC fowl having a determined genotype which correlates with resistance
CC to the preselected disease. The method is also useful for breeding
CC domesticated fowl to produce an offspring resistant to a preselected
CC disease by selecting a first domesticated fowl of a gender which is
CC resistant to a preselected disease, and mating the first domesticated
CC fowl with a second domesticated fowl of the opposite gender to produce
CC offspring. The present sequence is a PCR primer used for genotyping
CC fowl Mhc region.
XX
XX
SQ Sequence 21 BP; 4 A; 7 C; 6 G; 4 T; 0 other;
Query Match 72.0%; Score 14.4; DB 24; Length 21;
Best Local Similarity 93.8%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 5 CACGGCGCAGAGGAGC 20
DB 16 CACGGTGCAGAGGAGC 1
RESULT 8
AAI73383
ID AAI73383 standard; DNA; 50 BP.
XX
XX AAI73383;
XX
XX 09-NOV-2001 (first entry)
DT
XX Human silent SNP containing nucleic acid SEQ:324.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX WO200140521-A2.
XX
XX 07-JUN-2001.
```

XX 30-NOV-2000; 2000WO-US2758.  
PF 30-NOV-1999; 99US-0168138.  
PR 29-NOV-2000; 2000US-0726173.  
XX (CURA-) CURAGEN CORP.  
XX Shimkets RA, Leach M;  
PI WPI: 2001-356160/37.  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy -  
PS Claim 1; Page 153; 2653pp; English.  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA153114 to AA153329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides.  
CC For example, (I) may be used to treat disorders by rectifying mutations  
CC or deletions in a patient's genome that affect the activity of  
CC polypeptides by expressing inactive proteins or to supplement the  
CC patient's own production of polypeptide. Additionally, (I) and its  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays to detect and quantitate the presence of similar nucleic acids  
CC in samples, and therefore which patients may be in need of restorative  
CC therapy. The polypeptides encoded by (I) may be used as antigens in the  
CC production of antibodies specific for polymorphic polypeptides. The  
CC antibodies may also be used to down regulate expression and activity.  
CC The antibodies may also be used as diagnostic agents for detecting the  
CC presence of polymorphic polypeptides in samples.  
XX  
SO Sequence 50 BP; 5 A; 14 C; 28 G; 3 T; 0 other;  
Query Match 71.0%; Score 14.2; DB 22; Length 50;  
Best Local Similarity 84.2%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 CGAGCAGCGCGCAGAGGAG 19  
DB 30 CGAGCAGCGCGCGAGCAG 48  
RESULT 9  
AA177070  
ID AA177070 standard; cDNA; 51 BP.  
XX  
AC AA177070;  
XX  
DT 16-NOV-2000 (first entry)  
XX  
DE Human clone cg43921619 polymorphic site. SEQ ID NO:753.  
XX  
KW Human; single nucleotide polymorphism; SNP; chromosome 17;  
KW detection; identification; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT variation /tag\_a  
XX  
PN WO200029623-A2.  
XX  
PD 25-MAY-2000.  
XX  
PF 17-NOV-1999; 99WO-US27293.  
XX

PR 17-NOV-1998; 98US-0109024.  
PR 16-NOV-1999; 99US-0109024.  
XX (CURA-) CURAGEN CORP.  
XX Shimkets RA, Leach MD;  
PI WPI: 2000-387826/33.  
XX  
XX Human nucleic acids containing single nucleotide polymorphisms, useful  
PT for treating a subject suffering, or at risk from a pathology due to  
PT the presence of a sequence polymorphism -  
PS Claim 1; Page 385; 543pp; English.  
XX  
XX Sequences AA17504-A17509 represent 1192 human nucleic acid sequences  
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to  
CC 1112 (AA176318-A177429) are consecutive pairs of nucleotides which  
CC contain silent SNPs. Sequences 1113 to 1192 (AA177430-A177509) are  
CC consecutive pairs of nucleotides containing SNPs which result in changes  
CC in the corresponding amino acid sequences (A177449-B1028). The SNPs in  
CC sequences 1113 to 1128 (AA177430-A177445) lead to conservative amino acid  
CC changes, while those in sequences 1129 to 1186 (AA177446-A177503) result  
CC in non-conservative changes. The SNPs in sequences 1187 to 1192  
CC (AA177504-A17509) generate frameshift mutations. The invention also  
CC relates to a method of detecting a polymorphic site in a nucleic acid and  
CC a method of determining the relatedness of two nucleic acids. It also  
CC encompasses peptides containing polymorphic sites, antibodies raised  
CC against such peptides, and a method of detecting polymorphic  
CC proteins/peptides using the antibodies. The nucleic acids are useful for  
CC gene therapy of an individual having, suspected of having, or at risk of  
CC developing a pathological condition due to the presence of a sequence  
CC polymorphism. Such treatment would comprise administration of the  
CC wild-type nucleic acid sequence. Antibodies raised against polymorphic  
CC peptides can also be used in the treatment of such individuals.  
XX  
SO Sequence 51 BP; 15 A; 4 C; 24 G; 8 T; 0 other;  
Query Match 71.0%; Score 14.2; DB 21; Length 51;  
Best Local Similarity 84.2%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2 GAGCAGCGCGCAGAGGAGC 20  
DB 26 GAGCAGGGAGAGAGAGC 44  
RESULT 10  
AA173382  
ID AA173382 standard; DNA; 51 BP.  
XX  
AC AA173382;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:323.  
XX  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200140521-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 30-NOV-2000; 2000WO-US2758.  
XX  
PR 30-NOV-1999; 99US-0168138.  
PR 29-NOV-2000; 2000US-0726173.  
XX  
PA (CURA-) CURAGEN CORP.

XX	Shimkets RA, Leach M;
XX	
DR	WPI: 2001-356160/37.
XX	
PT	polymorphic nucleic acid sequences, useful in genetic testing and
XX	therapy -
PS	Claim 1; Page 153; 2653bp; English.
XX	
CC	AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC	sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC	AA53114 to AA53329 represent peptides related to human polymorphic
CC	polynucleotide sequences. The sequences can be used in gene and protein
CC	therapy, and in vaccine production. (I) and the polypeptides encoded by
CC	them may be used in the prevention, diagnosis and treatment of diseases
CC	associated with inappropriate expression of polymorphic polypeptides.
CC	For example, (I) may be used to treat disorders by rectifying mutations
CC	or deletions in a patient's genome that affect the activity of
CC	polypeptides by expressing inactive proteins or to supplement the
CC	patients own production of polypeptide. Additionally, (I) and its
CC	complementary sequences may also be used as DNA probes in diagnostic
CC	assays to detect and quantitate the presence of similar nucleic acids
CC	in samples, and therefore which patients may be in need of restorative
CC	therapy. The polypeptides encoded by (I) may be used as antigens in the
CC	production of antibodies specific for polymorphic polypeptides. The
CC	antibodies may also be used to down regulate expression and activity.
CC	The antibodies may also be used as diagnostic agents for detecting the
CC	presence of polymorphic polypeptides in samples.
XX	
SQ	Sequence 51 BP; 5 A; 14 C; 29 G; 3 T; 0 other;
XX	
Query Match	71.0%; Score 14.2; DB 22; Length 51;
Best Local Similarity	84.2%; Pred. No. 4.7e+03;
Matches 16; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
OY	1 CGAGCAGCGCGCAGAGAG 19
Db	31 CGAGCAGCGCGCGAGCAG 49
XX	
RESULT 11	
AA57918/C	
ID	AA57918 standard; DNA: 37 BP.
XX	
AC	AA57918;
XX	
DT	11-APR-2000 (first entry)
XX	
DE	Escherichia coli trpC gene 3' flanking region PCR primer N19.
XX	
KW	trpC gene; N-(5'-phosphoribosyl)-anthranilate isomerase;
KM	expression system; selectable marker; auxotroph complementation;
KW	PCR primer; ss.
XX	
OS	Escherichia coli.
XX	
PN	EP972838-A1.
XX	
PD	19-JAN-2000.
XX	
PF	08-JUL-1999; 99EP-0113182.
XX	
PR	15-JUL-1998; 98EP-0113156.
PR	09-OCT-1998; 98EP-0119078.
XX	
PA	(HOFF ) ROCHE DIAGNOSTICS GMBH.
XX	
PI	Kopetzki E, Schantz C;
XX	
DR	WPI: 2000-108129/10.
XX	
PT	Novel prokaryotic expression system, used to produce recombinant

PT proteins

XX Example 6; Page 13; 31pp; English.

XX

CC The present sequence is that of primer N19, which was used as

CC antisense primer in the PCR amplification of the 3' flanking region

CC of the *Escherichia coli* trpC gene (trpB) using chromosomal DNA as

CC template. The primer introduces a 3' SphI cleavage site into the

CC amplified product. The PCR product was used in the construction of

CC deletion plasmid pMAK705-trpD/B. A trpC auxotrophy marker was

CC introduced into a laboratory *E. coli* strain by directed deletion

CC via homologous recombination in order to create a non-revertible

CC trpC host characterised by an inactive N-(5'-phosphoribosyl)-

CC anthranilate isomerase. This host strain can be used in a novel

CC host/vector system of the invention. The invention provides a

CC stable prokaryotic (preferably *Escherichia coli*) host/vector system

CC (expression system) which avoids plasmid selection by antibiotics.

CC The selection principle is based on complementation of a stable

CC auxotrophy (e.g. trpC, pyrF) of the host cells by a yeast gene (e.g.

CC TRP1, URA3). A minimal prokaryotic expression vector that cannot be

CC homologously recombined with the genome of prokaryotic organisms

CC includes an origin of replication, an auxotrophy marker gene, a

CC promoter that is functionally active in prokaryotes; and a foreign

CC gene to be expressed under the control of the promoter. The new

CC expression system is used for the production of recombinant proteins.

XX

SQ Sequence 37 BP; 8 A; 11 C; 11 G; 7 T; 0 other;

Query Match 69.0%; Score 13.8; DB 21; Length 37;

Best Local Similarity 88.2%; Pred. No. 7e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

OY 1 CGAGCAGCGCGCAGAGG 17  
|||||  
Db 28 CGAGCAGCGCGCAGCGG 12

RESULT 12

ABN56998

ID ABN56998 standard; DNA; 65 BP.

XX

AC ABN56998;

XX

DT 15-JUL-2002 (first entry)

XX

DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:29746.

XX

HW Human; mouse; rat; splice transcript; detection; RNA transcript;

XX

KW splice variant; transcriptome; oligonucleotide library; ss.

XX

OS Mus musculus.

XX

PN WO200210449-A2.

XX

PD 07-FEB-2002.

XX

PF 20-JUL-2001; 2001WO-IB01903.

XX

PR 28-JUL-2000; 2000US-221607P.

XX

PR 02-MAY-2001; 2001US-287724P.

XX

PA (COMP-) COMPUGEN INC.

XX

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX

DR WPI: 2002-257383/30.

XX

PT New oligonucleotide libraries comprising oligonucleotides which

PT selectively hybridize to mRNAs transcribed from a transcription unit of

PT a genome, useful for detecting tissue-, pathology-, and

PT developmental-specific genes

XX

SS Example 1; SEQ ID 29746; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the  
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises  
CC several oligonucleotides, each capable of hybridizing selectively to a  
CC set of messenger RNAs transcribed from a given transcription unit of  
CC the genome, which encodes one or more messenger RNA splice variants.  
CC The oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterizing the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a  
CC particular biological or pathological state, and so allowing the  
CC detection of tissue- and pathology-specific genes such as those genes  
CC only expressed in specific tissue under a specific pathological  
CC condition; to detect developmental specific genes; and to detect RNA  
CC transcripts and splice variants of a transcriptome of a patient suffering  
CC from a particular disorder. ABN27253 to ABN59589 represent  
CC oligonucleotide sequences from rats, humans and mice, which are used in  
CC the exemplification of the present invention.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).  
XX  
SQ Sequence 65 BP; 17 A; 17 C; 24 G; 7 T; 0 other;  
Query Match 69.0%; Score 13.8; DB 24; Length 65;  
Best Local Similarity 88.2%; Pred. No. 6.9e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GAGCAGCGCGCAGAGCA 18  
| | | | | | | | | | | | | | | | | |  
Db 37 GAGCATGCGCGCAGGGA 53  
RESULT 13  
AAAX24557  
ID AAAX24557 standard; DNA; 23 BP.  
XX  
AC AAAX24557;  
XX  
DT 21-JUN-1999 (first entry)  
XX  
DE Human SR-BI gene exon 1 PCR primer.  
XX  
KW SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;  
KW restenosis; congestive heart failure; atherosclerosis; cholesterol;  
KW low density lipoprotein; LDL; high density lipoprotein; HDL;  
KW diagnosis; body mass index; obesity; cachexia; gallstone; PCR;  
KW primer; ss.  
XX  
KM  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9902735-A2.  
XX  
PD 21-JAN-1999.  
XX  
PE 10-JUL-1998; 98WO-US14354.  
XX  
PR 27-FEB-1998; 98US-0031626.  
PR 10-JUL-1997; 97US-0890979.  
XX  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
PA (UYTU-) UNIV TUFTS.  
XX  
PI Acton SL, Ordovas JM;  
XX  
DR WPI; 1999-120935/10.  
XX  
PT Detecting genetic predisposition for body mass disorders - by

PT identifying allelic variants of a polymorphic region of the SR-BI  
PT gene  
XX  
PS Example 5; Page 72; 102pp; English.  
XX  
XX A PCR primer pair (see also AAAX24556) is designed for the  
CC amplification of exon 1 (see AAAX24498) of the human SR-BI gene.  
CC A G/A polymorphism has been detected at nucleotide 146 of this  
CC exon. PCR amplification followed by AluI digestion yields  
CC a 263 bp product in GG individuals, 263, 192 and 71 bp products  
CC in GA individuals, and 192 and 71 bp products in AA individuals.  
CC The invention is based on the discovery of the genomic structure of  
CC the human SR-BI gene (see AAAX24498-509) and on the identification of  
CC polymorphic regions within the gene which are associated with  
CC abnormal body mass index (BMI) and abnormal lipoprotein levels and  
CC hence with disorders such as obesity, cachexia, cardiovascular  
CC disorders and gallstone formation. The invention provides methods  
CC for determining whether a subject has, or is at risk of developing,  
CC a disease associated with a specific allele of a polymorphic region  
CC of an SR-BI gene. Kits comprising the relevant probe or primer are  
CC claimed.  
XX  
SQ Sequence 23 BP; 6 A; 10 C; 6 G; 1 T; 0 other;  
Query Match 68.0%; Score 13.6; DB 20; Length 23;  
Best Local Similarity 80.0%; Pred. No. 8.6e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CGAGCAGCGCGCAGAGC 20  
| | | | | | | | | | | | | | | | | |  
Db 4 CCAGCAGCAGCGCACAGTGC 23  
RESULT 14  
AAAX24649  
ID AAAX24649 standard; DNA; 23 BP.  
XX  
AC AAAX24649;  
XX  
DT 21-JUN-1999 (first entry)  
XX  
DE Human SR-BI gene exon 1 PCR primer.  
XX  
KW SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;  
KW restenosis; congestive heart failure; atherosclerosis; cholesterol;  
KW low density lipoprotein; LDL; high density lipoprotein; HDL;  
KW diagnosis; body mass index; obesity; cachexia; gallstone; PCR;  
KW primer; ss.  
XX  
KM  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9902736-A2.  
XX  
PD 21-JAN-1999.  
XX  
PE 10-JUL-1998; 98WO-US14359.  
XX  
PR 27-FEB-1998; 98US-0032894.  
PR 10-JUL-1997; 97US-0890980.  
XX  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
PA Acton SL;  
XX  
DR WPI; 1999-120936/10.  
XX  
PT New nucleic acids comprising intronic sequence of a human scavenger  
PT receptor-BI (SR-BI) gene - useful for prognosis, diagnosis and  
PT treatment of SR-BI associated diseases or conditions  
XX  
PS Claim 10; Page 71; 103pp; English.  
XX



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## OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:53:51 : Search time 21.55 Seconds

(Without alignments)  
284.619 Million cell updates/sec

Title: US-09-296-264-2

Sequence: 1 cgcacagcgcgcagcagcagc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

- 1: /cgn2\_6/ptodata/1/lna/5A.COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/lna/5B.COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/lna/6A.COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/lna/6B.COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/lna/PTUS.COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/lna/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	13.8	69.0	37 4 US-09-344-888A-19	Sequence 19, Appl
2	13.6	68.0	23 3 US-09-032-894-90	Sequence 90, Appl
3	13.6	68.0	23 4 US-09-031-626-90	Sequence 90, Appl
4	13.6	68.0	27 1 US-08-170-095B-36	Sequence 36, Appl
5	13.6	68.0	27 6 5428007-6	Patent No. 5428007
6	13.6	68.0	45 1 US-08-785-448-6	Sequence 6, Appl
7	13.6	68.0	45 2 US-08-925-927-6	Sequence 6, Appl
8	13.6	68.0	45 2 US-08-875-154-8	Sequence 6, Appl
9	13.6	68.0	45 3 US-09-120-576-6	Sequence 6, Appl
10	13.6	68.0	60 1 US-08-009-265-17	Sequence 17, Appl
11	13.6	68.0	75 1 US-08-009-265-42	Sequence 42, Appl
12	13.6	68.0	75 2 US-08-322-679-10	Sequence 10, Appl
13	13.6	68.0	75 4 US-08-686-993A-22	Sequence 22, Appl
14	13.6	68.0	78 6 5457037-7	Patent No. 5457037
15	13.2	66.0	43 4 US-09-380-190A-46	Sequence 46, Appl
16	13.2	66.0	44 4 US-09-380-120C-13	Sequence 13, Appl
17	13.2	66.0	92 1 US-08-487-141B-109	Sequence 109, App
18	13.2	65.0	27 4 US-09-529-279-7	Sequence 7, Appl
19	13.2	65.0	37 1 US-08-253-785-12	Sequence 12, Appl
20	13.2	65.0	45 1 US-08-253-785-13	Sequence 13, Appl
21	12.8	64.0	20 4 US-09-435-296-13	Sequence 13, Appl
22	12.8	64.0	75 2 US-09-073-032-4	Sequence 4, Appl
23	12.6	63.0	30 3 US-08-929-856-63	Sequence 63, Appl
24	12.6	63.0	33 4 US-09-349-627-3	Sequence 3, Appl
25	12.6	63.0	36 3 US-08-767-942A-30	Sequence 30, Appl
26	12.6	63.0	52 1 US-08-685-793-13	Sequence 13, Appl
27	12.6	63.0	52 1 US-08-685-793-20	Sequence 20, Appl

28	12.6	63.0	53 1 US-08-434-743-3	Sequence 3, Appl
29	12.6	63.0	53 1 US-08-685-793-5	Sequence 5, Appl
30	12.6	63.0	56 1 US-08-685-793-9	Sequence 9, Appl
31	12.6	63.0	60 1 US-08-349-696-4	Sequence 4, Appl
32	12.6	63.0	60 1 US-08-233-009-4	Sequence 4, Appl
33	12.6	63.0	60 1 US-08-560-231-4	Sequence 4, Appl
34	12.6	63.0	60 4 US-09-080-704A-4	Sequence 4, Appl
35	12.6	63.0	61 3 US-09-023-228B-110	Sequence 110, App
36	12.6	63.0	61 4 US-09-163-025B-110	Sequence 110, App
37	12.6	63.0	99 1 US-08-472-255A-50	Sequence 50, Appl
38	12.6	63.0	99 1 US-08-479-724A-50	Sequence 50, Appl
39	12.6	63.0	99 3 US-08-472-256B-50	Sequence 50, Appl
40	12.6	63.0	99 4 US-08-952-793-50	Sequence 50, Appl
41	12.6	63.0	99 5 PCT-US96-09455A-50	Sequence 50, Appl
42	12.4	62.0	20 1 US-08-468-447-12	Sequence 12, Appl
43	12.4	62.0	20 1 US-08-469-851A-12	Sequence 12, Appl
44	12.4	62.0	20 1 US-08-467-597A-12	Sequence 12, Appl
45	12.4	62.0	20 1 US-08-468-569A-12	Sequence 12, Appl

## ALIGNMENTS

RESULT 1  
US-09-344-888A-19/C  
Sequence 19, Application US/09344888A  
Patent No. 6291245  
GENERAL INFORMATION:  
APPLICANT: Kopetzki, Erhard  
TITLE OF INVENTION: New Host-Vector System  
FILE REFERENCE: CD20315  
CURRENT APPLICATION NUMBER: US/09/344,888A  
CURRENT FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: 1998113156.8  
PRIOR FILING DATE: 1998-07-16  
PRIOR APPLICATION NUMBER: 1998119078.8  
PRIOR FILING DATE: 1998-10-09  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 19  
LENGTH: 37  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-344-888A-19

Query Match 69.0%; Score 13.8; DB 4; Length 37;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGACACGCGCAGAGG 17  
Db 28 CGACACGCGCAGAGG 12  
|||||

RESULT 2  
US-09-032-894-90  
Sequence 90, Application US/09032894  
Patent No. 6130041  
GENERAL INFORMATION:  
APPLICANT: Action, Susan L.  
TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR  
FILE REFERENCE: MTA-005.03  
CURRENT APPLICATION NUMBER: US/09/032,894  
CURRENT FILING DATE: 1998-02-27  
EARLIER APPLICATION NUMBER: 08/890,980  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 90  
LENGTH: 23

TYPE: DNA  
ORGANISM: Human  
US-09-032-894-90

Query Match 68.0%; Score 13.6; DB 3; Length 23;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGGAGC 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4 CCAGCAGCGCGCAGAGTACG 23

RESULT 3  
US-09-031-626-90  
Sequence 90, Application US/09031626  
Patent No. 6228581  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan L.  
APPLICANT: Ordovas, Jose M.  
TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND  
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS  
FILE REFERENCE: MIA-005.04  
CURRENT APPLICATION NUMBER: US/09/031.626  
CURRENT FILING DATE: 1998-02-27  
EARLIER APPLICATION NUMBER: 08/890.979  
EARLIER FILING DATE: 1997-07-10  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 90  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Human  
US-09-031-626-90

Query Match 68.0%; Score 13.6; DB 4; Length 23;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGGAGC 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4 CCAGCAGCGCGCAGAGTACG 23

RESULT 4  
US-08-170-095B-36  
Sequence 36, Application US/08170095B  
Patent No. 5563254  
GENERAL INFORMATION:  
APPLICANT: Hoffman, Stephen J.  
APPLICANT: Nagai, Kiyoshi  
TITLE OF INVENTION: Blood Substitutes  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Somatogen, Inc.  
STREET: 2545 Central Avenue  
CITY: Boulder  
STATE: Colorado  
ZIP: 80301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: System 7.0.1  
SOFTWARE: Microsoft Word 5.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/170.095B  
FILING DATE: December 20, 1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5563254ak, Henry P.  
REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: Hoffman 2A/CONT2  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 303-541-3322  
TELEFAX: 303-444-3013  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown to applicant  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: beta globin sequence fragment  
HYPOTHETICAL: no  
US-08-170-095B-36

Query Match 68.0%; Score 13.6; DB 1; Length 27;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGGAGC 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 6 CCAGCAGCGTCCCGCAGGAGC 25

RESULT 5  
5428007-6  
Patent No. 5428007  
APPLICANT: FISCHER, JAMES J.; BASERGA, SUSAN J.  
TITLE OF INVENTION: GENETICALLY ENGINEERED LOW OXYGEN  
AFFINITY MUTANTS OF HUMAN HEMOGLOBIN  
NUMBER OF SEQUENCES: 7  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/235.118  
FILING DATE: 28-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 959,286  
FILING DATE: 09-OCT-1992  
APPLICATION NUMBER: 417,949  
FILING DATE: 06-OCT-1989  
SEQ ID NO: 6  
LENGTH: 27  
5428007-6

Query Match 68.0%; Score 13.6; DB 6; Length 27;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGGAGC 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 6 CCAGCAGCGTCCCGCAGGAGC 25

RESULT 6  
US-08-785-448-6  
Sequence 6, Application US/08785448  
Patent No. 5763187  
GENERAL INFORMATION:  
APPLICANT: Sioma, Alan P.  
APPLICANT: Widner, William R.  
TITLE OF INVENTION: Bacterial Donor Cell Useful  
TITLE OF INVENTION: In Conjugation  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5763187o No. 5763187disk of No. 5763187th America  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/08/785,448  
FILING DATE: 17-JAN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Agtis, Cheryl H  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 4666,200-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-785-448-6

Query Match 68.0%; Score 13.6; DB 1; Length 45;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCGCAGAGGAGC 20  
DB 16 CGGCGCCGCGGTAGAGGATC 35

RESULT 7  
US-08-925-927-6  
Sequence 6, Application US/08925927  
Patent No. 5843720  
GENERAL INFORMATION:  
APPLICANT: Tangney, Martin  
APPLICANT: Hansen, Christian  
APPLICANT: Pedersen, Poul Erik  
APPLICANT: Jorgensen, Per Lina  
APPLICANT: Jorgensen, Steen Troels  
TITLE OF INVENTION: Introduction of DNA Into Bacillus  
TITLE OF INVENTION: By Conjugation  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 58437200 No. 5843720disk of No. 5843720th America  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/925,927  
FILING DATE: 08-SEP-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Lambiris, Elias J  
REGISTRATION NUMBER: 33,728  
REFERENCE/DOCKET NUMBER: 4125,204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-925-927-6

Query Match 68.0%; Score 13.6; DB 2; Length 45;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCGCAGAGGAGC 20  
DB 16 CGGCGCCGCGGTAGAGGATC 35

RESULT 8  
US-08-875-154-8  
Sequence 8, Application US/08875154  
Patent No. 5882888  
GENERAL INFORMATION:  
APPLICANT: Jorgensen, Steen Troels  
TITLE OF INVENTION: DNA Integration By Transporation  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 58828880 No. 5882888disk of No. 5882888th America, Inc.  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,154  
FILING DATE: 17-JUL-1997

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lambiris, Elias J  
REGISTRATION NUMBER: 33,728  
REFERENCE/DOCKET NUMBER: 4381,204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "LMN2043"  
US-08-875-154-8

Query Match 68.0%; Score 13.6; DB 2; Length 45;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCGCAGAGGAGC 20  
DB 16 CGGCGCCGCGGTAGAGGATC 35

RESULT 9  
US-09-120-576-6  
Sequence 6, Application US/09120576  
Patent No. 6066473  
GENERAL INFORMATION:  
APPLICANT: Tangney, Martin  
APPLICANT: Hansen, Christian  
APPLICANT: Pedersen, Poul Erik  
APPLICANT: Jorgensen, Steen Troels  
TITLE OF INVENTION: Introduction Of DNA Into Bacillus  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 60664730 No. 6066473disk of No. 6066473th America  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/120.576  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/925.927  
FILING DATE: 08-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lambiris, Elias J  
REGISTRATION NUMBER: 33.728  
REFERENCE/DOCKET NUMBER: 4125.204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-120-576-6

Query Match 68.0%; Score 13.6; DB 3; Length 45;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGAGC 20  
||| ||||| ||||| |  
DB 16 CGGCGCGCGCGTGAAGAGATC 35

RESULT 10  
US-08-009-265-17/c  
Sequence 17, Application US/08009265  
Patent No. 5547871  
GENERAL INFORMATION:  
APPLICANT: Black Dr., Bruce C.  
TITLE OF INVENTION: Heterologous Signal Sequences For  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: 1937 West Main Street, P.O. Box 60  
CITY: Stamford  
STATE: CT  
COUNTRY: USA  
ZIP: 06904-0060  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/009.265  
FILING DATE: 19930125  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gordon Mr., Alan M.  
REGISTRATION NUMBER: 30637  
REFERENCE/DOCKET NUMBER: 31868-00

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 203-321-2971  
TELEFAX: 203-321-2971  
TELEX: 710-474-4059  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 60 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Drosophila melanogaster  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 13..60  
US-08-009-265-17

Query Match 68.0%; Score 13.6; DB 1; Length 60;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGAGC 20  
||| ||||| ||||| |  
DB 46 CGAGCAGCGCGCAGATCATC 27

RESULT 11  
US-08-009-265-42/c  
Sequence 42, Application US/08009265  
Patent No. 5547871  
GENERAL INFORMATION:  
APPLICANT: Black Dr., Bruce C.  
TITLE OF INVENTION: Heterologous Signal Sequences For  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: 1937 West Main Street, P.O. Box 60  
CITY: Stamford  
STATE: CT  
COUNTRY: USA  
ZIP: 06904-0060  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/009.265  
FILING DATE: 19930125  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gordon Mr., Alan M.  
REGISTRATION NUMBER: 30637  
REFERENCE/DOCKET NUMBER: 31868-00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 203-321-2971  
TELEFAX: 203-321-2971  
TELEX: 710-474-4059  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 75 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:

ORGANISM: Drosophila melanogaster  
US-08-009-265-42

Query Match 68.0%; Score 13.6; DB 1; Length 75;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCGCAGAGAGC 20  
|||||  
DB 46 CGAGCAGCGCGCAGATCATC 27

RESULT 12  
US-08-322-679-10/C  
Sequence 10, Application US/08322679  
Patent No. 5965123

GENERAL INFORMATION:

APPLICANT: Ahmed, Fakhruddin  
TITLE OF INVENTION: Coated Pesticidal Agents, Processes For  
TITLE OF INVENTION: Their Preparation And Compositions Containing Them  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/322,679  
FILING DATE: 13-OCT-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Hogan, John W.  
REGISTRATION NUMBER: 32,703  
REFERENCE/DOCKET NUMBER: 32,458  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3195  
TELEFAX: 201-831-3305

INFORMATION FOR SEQ. ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 75 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-322-679-10

Query Match 68.0%; Score 13.6; DB 2; Length 75;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCGCAGAGAGC 20  
|||||  
DB 46 CGAGCAGCGCGCAGATCATC 27

RESULT 13  
US-08-686-993A-22/C  
Sequence 22, Application US/08686993A  
Patent No. 6355240

GENERAL INFORMATION:  
APPLICANT: Dietz, Peter  
TITLE OF INVENTION: ENHANCED INSECTICIDAL INSECT VIRUS THROUGH THE  
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEINS WITH EARLY  
TITLE OF INVENTION: PROMOTERS

FILE REFERENCE: 0646/0D616  
CURRENT APPLICATION NUMBER: US/08/686,993A  
CURRENT FILING DATE: 1996-07-25  
NUMBER OF SEQ. ID NOS: 35  
SOFTWARE: Patentin Ver. 2.1  
SEQ. ID NO: 22  
LENGTH: 75  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: cDNA  
US-08-686-993A-22

Query Match 68.0%; Score 13.6; DB 4; Length 75;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCGCAGAGAGC 20  
|||||  
DB 46 CGAGCAGCGCGCAGATCATC 27

RESULT 14  
5457037-7/C  
Patent No. 5457037

APPLICANT: TOGNONI, ANGELO;CARRERA, PAOLO;CAMERINI, BARBARA;  
GALLI, GIULIANO;LUCCHESI, GIUSEPPE;GRANDI, GUIDO;DI GENNARO, CARLO  
TITLE OF INVENTION: CLONING OF THE GENE CODING THE ISOMYLAISE  
ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME  
NUMBER OF SEQUENCES: 7  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/1,797  
FILING DATE: 08-JAN-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 749,621  
FILING DATE: 19-AUG-1991  
APPLICATION NUMBER: 224,114  
FILING DATE: 25-JUL-1988  
SEQ. ID NO: 7  
LENGTH: 78  
5457037-7

Query Match 68.0%; Score 13.6; DB 6; Length 78;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCGCAGAGAGC 20  
|||||  
DB 49 CGAGCAGCGCGCAGCCNAGC 30

RESULT 15  
US-09-380-190A-46  
Sequence 46, Application US/09380190A  
Patent No. 6410220

GENERAL INFORMATION:  
APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.  
TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES  
THEREOF  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.  
STREET: 119 NORTH FOURTH STREET, SUITE 203  
CITY: MINNEAPOLIS  
STATE: MINNESOTA  
COUNTRY: USA  
ZIP: 55401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,190A  
FILING DATE: 26-Aug-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/03918  
FILING DATE: 28-FEB-98  
ATTORNEY/AGENT INFORMATION:  
NAME: MUELLING, ANN M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 228,00010201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-09-380-190A-46

Query Match 66.0%; Score 13.2; DB 4; Length 43;  
Best Local Similarity 83.3%; Pred. No. 2.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2 GAGCAGGCGCAGAGAG 19  
||||| |  
Db 13 GAGCAGGCGTGAAGAG 30

Search completed: November 23, 2002, 06:35:58  
Job time : 24.55 secs



```
APPLICANT: Conner, Timothy
APPLICANT: Dubois, Patricia
APPLICANT: Malven, Marianne
APPLICANT: Masucci, James
TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRESSION
FILE REFERENCE: 38-21(15856)B
CURRENT APPLICATION NUMBER: US/09/894,633A
PRIOR FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: 60/214,357
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 09/894,633
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.0
SEQ ID NO 18
LENGTH: 27
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(27)
OTHER INFORMATION: synthetic primer sequence
US-09-894-633A-18
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Query Match          76.0%; Score 15.2; DB 10; Length 27;
Best Local Similarity 85.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
OY 1 CGAGCAGCGCGCAGAGAGC 20
    ||||| ||||| ||||| |||||
DB 7 CGAGCAGCGCGCAGAGAGATC 26
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RESULT 3
US-09-886-607-14/C
Sequence 14, Application US/09886607
Patent No. US20020083482A1
GENERAL INFORMATION:
APPLICANT: Miller, Marcia
APPLICANT: Afanassieff, Marielle
APPLICANT: Briles, W. Elwood
TITLE OF INVENTION: Method for Breeding Disease Resistant Domesticated Fowl
FILE REFERENCE: 1954-376
CURRENT APPLICATION NUMBER: US/09/886,607
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 09/244,093
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: US 09/619,757
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 08/774,025
PRIOR FILING DATE: 1996-12-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 21
TYPE: DNA
ORGANISM: Gallus sp.
US-09-886-607-14
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Query Match          72.0%; Score 14.4; DB 10; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 5 CACGGCGCAGAGAGC 20
    ||||| ||||| ||||| |||||
DB 16 CACGGCGCAGAGAGC 1
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```
RESULT 4
US-10-158-895-7
Sequence 7, Application US/10158895
Patent No. US20020155624A1
GENERAL INFORMATION:
```

```
APPLICANT: ONO, KOICHIRO
APPLICANT: OHTOMO, TOSHIHIKO
APPLICANT: TSUCHIYA, MASAYUKI
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
FILE REFERENCE: 053466/0278
CURRENT APPLICATION NUMBER: US/10/158,895
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US/09/529,279
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: PCT/JP98/04796
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: JP 9/290188
PRIOR FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-158-895-7
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Query Match          65.0%; Score 13; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 7 CGGCGCAGAGAG 19
    ||||| ||||| |||||
DB 14 CGGCGCAGAGAG 26
```

```
RESULT 5
US-09-972-809-4
Sequence 4, Application US/09972809
Patent No. US20020151490A1
GENERAL INFORMATION:
APPLICANT: Sundee, Cheryl A.
TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
FILE REFERENCE: 07039/183001
CURRENT APPLICATION NUMBER: US/09/972,809
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/428,226
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/045,607
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 75
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically derived primer
US-09-972-809-4
```

```
Query Match          64.0%; Score 12.8; DB 10; Length 75;
Best Local Similarity 87.5%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 1 CGAGCAGCGCGCAGAG 16
    ||||| ||||| |||||
DB 32 CGAGCAGCGCGCAGAG 47
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```
RESULT 6
US-09-864-761-19378
Sequence 19378, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
```

APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aecomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 19378  
LENGTH: 88  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC011297.1  
OTHER INFORMATION: EXPRESSED IN B1474, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.99  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.9  
OTHER INFORMATION: EST\_HUMAN HIT: BF115285.1, EVALUATE 3.00e-16  
OTHER INFORMATION: NT\_HIT: J03061.1, EVALUATE 2.00e-16  
OTHER INFORMATION: SWISSPROT HIT: Q90663, EVALUATE 9.30e+00  
US-09-864-761-19378  
Query Match 64.0%; Score 12.8; DB 10; Length 88;  
Best Local Similarity 87.5%; Pred. No. 1.9e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 7  
US-09-866-108-4429  
Sequence 4429, Application US/09866108  
Patent No. US20020048800A1  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharron G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AECOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 60/266,860  
PRIOR FILING DATE: 2001-02-05  
NUMBER OF SEQ ID NOS: 15752  
SOFTWARE: Aecomica Sequence Listing Engine  
SEQ ID NO 4429  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108-4429  
Query Match 63.0%; Score 12.6; DB 10; Length 25;  
Best Local Similarity 78.9%; Pred. No. 2.3e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 8  
US-09-866-108-4430  
Sequence 4430, Application US/09866108  
Patent No. US20020048800A1  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharron G.  
US-09-866-108-4430  
Query Match 64.0%; Score 12.8; DB 10; Length 88;  
Best Local Similarity 87.5%; Pred. No. 1.9e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

1  APPLICANT: HANZEL, David K.
2  APPLICANT: RANK, David R.
3  APPLICANT: CHEN, Wensheng
4  APPLICANT: SHANNON, Mark
5  TITLE OF INVENTION: MOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
6  FILE REFERENCE: AECOMICA-7
7  CURRENT APPLICATION NUMBER: US/09/866,108
8  CURRENT FILING DATE: 2001-05-25
9  PRIOR APPLICATION NUMBER: US 60/207,456
10 PRIOR FILING DATE: 2000-05-26
11 PRIOR APPLICATION NUMBER: GB 24263.6
12 PRIOR FILING DATE: 2000-10-04
13 PRIOR APPLICATION NUMBER: US 60/236,359
14 PRIOR FILING DATE: 2000-09-27
15 PRIOR APPLICATION NUMBER: PCT/US01/00666
16 PRIOR FILING DATE: 2001-01-30
17 PRIOR APPLICATION NUMBER: PCT/US01/00667
18 PRIOR FILING DATE: 2001-01-30
19 PRIOR APPLICATION NUMBER: PCT/US01/00664
20 PRIOR FILING DATE: 2001-01-30
21 PRIOR APPLICATION NUMBER: PCT/US01/00669
22 PRIOR FILING DATE: 2001-01-30
23 PRIOR APPLICATION NUMBER: PCT/US01/00665
24 PRIOR FILING DATE: 2001-01-30
25 PRIOR APPLICATION NUMBER: PCT/US01/00668
26 PRIOR FILING DATE: 2001-01-30
27 PRIOR APPLICATION NUMBER: PCT/US01/00663
28 PRIOR FILING DATE: 2001-01-30
29 PRIOR APPLICATION NUMBER: PCT/US01/00662
30 PRIOR FILING DATE: 2001-01-30
31 PRIOR APPLICATION NUMBER: PCT/US01/00661
32 PRIOR FILING DATE: 2001-01-30
33 PRIOR APPLICATION NUMBER: PCT/US01/00670
34 PRIOR FILING DATE: 2001-01-30
35 PRIOR APPLICATION NUMBER: US 60/234,687
36 PRIOR FILING DATE: 2000-09-21
37 PRIOR APPLICATION NUMBER: US 60/266,860
38 PRIOR FILING DATE: 2001-02-05
39 NUMBER OF SEQ ID NOS: 15752
40 SOFTWARE: Aecomica Sequence Listing Engine
41 SEQ ID NO 4430
42 LENGTH: 25
43 TYPE: DNA
44 ORGANISM: Homo sapiens
45 US-09-866-108-4430

```

RESULT 9  
 US-09-866-108-4431  
 : Sequence 4431, Application US/09866108  
 : Patient No. US20020048800A1  
 : GENERAL INFORMATION:  
 : APPLICANT: GU, Yizhong  
 : APPLICANT: JI, Yonggang  
 : APPLICANT: PENN, Sharon G.  
 : APPLICANT: HANZEL, David K.  
 : APPLICANT: RANK, David R.  
 : APPLICANT: CHEN, Wensheng  
 : APPLICANT: SHANNON, Mark  
 : TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
 : FILE REFERENCE: AEMOICA-7  
 : CURRENT APPLICATION NUMBER: US/09/866,108  
 : CURRENT FILING DATE: 2001-05-25  
 : PRIOR APPLICATION NUMBER: US 60/207,456  
 : PRIOR FILING DATE: 2000-05-26

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1      PRIOR APPLICATION NUMBER: GB 24265.6
2      PRIOR FILING DATE: 2000-10-04
3      PRIOR APPLICATION NUMBER: US 60/236,359
4      PRIOR FILING DATE: 2000-09-27
5      PRIOR APPLICATION NUMBER: PCT/US01/00666
6      PRIOR FILING DATE: 2001-01-30
7      PRIOR APPLICATION NUMBER: PCT/US01/00667
8      PRIOR FILING DATE: 2001-01-30
9      PRIOR APPLICATION NUMBER: PCT/US01/00664
10     PRIOR FILING DATE: 2001-01-30
11     PRIOR APPLICATION NUMBER: PCT/US01/00669
12     PRIOR FILING DATE: 2001-01-30
13     PRIOR APPLICATION NUMBER: PCT/US01/00665
14     PRIOR FILING DATE: 2001-01-30
15     PRIOR APPLICATION NUMBER: PCT/US01/00668
16     PRIOR FILING DATE: 2001-01-30
17     PRIOR APPLICATION NUMBER: PCT/US01/00663
18     PRIOR FILING DATE: 2001-01-30
19     PRIOR APPLICATION NUMBER: PCT/US01/00662
20     PRIOR FILING DATE: 2001-01-30
21     PRIOR APPLICATION NUMBER: PCT/US01/00661
22     PRIOR FILING DATE: 2001-01-30
23     PRIOR APPLICATION NUMBER: PCT/US01/00670
24     PRIOR FILING DATE: 2001-01-30
25     PRIOR APPLICATION NUMBER: US 60/234,687
26     PRIOR FILING DATE: 2000-09-21
27     PRIOR APPLICATION NUMBER: US 60/266,860
28     PRIOR FILING DATE: 2001-02-05
29     NUMBER OF SEQ ID NOS: 15752
30     SOFTWARE: Acomica Sequence Listing Engine
31     SEQ ID NO 4431
32     LENGTH: 25
33     TYPE: DNA
34     ORGANISM: Homo sapiens
35     US-09-866-108-4431

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```

Query Match      63.0%;  Score 12.6;  DB 10;  Length 25;
Best Local Similarity  78.9%;  Pred. No.2.3e+03;
Matches 15;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;

OY      2  GAGCAGGGCGCAGAGGAGC 20
          ||| | ||||| |||
Db      5  GGGCAGGAAGCAGAGAGGC 23

RESULT 10
US-09-866-108-4432
; Sequence 4432, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

```



PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 60/266,860  
PRIOR FILING DATE: 2001-02-05  
NUMBER OF SEQ ID NOS: 15752  
SOFTWARE: Aeomica Sequence Listing Engine  
SEQ ID NO 4432  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108-4432

Query Match 63.0%; Score 12.6; DB 10; Length 25;  
Best Local Similarity 78.9%; Pred. No. 2.3e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GAGCAGCGCGCAGAGAGC 20  
Db 4 GGCAGAGAGCAGAGAGC 22

RESULT 11  
US-09-866-108-4433  
Sequence 4433, Application US/09866108  
Patent No. US20020048800A1  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharon G.  
APPLICANT: HANZEL, David R.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AEOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 60/266,860  
PRIOR FILING DATE: 2001-02-05  
NUMBER OF SEQ ID NOS: 15752  
SOFTWARE: Aeomica Sequence Listing Engine  
SEQ ID NO 4433  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108-4433

Query Match 63.0%; Score 12.6; DB 10; Length 25;  
Best Local Similarity 78.9%; Pred. No. 2.3e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GAGCAGCGCGCAGAGAGC 20  
Db 3 GGCAGAGAGCAGAGAGC 21

RESULT 12  
US-09-866-108-4434  
Sequence 4434, Application US/09866108  
Patent No. US20020048800A1  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharon G.  
APPLICANT: HANZEL, David R.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AEOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
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PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
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PRIOR APPLICATION NUMBER: PCT/US01/00661  
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PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 60/266,860  
PRIOR FILING DATE: 2001-02-05  
NUMBER OF SEQ ID NOS: 15752  
SOFTWARE: Aeomica Sequence Listing Engine

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; SEQ ID NO 4434
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4434
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Query Match      63.0%; Score 12.6; DB 10; Length 25;
Best Local Similarity 78.9%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY      2 GAGCAGCGCCAGAGGAGC 20
DB      2 GGGCAGGAAGCAGAGGAGC 20
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## RESULT 13

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US-09-866-108-4435
; Sequence 4435, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR APPLICATION NUMBER: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4435
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4435
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Query Match      63.0%; Score 12.6; DB 10; Length 25;
Best Local Similarity 78.9%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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DB      1 GGGCAGGAAGCAGAGGAGC 19
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; Sequence 450, Application US/0978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; PRIOR APPLICATION NUMBER: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 63.0%; Score 12.6; DB 9; Length 43;  
Best Local Similarity 78.9%; Pred. No. 2.3e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGCAGCGGCAGAGAC 20  
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Db 8 GAGCAGCGGAGGAGCAGC 26

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US-09-978-697-450

Sequence 450, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James:  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC27  
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Query Match 53.0%; Score 12.6; DB 9; Length 43;  
Best Local Similarity 78.9%; Pred. No. 2.3e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAGCAGCGCGCAGAGCAGC 20  
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Db 8 GAGCAGCGCGGAGAGCGCAGC 26

Search completed: November 23, 2002, 06:42:01  
Job time : 18.25 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

# OM nucleic - nucleic search, using sw model

Run on: November 25, 2002, 09:10:06 ; Search time 755.55 Seconds  
(without alignments)  
428.707 Million cell updates/sec

Title: US-09-296-264-2

Perfect score: 20

Sequence: 1 cgaagcagcgcagcagcagc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : EST: \*

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3:	em_estlin:*
4:	em_estcmu:*
5:	em_estlov:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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5	14.8	74.0	96 17	GA270142
6	14.2	71.0	55 17	BH643795 1008060C0

c 7	14.2	71.0	79 14	BQ167594	BQ167594 WHE0077.H
c 8	13.8	69.0	92 17	A2595307	A2595307 IM0407P17
c 9	13.8	69.0	92 17	CNS03900	A1234251 Tetracodon
c 10	13.8	69.0	95 17	BH173450	BH173450 0104C7.ma
c 11	13.8	69.0	98 13	BI768381	BI768381 603053690
c 12	13.6	68.0	46 9	AA008276	AA008276 mg69b08.r
c 13	13.6	68.0	50 9	AU104090	AU104090 AU104090
c 14	13.6	68.0	81 13	BM490089	BM490089 p9p2n.pk0
c 15	13.6	68.0	81 17	BH849516	BH849516 SAKL_0598
c 16	13.6	68.0	86 17	BH796584	BH796584 1008094H0
c 17	13.6	68.0	87 17	A2918012	A2918012 1006002H0
c 18	13.6	68.0	93 14	BQ564305	BQ564305 g114c02.y
c 19	13.4	67.0	25 17	A2374695	A2374695 1M0127I08
c 20	13.4	67.0	74 9	AA492659	AA492659 v177a03.r
c 21	13.4	67.0	88 9	AA574321	AA574321 nf45f03.s
c 22	13.2	66.0	42 17	A2633442	A2633442 1M0488N08
c 23	13.2	66.0	75 17	CNS01XAO	AL171467 Tetracodon
c 24	13.2	66.0	79 9	A1000040	A1000040 os46c07.s
c 25	13.2	66.0	85 9	AA128241	AA128241 z192f09.r
c 26	13.2	66.0	86 12	BF528126	BF528126 602042896
c 27	13.2	66.0	95 17	BH216187	BH216187 1006041A0
c 28	13.2	66.0	100 10	AW998118	AW998118 RC0-BN005
c 29	12.8	64.0	54 17	A2584073	A2584073 1M0388D22
c 30	12.8	64.0	63 14	BQ761521	BQ761521 EBF08.SQ
c 31	12.8	64.0	88 9	AA883676	AA883676 am12f05.s
c 32	12.8	64.0	88 14	D38686	D38686 HUMC1254.Hu
c 33	12.8	64.0	93 9	A1400715	A1400715 t993h01.x
c 34	12.8	64.0	94 17	A2921327	A2921327 1006029D0
c 35	12.8	64.0	96 14	R59502	R59502 yh17f12.r1
c 36	12.8	64.0	100 17	A2819462	A2819462 2M0091A10
c 37	12.6	63.0	33 17	A2486766	A2486766 1M0315H10
c 38	12.6	63.0	47 13	BI082347	BI082347 602877544
c 39	12.6	63.0	47 17	BH811174	BH811174 SAKL_0575
c 40	12.6	63.0	50 9	AU106272	AU106272 AU106272
c 41	12.6	63.0	50 9	AU106275	AU106275 AU106275
c 42	12.6	63.0	50 9	AU106276	AU106276 AU106276
c 43	12.6	63.0	50 9	AU106279	AU106279 AU106279
c 44	12.6	63.0	50 9	AU106287	AU106287 AU106287
c 45	12.6	63.0	50 9	AA250719	AA250719 mx79b08.r

## ALIGNMENTS

RESULT 1  
AA197619  
LOCUS  
DEFINITION  
AA197619  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AA197619 94 bp mRNA linear EST 19-FEB-1997  
mu19a03.r1 Scores: thymus\_2nbmt Mus musculus cDNA clone IMAGE:639820  
5' mRNA sequence.  
AA197619  
AA197619.1 GI:1793270  
EST.  
house mouse.  
Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 94)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.  
The WashU-HMNI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMNI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through INL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:391812  
Seq primer: -28M13 rev2 from Amerisham  
High quality sequence stop: 81.  
Location/Qualifiers

1.94

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_image="IMAGE:639820"  
/clone\_lib="Soares\_thymus\_2NDMT"  
/sex="male"  
/tissue\_type="Thymus"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. RNA  
provided by Dr. Bertrand Jordan. Library went through two  
rounds of normalization, and was constructed by Bento  
Soares and M.Patima Bonaldo."

BASE COUNT 12 a 32 c 34 g 16 t  
ORIGIN

Query Match 92.0%; Score 18.4; DB 9; Length 94;  
Best Local Similarity 95.0%; Pred. No. 1e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCGCAGAGAGC 20  
|||||  
Db 3 CGAGCAGCGCGCGAGAGAGC 22

RESULT 2 52 bp mRNA linear EST 21-DEC-2000  
AM693858  
LOCUS NF069H05ST.F1047 Developing stem Medicago truncatula cDNA clone  
DEFINITION  
ACCESSION AM693858  
VERSION AM693858  
KEYWORDS EST.  
SOURCE  
ORGANISM Medicago truncatula

barrel medic.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 52)

He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell  
,C.J., Flores,H.R., Imman,U.T., Weiler,U.W., May,G.D. and Dixon  
,R.A.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula stem library  
Unpublished (2000)  
On Apr 14, 2000 this sequence version replaced gi:7568595.

CONTACT: Dixon RA  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7302  
Fax: 580 221 7380  
Email: radixon@noble.org

Insert Length: 685 Std Error: 0.00  
Plate: 069 row: H column: 05  
Seq primer: TCACACAGGAACACCTATGAC.

FEATURES  
source  
1.52  
/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/clone="NF069H05ST"

/clone\_lib="Developing stem"  
/tissue\_type="stem"  
/dev\_stage="Pooled developmental"  
/note="Vector: Lambda Zap; Contains a mixture of  
internodal stem segments"

BASE COUNT 14 a 18 c 14 g 6 t  
ORIGIN

Query Match 79.0%; Score 15.8; DB 10; Length 52;  
Best Local Similarity 89.5%; Pred. No. 9.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCGCAGAGAGC 19  
|||||  
Db 21 CGAGCAGCGCGAGAGAGAGC 39

RESULT 3 55 bp mRNA linear EST 17-JUL-2001  
BI250613  
LOCUS 602993676F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:5149483 5',  
DEFINITION  
ACCESSION BI250613  
VERSION BI250613.1 GI:14799130  
KEYWORDS EST.  
SOURCE  
ORGANISM Mus musculus

house mouse.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 55)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: Lotnar Hennighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: LLAM1369 row: 9 column: 20  
High quality sequence start: 2  
High quality sequence stop: 55.  
Location/Qualifiers

1.55  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_image="IMAGE:5149483"  
/clone\_lib="NCI\_CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: PCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Lotnar Hennighausen/Robin Humphreys,  
NIH"

BASE COUNT 8 a 19 c 17 g 11 t  
ORIGIN

Query Match 76.0%; Score 15.2; DB 13; Length 55;  
Best Local Similarity 85.0%; Pred. No. 1.6e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCGCAGAGAGC 20  
|||||  
Db 41 CGGCGCAGCGAGAGAGACC 22

RESULT 4





BASE COUNT 3 a 30 c 12 g 10 t  
 ORIGIN  
 Query Match 71.0%; Score 14.2; DB 17; Length 55;  
 Best Local Similarity 84.2%; Pred. No. 4e+04; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GAGCAGCGCGCAGAGGAGC 20  
 ||||| ||||| ||||| |||||  
 Db 35 GAGCAGCGCGCAGAGGAGC 17

RESULT 7  
 B0167594/c 79 bp mRNA linear EST 25-APR-2002  
 LOCUS B0167594  
 DEFINITION WHE0077\_H03\_P05K Wheat endosperm cDNA library Triticum aestivum  
 CDNA clone WHE0077\_H03\_P05, mRNA sequence.  
 ACCESSION B0167594  
 VERSION B0167594.1 GI:20312113  
 KEYWORDS EST.  
 SOURCE bread wheat.  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
 ; Triticeae; Triticum.  
 1 (bases 1 to 79)  
 Altenbach,S., Anderson,O.D., Chao,S., Gallig,G., Han,P.S., Hsia  
 C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and  
 Tong,J.C.  
 The structure and function of the expressed portion of the wheat  
 genomes - Endosperm cDNA library  
 Unpublished (2000)  
 Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific  
 West Area, Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105595773  
 Fax: 5105595818  
 Email: oanderson@wpr.usda.gov  
 This EST was generated by sequencing from the 3' end of the clone.  
 Sequences have been trimmed to remove vector sequence and low  
 quality sequence with phred score less than 20.  
 Seg primer: Stragene's KS primer.  
 Location/Qualifiers  
 1..79  
 /organism="Triticum aestivum"  
 /cultivar="Cheyenne"  
 /db\_xref="taxon:4565"  
 /clone="WHE0077\_H03\_P05"  
 /clone\_1lb="Wheat endosperm cDNA library"  
 /tissue\_type="Endosperm"  
 /dev\_stage="5 to 30 days post anthesis seed"  
 /lab\_host="E. coli SOLR"  
 /note="Vector: Lambda ZAP II, excised phagemid; Site-1:  
 EcoRI; Seeds collected, endosperm isolated, and RNA  
 prepared by Susan Altenbach. Library constructed by  
 Stragene, Inc. Plasmid DNA preparations and DNA  
 sequencing were performed in the OD Anderson lab."

BASE COUNT 11 a 31 c 23 g 14 t  
 ORIGIN  
 Query Match 71.0%; Score 14.2; DB 14; Length 79;  
 Best Local Similarity 84.2%; Pred. No. 4.2e+04; Mismatches 3; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GAGCAGCGCGCAGAGGAGC 20  
 ||||| ||||| ||||| |||||  
 Db 58 GAGCGCGCGCAGAGGAGC 40

RESULT 8  
 A2595307/c

LOCUS A2595307 92 bp DNA linear GSS 13-DEC-2000  
 DEFINITION lM0407P17R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0407P17 R, DNA sequence.  
 ACCESSION A2595307  
 VERSION A2595307.1 GI:11717497  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 92)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly  
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.  
 and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0407 row: P column: 17  
 Seg primer: CACACAGCAACACCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 92.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0407P17"  
 /clone\_1lb="Mouse 10kb plasmid UUC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD2 (g114732114(gb)AF129072.1), a copy-number  
 inducible derivative of plasmid RL. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted-vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 15 a 21 c 26 g 30 t  
 ORIGIN  
 Query Match 69.0%; Score 13.8; DB 17; Length 92;  
 Best Local Similarity 88.2%; Pred. No. 6.2e+04; Mismatches 2; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGCAGCGCGCAGAGGAGC 19  
 ||||| ||||| ||||| |||||  
 Db 88 AACACGCGCGCAGAGGAGC 72

RESULT 9  
 CNS03900/c







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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

(without alignments)  
1926.063 Million cell updates/sec

Sequence: 1 ggacgagggcgagcacggcg 20

Gapor 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 995600

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Minimum DB seq length: 0
Maximum DB seq length: 100
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Post-processing: Minimum Match 0%

### Listing first 45 summaries

Database :

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1:  gb.ba:*
2:  gb_htg:*
3:  gb_in:*
4:  gb.om:*
5:  gb.ov:*
6:  gb.pat:*
7:  gb.ph:*
8:  gb.pl:*
9:  gb.pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15:  gb.ba:*
16:  em.fun:*
17:  em_hum:*
18:  em_in:*
19:  em_mn:*
20:  em.om:*
21:  em.or:*
22:  em.ov:*
23:  em.pat:*
24:  em.ph:*
25:  em.pl:*
26:  em.ro:*
27:  em.scs:*
28:  em.un:*
29:  em.vl:*
30:  em_htg_hum:*
31:  em_htg_in:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_htg:*
39:  em_htg_hum:*
40:  em_htg_mus:*
41:  em_htg_other:*

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Pred. No. is the number of results predicted by chance to have a

Query No.	Score	Match	Length	ID	Description
1	16.8	84.0	51	6	AX156995 Sequence
2	15.2	76.0	99	6	A23183 Artificial
3	14.2	71.0	26	6	AX146654 Sequence
4	14.2	71.0	40	6	AX490799 Sequence
5	14.2	71.0	45	6	AX128401 Sequence
6	14.2	71.0	45	6	AX429834 Sequence
7	14.2	71.0	65	6	AR038667 Sequence
8	14.2	71.0	66	6	AR038665 Sequence
9	14.2	71.0	78	14	AF362846 HIV-1 Iso
10	14.2	71.0	78	14	AF362847 HIV-1 Iso
11	14.2	71.0	78	14	AF362848 HIV-1 Iso
12	13.8	69.0	60	6	AR009383 Sequence
13	13.8	69.0	78	6	AE67678 Sequence 8
14	13.6	68.0	30	6	AR063475 Sequence
15	13.6	68.0	30	6	I28155 Sequence 12
16	13.6	68.0	37	6	AX356235 Sequence
17	13.6	68.0	49	11	AL823803 Sequence
18	13.6	68.0	64	9	HUMMACU L37707 Homo sapien
19	13.6	68.0	86	6	AX236733 Sequence
20	13.6	68.0	90	6	AX236627 Sequence
21	13.6	68.0	100	11	AF235063 Sequence 3
22	13.2	66.0	21	6	AB6893 Sequence 1
23	13.2	66.0	21	6	AB93725 Sequence 1
24	13.2	66.0	21	6	AR088407 Sequence
25	13.2	66.0	27	6	AX207516 Sequence
26	13.2	66.0	27	6	AX207554 Sequence
27	13.2	66.0	60	6	AR009382 Sequence
28	13.2	66.0	75	14	AF178663 HIV-1 LCV
29	13.2	66.0	81	14	AF362871 HIV-1 Iso
30	13.2	66.0	81	14	AF362873 HIV-1 Iso
31	13.2	66.0	81	14	AF362874 HIV-1 Iso
32	13	65.0	37	6	AR170305 Sequence
33	13	65.0	37	6	AX007133 Sequence
34	13	65.0	37	6	E51079 Novel Esche
35	12.6	63.0	22	6	AX328831 Sequence
36	12.6	63.0	23	6	AR106710 Sequence
37	12.6	63.0	23	6	AR202521 Sequence
38	12.6	63.0	23	6	I24358 Sequence 8
39	12.6	63.0	24	6	BD004778 Novel YEG
40	12.6	63.0	24	6	E36097 Novel polyp
41	12.6	63.0	25	6	E38429 Novel polyp
42	12.6	63.0	25	6	AX083192 Sequence
43	12.6	63.0	25	6	AX107065 Sequence
44	12.6	63.0	25	6	AX155273 Sequence
45	12.6	63.0	25	6	AX206869 Sequence

## RESULT 1

LOCUS	AX156995	51 bp	DNA	1 linear	PAT 22-JUN-2001
DEFINITION	Sequence 323 from Patent WO0140521.				

VERSION AX156995.1 GI:14538326

SOURCE ORGANISM	human.
Homo sapiens	

REFERENCE  
AUTHORS  
TITLE

Nucleic acids containing single nucleotide polymorphisms and  
Shinkre,S.R.A. and Leach,M.  
1 (pages 1 to 51)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

JOURNAL Patent: WO 0140521-A 323 07-JUN-2001;  
Curagen Corporation (US)  
Location/Qualifiers  
FEATURES  
source 1..51  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
misc.feature 26  
/note="1 of 2 allelic variants (324 is other entry)  
Accession number cg20436198"  
BASE COUNT 5 a 14 c 29 g 3 t  
ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 51;  
Best Local Similarity 90.0%; Pred. No. 2.8e+04;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGACGAGCGCGACGCGCG 20  
||||| ||||| ||||| |||||  
Db 22 GGACGCGCGCGACGCGCG 41

RESULT 2  
A23183/c A23183 99 bp DNA linear PAT 11-JAN-1995  
LOCUS A23183  
DEFINITION Artificial DNA for DNA adapter (1d. 7).  
ACCESSION A23183  
VERSION A23183.1 GI:833251  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 99)  
AUTHORS Stern, A., Hagemann, I. and Ziegler-Landesberger, D.  
TITLE Method of introduction of nucleic acids in cells  
JOURNAL Patent: EP 0544292-A 7 02-JUN-1993;  
BOEHRINGER MANNHEIM GMBH  
Location/Qualifiers  
FEATURES  
source 1..99  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
BASE COUNT 13 a 36 c 27 g 23 t  
ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 99;  
Best Local Similarity 85.0%; Pred. No. 9.5e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGCGCGACGCGCG 20  
||||| ||||| ||||| |||||  
Db 88 GGACGCGCGCGACGCGCG 69

RESULT 3  
AX146654/c AX146654 26 bp DNA linear PAT 31-MAY-2001  
LOCUS AX146654  
DEFINITION Sequence 5 from Patent WO0134818.  
ACCESSION AX146654  
VERSION AX146654.1 GI:14285047  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Johal, G.S. and Multani, D.S.  
TITLE Sorghum dwarfing genes and methods of use  
JOURNAL Patent: WO 0134818-A 5 17-MAY-2001;  
Johal, Gurmukh S. (US); Multani, Dilbag S. (US)  
Location/Qualifiers  
FEATURES  
source 1..26  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="oligonucleotide primer designed from sequence of  
Zea mays Br2 gene"

BASE COUNT 0 a 12 c 6 g 8 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 26;  
Best Local Similarity 84.2%; Pred. No. 2.8e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGCGCGACGCGCG 20  
||||| ||||| ||||| |||||  
Db 24 GACGAGCGCGACGCGCG 6

RESULT 4  
AX490799/c AX490799 40 bp DNA linear PAT 16-AUG-2002  
LOCUS AX490799  
DEFINITION Sequence 13 from Patent WO0246400.  
ACCESSION AX490799  
VERSION AX490799.1 GI:22323749  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Kranz, D.M., Starwalt, S. and Bluestone, J.A.  
TITLE Mutated Class II major histocompatibility proteins  
JOURNAL Patent: WO 0246400-A 13 13-JUN-2002;  
The Board of Trustees of the University of Illinois (US)  
Location/Qualifiers  
FEATURES  
source 1..40  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Synthetic nucleotide primer"  
BASE COUNT 4 a 19 c 12 g 5 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 40;  
Best Local Similarity 84.2%; Pred. No. 2.6e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGCGCGACGCGCG 20  
||||| ||||| ||||| |||||  
Db 39 GACGTGGCGCGACTACCGCG 21

RESULT 5  
AX128401 AX128401 45 bp DNA linear PAT 15-MAY-2001  
LOCUS AX128401  
DEFINITION Sequence 62 from Patent WO0130843.  
ACCESSION AX128401  
VERSION AX128401.1 GI:14134909  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Barbas, C.F., Kadan, M. and Beeri, R.  
TITLE Ligand activated transcriptional regulator proteins  
JOURNAL Patent: WO 0130843-A 62 03-MAY-2001;  
Novartis AG (CH); The Scripps Research Institute (US)  
Location/Qualifiers  
FEATURES  
source 1..45  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Recombinant molecule"  
BASE COUNT 9 a 14 c 17 g 5 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 45;  
Best Local Similarity 84.2%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGCGCGACGCGCG 19  
||||| ||||| ||||| |||||



Db 3 GGAGGAGCGCGCCGCCGC 21

RESULT 6  
LOCUS AX429834 45 bp DNA linear PAT 21-JUN-2002  
DEFINITION Sequence 26 from Patent WO0206463.  
ACCESSION AX429834  
VERSION AX429834.1 GI:21541010  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..45  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="Synthesized"

BASE COUNT 9 a 14 c 17 g 5 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 45;  
Best Local Similarity 84.2%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GGAGGAGCGCGCGCCGCCGC 19  
Db 3 GGAGGAGCGCGCGCCGCCGC 21

RESULT 7  
LOCUS AR038667 65 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 5 from patent US 5807675.  
ACCESSION AR038667  
VERSION AR038667.1 GI:5958030  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..65  
/organism="unknown"  
/db\_xref="taxon:32644"

BASE COUNT 16 a 15 c 23 g 11 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 65;  
Best Local Similarity 84.2%; Pred. No. 2.4e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GAGCAGGCGCGAGCAGCGCG 20  
Db 3 GAGCAGGCGCGAGCAGCGCG 21

RESULT 8  
LOCUS AR038665/c 66 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 3 from patent US 5807675.  
ACCESSION AR038665  
VERSION AR038665.1 GI:5958028  
KEYWORDS  
SOURCE  
Unknown.

ORGANISM Unknown.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..66  
/organism="unknown"

BASE COUNT 14 a 26 c 8 g 18 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 66;  
Best Local Similarity 84.2%; Pred. No. 2.4e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GAGCAGGCGCGAGCAGCGCG 20  
Db 28 GAGCAGGCGCGAGCAGCGCG 10

RESULT 9  
LOCUS AF362846 78 bp RNA linear VRL 09-MAY-2001  
DEFINITION HIV-1 isolate 3040p1 from USA envelope glycoprotein, V3 region (env) gene, partial cds.  
ACCESSION AF362846  
VERSION AF362846.1 GI:14010375  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..78  
/organism="Human immunodeficiency virus type 1"  
/viralon  
/isolate="3040p1"  
/db\_xref="taxon:11676"  
/tissue\_type="blood plasma"  
/country="USA"  
/gene="env"  
/note="V3 region"  
/codon\_start=1  
/product="envelope glycoprotein"  
/protein\_id="AAK51973.1"  
/db\_xref="GI:14010376"  
/translation="NNNTRRSIQIGPRAWHTTITGDIR"

BASE COUNT 39 a 10 c 18 g 11 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 14; Length 78;  
Best Local Similarity 84.2%; Pred. No. 2.3e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGCGGAGCAGCGC 19  
||||| ||||| ||||| |||||  
Db. 31 GGACGAGCGGAGCAGCATGCG 49

RESULT 10  
AF362847 78 bp RNA linear VRL 09-MAY-2001  
LOCUS HIV-1 isolate 3040P2 from USA envelope glycoprotein, V3 region  
DEFINITION (env) gene, partial cds.  
ACCESSION AF362847  
VERSION AF362847.1 GI:14010377  
KEYWORDS Human immunodeficiency virus type 1.  
SOURCE Human immunodeficiency virus type 1.  
ORGANISM Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate

REFERENCE  
AUTHORS 1 (bases 1 to 78)  
TITLE Human immunodeficiency virus type 1.  
JOURNAL J. Virol. 75 (10), 4936-4940 (2001)  
MEDLINE 21211648  
PUBMED 11312368  
REFERENCE 2 (bases 1 to 78)  
AUTHORS Freil,S.A., Williams,J.M., Nelson,J.A., Patton,L.L., Fiscus,S.A.,  
Svanstrom,R. and Shugars,D.C.  
TITLE Characterization of human immunodeficiency virus type 1 in saliva  
JOURNAL and blood plasma by V3-specific heteroduplex tracking assay and  
MEDLINE genotype analyses  
PUBMED J. Virol. 75 (10), 4936-4940 (2001)  
REFERENCE 21211648  
PUBMED 11312368  
REFERENCE 2 (bases 1 to 78)  
AUTHORS Freil,S.A., Williams,J.M., Nelson,J.A., Patton,L.L., Fiscus,S.A.,  
Svanstrom,R. and Shugars,D.C.  
TITLE Direct Submission  
JOURNAL Submitted (21-MAR-2001) Dentistry and Microbiology, University of  
MEDLINE North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA  
PUBMED Location/Qualifiers  
FEATURES  
source 1..78  
/organism="Human immunodeficiency virus type 1"  
/virlon  
/isolate="3040P2"  
/db\_xref="taxon:11676"  
/tissue\_type="blood plasma"  
/country="USA"  
<1..>78  
/gene="env"  
/gene="env"  
<1..>78  
/gene="env"  
/note="V3 region"  
/codon\_start=1  
/product="envelope glycoprotein"  
/protein\_id="AAK51974.1"  
/db\_xref="GI:14010378"  
/translation="NNNTRRSIQIGPGRAWHTTTRIGDIR"  
BASE COUNT 39 a 11 c 18 g 10 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 14; Length 78;  
Best Local Similarity 84.2%; Pred. No. 2.3e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGCGGAGCAGCGC 19  
||||| ||||| ||||| |||||  
Db 31 GGACGAGCGGAGCAGCATGCG 49

RESULT 11  
AF362848 78 bp RNA linear VRL 09-MAY-2001  
LOCUS HIV-1 isolate 3040P3 from USA envelope glycoprotein, V3 region  
DEFINITION (env) gene, partial cds.  
ACCESSION AF362848  
VERSION AF362848.1 GI:14010379  
KEYWORDS Human immunodeficiency virus type 1.  
SOURCE Human immunodeficiency virus type 1.  
ORGANISM Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate

REFERENCE  
AUTHORS 1 (bases 1 to 78)  
TITLE Human immunodeficiency virus type 1.  
JOURNAL J. Virol. 75 (10), 4936-4940 (2001)  
MEDLINE 21211648  
PUBMED 11312368  
REFERENCE 2 (bases 1 to 78)  
AUTHORS Freil,S.A., Williams,J.M., Nelson,J.A., Patton,L.L., Fiscus,S.A.,  
Svanstrom,R. and Shugars,D.C.  
TITLE Direct Submission  
JOURNAL Submitted (21-MAR-2001) Dentistry and Microbiology, University of  
MEDLINE North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA  
PUBMED Location/Qualifiers  
FEATURES  
source 1..78  
/organism="Human immunodeficiency virus type 1"  
/virlon  
/isolate="3040P3"  
/db\_xref="taxon:11676"  
/tissue\_type="blood plasma"  
/country="USA"  
<1..>78  
/gene="env"  
/gene="env"  
<1..>78  
/gene="env"  
/note="V3 region"  
/codon\_start=1  
/product="envelope glycoprotein"  
/protein\_id="AAK51975.1"  
/db\_xref="GI:14010380"  
/translation="NNNTRRSIQIGPGRAWHTTTRIGDIR"  
BASE COUNT 39 a 11 c 18 g 10 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 14; Length 78;  
Best Local Similarity 84.2%; Pred. No. 2.3e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGCGGAGCAGCGC 19  
||||| ||||| ||||| |||||  
Db 31 GGACGAGCGGAGCAGCATGCG 49

RESULT 12  
AR009383 60 bp DNA linear PAT 04-DEC-1998  
LOCUS AR009383  
DEFINITION Sequence 151 from patent US 5756291.  
ACCESSION AR009383  
VERSION AR009383.1 GI:3968188  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 60)  
AUTHORS Griffin,L., Albrecht,G., Latham,J., Leung,L., Vermaas,E. and  
Toole,J.J.  
TITLE Aptamers specific for biomolecules and methods of making  
JOURNAL Patent: US 5756291-A 151 26-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..60  
/organism="unknown"  
BASE COUNT 13 a 6 c 32 g 9 t  
ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 60;  
Best Local Similarity 88.2%; Pred. No. 3.4e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGACGAGCGGAGCAGC 17  
||||| ||||| ||||| |||||

Db 28 GGAGGCGGCGAGGCG 44

RESULT 13

LOCUS A67678/c 78 bp DNA linear PAT 05-MAY-1999

DEFINITION Sequence 8 from Patent WO9743428.

ACCESSION A67678

VERSION A67678.1 GI:4756541

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 78)

AUTHORS Merotz,B., Baudino,S., Gruber,V., Bournat,P., Lenee,P., Riviere,M.E. and Audommet,J.F.

TITLE TRANSGENIC PLANTS EXPRESSING RABIES GLYCOPROTEIN G, AND GLYCOPROTEINS THUS OBTAINED

JOURNAL Patent: WO 9743428-A 8 20-NOV-1997; BIOCEM (FR)

COMMENT Other publication FR 2748480 19971114.

FEATURES

source Location/Qualifiers

1..78

/organism="unidentified"

/db\_xref="taxon:32644"

BASE COUNT 10 a 32 c 26 g 10 t

ORIGIN

Query Match 69.0%; Score 13.6; DB 6; Length 78;

Best Local Similarity 88.2%; Pred. No. 3.2e+05;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CGAGGCGGCGAGGCGG 20

Db 58 CGAGGCGGCGAGGCGG 42

RESULT 14

AR063475

LOCUS AR063475 30 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 12 from patent US 5846706.

ACCESSION AR063475

VERSION AR063475.1 GI:5992783

KEYWORDS

SOURCE unknown.

ORGANISM unknown.

REFERENCE 1 (bases 1 to 30)

AUTHORS Greenberg,S.J. and Evans,M.Jo.

TITLE Rapid and sensitive detection of herpes simplex virus

JOURNAL Patent: US 5846706-A 12 08-DEC-1998;

FEATURES

source Location/Qualifiers

1..30

/organism="unknown"

BASE COUNT 7 a 6 c 17 g 0 t

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 30;

Best Local Similarity 80.0%; Pred. No. 4.5e+05;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGCGGCGAGGCGG 20

Db 1 GGACGAGGCGGCGAGGCGG 20

RESULT 15

I28155

LOCUS I28155 30 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 12 from patent US 5569583.

ACCESSION I28155

VERSION I28155.1 GI:1818931

KEYWORDS

SOURCE unknown.

ORGANISM unknown.

REFERENCE 1 (bases 1 to 30)

AUTHORS Greenberg,S.J. and Evans,M.J.

TITLE Rapid and sensitive detection of cytomegalovirus

JOURNAL Patent: US 5569583-A 12 29-OCT-1996;

FEATURES

source Location/Qualifiers

1..30

/organism="unknown"

BASE COUNT 7 a 6 c 17 g 0 t

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 30;

Best Local Similarity 80.0%; Pred. No. 4.5e+05;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGCGGCGAGGCGG 20

Db 1 GGACGAGGCGGCGAGGCGG 20

Search completed: December 3, 2002, 18:12:09

Job time : 309.2 secs

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xx Claim 4; Page 16; 57bp; English.

ps Sequences AA231431-460 represent antisense oligonucleotides which

cc Inhibit human neutropilin expression. The antisense oligonucleotides can

cc be used to inhibit the growth or metastasis of a mammalian tumor and

cc inhibit neovascularisation. The oligonucleotides may be used to treat

cc various forms of cancers or tumors, such as sarcomas, melanomas,

cc adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell

cc carcinomas of the mouth, throat, larynx and lung, genitourinary cancers

cc such as cervical and bladder cancer, hematopoietic cancers, colon cancer,

cc breast cancer, pancreatic cancer, renal cancer, brain cancer, skin

cc cancer, liver cancer, head and neck cancers, and nervous system cancers,

cc as well as benign lesions such as papillomas. The methods may be used to

cc treat neovascularisation disorders such as diabetic retinopathy, and

cc retinopathy of prematurity and age related macular degeneration.

xx

sq Sequence 20 BP; 4 A; 5 C; 11 G; 0 U; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGACGAGGCGGACGACGCG 20

DB 1 GGACGAGGCGGACGACGCG 20

RESULT 2

AA173382

ID AA173382 standard; DNA; 51 BP.

XX AA173382;

XX 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:323.

XX

KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

KW quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

XX

PN WO200140521-A2.

PD 07-JUN-2001.

XX

PF 30-NOV-2000; 2000WO-US32758.

XX

PR 30-NOV-1999; 99US-0168138.

PR 29-NOV-2000; 2000US-0726173.

XX

PA (CUBA-) CUBAGEN CORP.

XX

PI Shinkets RA, Leach M;

PI

DR WPI; 2001-356160/37.

XX

PT Polymorphic nucleic acid sequences, useful in genetic testing and

PT therapy -

PS

XX Claim 1; Page 153; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173114 to AA1753129 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (I) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides.

CC For example, (I) may be used to treat disorders by rectifying mutations

CC or deletions in a patient's genome that affect the activity of

CC polypeptides by expressing inactive proteins or to supplement the

CC patients own production of polypeptide. Additionally, (I) and its

CC complementary sequences may also be used as DNA probes in diagnostic

CC assays to detect and quantitate the presence of similar nucleic acids

CC in samples, and therefore which patients may be in need of restorative

CC therapy. The polypeptides encoded by (I) may be used as antigens in the

CC production of antibodies specific for polymorphic polypeptides. The

CC antibodies may also be used to down regulate expression and activity.

CC The antibodies may also be used as diagnostic agents for detecting the

CC presence of polymorphic polypeptides in samples.

xx

sq Sequence 51 BP; 5 A; 14 C; 29 G; 3 T; 0 other;

Query Match 84.0%; Score 16.8; DB 22; Length 51;

Best Local Similarity 90.0%; Pred. No. 4.9e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGACGAGGCGGACGACGCG 20

DB 22 GGACGAGGCGGACGACGCG 41

RESULT 3

AA042957/c

ID AA042957 standard; DNA; 95 BP.

XX AA042957;

XX 07-SEP-1993 (first entry)

DE Encodes 8 Arg C-terminal extension of G-CSF.

XX

KW Granulocyte Colony Stimulating Factor; Cell-homing factor;

KW fusion protein; targeting; gene therapy; ds.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT misc-feature 63..86

FT /tag= "a

FT /note= "8 Arg codons -

FT there is a 4-nucleotide overhang at the

FT 5' end of the coding strand and a 4-nt

FT overhang (5'-AGCT-3') at the 5' end of the

FT complementary strand"

FT

XX

PN EP544292-A.

PD 02-JUN-1993.

XX

PF 26-NOV-1992; 92EP-0120205.

XX

PR 27-NOV-1991; 91DE-4139001.

XX

PA (BOE ) BOEHRINGER MANNHEIM GMBH.

XX

PI Hagemann I, Stern A, Ziegler-Landesberger D;

PI

DR WPI; 1993-177078/22.

XX

PT Cell introduction of cell homing factor-polycation-nucleic acid

PT complex - of linear genetic cell homing factor-polycation fusion

PT having ionic interaction with nucleic acid, the polycation part

PT having at least three lysine and arginine

XX

PS Example 2; Page 6; 17pp; German.

XX

CC This sequence codes for the C-terminal region of G-CSF fused to 8

CC Arginine residues and a proline residue. The basic nature of

CC the extension ("polycation chain") results in ionic interaction of

CC the fusion protein with DNA to form a complex. The G-CSF acts to

CC target the complex to e.g. NFS60 cells where the associated DNA can

CC be taken up by those cells at a much higher rate than when the basic



ID AA298666 standard; DNA; 30 BP.  
XX  
XX AA298666;  
AC  
XX  
XX 05-JUN-2000 (first entry)  
DT  
XX  
XX Escherichia coli K12 DNAJ gene fragment probe sequence.  
DE  
XX  
XX Specific binding assay; DNAJ; analyte determination; antigen;  
KM happen; drug; cancer marker; pesticide; chemiluminescent compound;  
KW pollutant; probe; ss.  
XX  
XX Escherichia coli.  
OS  
XX  
XX EP984282-A2.  
PN  
XX  
XX 08-MAR-2000.  
PD  
XX  
XX 21-MAY-1992; 99EP-0121551.  
PF  
XX  
XX 22-MAY-1991; 91US-0704569.  
PR 20-JUN-1991; 91US-0718490.  
PR 21-MAY-1992; 92EP-0304630.  
XX  
XX (DADE-) DADE BEHRING MARBURG GMBH.  
PA  
XX  
XX Ullman EF, Kirakossian H, Pease JS, Wagner DB, Daniloff Y;  
PI  
XX  
XX WPI: 2000-225922/20.  
DR  
XX  
XX Particles containing a chemiluminescent donor and a fluorescent  
PT acceptor are useful in specific binding assays to determine antigens,  
PT haplens, enzymes, hormones, cancer markers or nutritional markers -  
XX  
XX  
XX Example 5; Page 66; 79pp; English.  
PS  
XX  
XX This sequence represents a probe for a fragment of the Escherichia coli  
CC DNAJ gene. The fragment is used as an example target sequence in a method  
CC for determining analyte in a sample using the particles of the invention.  
CC The invention relates to particles (I) containing a compound (II) and a  
CC fluorescent compound (III). Compound II reacts with singlet oxygen to  
CC form a metastable intermediate that can decompose with simultaneous or  
CC subsequent emission of light. The fluorescent compound (III) is excited  
CC by activated compound (II) and emits at a wavelength longer than the  
CC emission wavelength of compound (II). The particles are useful in  
CC specific binding assays. The assays can be used to determine antigens or  
CC haplens, e.g. blood group or HLA antigens or bacterial, fungal, protozoal  
CC or viral antigens, other proteins e.g. immunoglobulins, cytokines,  
CC enzymes, hormones, cancer markers or nutritional markers, microorganisms,  
CC drugs, metabolites, pesticides, pollutants or polynucleotides. The longer  
CC emission wavelength of (III) eliminates interference from serum  
CC components when the particles are used in specific binding assays in the  
CC presence of such components.  
XX  
XX Sequence 30 BP; 2 A; 14 C; 8 G; 6 T; 0 other;  
SQ  
Query Match 71.0%; Score 14.2; DB 21; Length 30;  
Best Local Similarity 84.2%; Pred. No. 5.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GACGAGCGCGACGCGCG 20  
DB 28 GACGCGCGCGACGATGCGC 10

DE Single chain Class II MHC, I-Ag7 mutagenic primer 4.  
XX  
XX Major histocompatibility complex; MHC; combinatorial library;  
KM I-Ag7; insulin-dependent diabetes mellitus; autoimmune disease;  
KW antidiabetic; diagnosis; mutagenesis; PCR; primer; ss.  
XX  
XX Synthetic.  
OS  
XX  
XX WO200246400-A2.  
PN  
XX  
XX 13-JUN-2002.  
PD  
XX  
XX 10-DEC-2001; 2001WO-US47830.  
PF  
XX  
XX 08-DEC-2000; 2000US-254248P.  
PR  
XX  
XX (UNITI ) UNIV ILLINOIS FOUNO.  
PA  
XX  
XX Kranz DM, Starwalt S, Bluestone JA;  
PI  
XX  
XX WPI: 2002-537566/57.  
DR  
XX  
XX Novel isolated mutant major histocompatibility complex class II  
PT chimeric protein displayed on recombinant yeast cell surface has  
PT improved stability or T-cell receptor binding, useful for treating  
PT autoimmune disease -  
XX  
XX  
XX Example 3; Page 27; 66pp; English.  
PS  
XX  
XX The present sequence is mutagenic primer 3 for positions beta-56  
CC and beta-57 of a single chain (sc) Class II major histocompatibility  
CC complex (MHC) haplotype I-Ag7 construct. A site-directed mutagenesis  
CC strategy involving PCR sewing and yeast homologous recombination was  
CC used to mutate residues beta-56 and -57. Mutant libraries of sc MHC  
CC Class II protein were generated and displayed on the cell surface of  
CC recombinant yeast cells, and stabilised I-Ag7 proteins were  
CC identified. Haplotype I-Ag7 is associated with the development of  
CC insulin-dependent diabetes mellitus (IDDM) in the non-obese (NOD)  
CC mouse model of IDDM. The present invention allows the creation and  
CC isolation of stabilised variants of Class II peptide-MHC complexes.  
CC Stabilised variants of single chain I-Ag7, in association with each  
CC of 3 peptides of interest (BDC2.5(A), GAD65(78-95) and B9-23  
CC insulin), have been produced. These can be used in diagnostic  
CC tests of IDDM, in imaging tests, and in the treatment or prevention  
CC of IDDM.  
XX  
XX Sequence 40 BP; 4 A; 19 C; 12 G; 5 T; 0 other;  
SQ  
Query Match 71.0%; Score 14.2; DB 24; Length 40;  
Best Local Similarity 84.2%; Pred. No. 5.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GACGAGCGCGACGCGCG 20  
DB 39 GACGTGGCGGAGTACCGCG 21

RESULT 7  
ABN84043/C  
ID ABN84043 standard; DNA; 40 BP.  
XX  
XX  
XX ABN84043;  
AC  
XX  
XX 23-SEP-2002 (first entry)  
DT  
XX

RESULT 8  
AAD06100  
ID AAD06100 standard; DNA; 45 BP.  
XX  
XX  
XX AAD06100;  
AC  
XX  
XX 31-JUL-2001 (first entry)  
DT  
XX  
XX Drosophila ECR coding region amplifying primer, (ASCI)-ECR.  
DE  
XX  
XX Fusion protein; nucleotide-binding domain; NBD;  
KM ligand-binding domain; LBD; transcription regulation domain; TRD;  
KM zinc finger protein; ZFP; ligand-activated transcriptional regulator;  
KM gene regulation; gene therapy; cell proliferative disorder; cancer;  
KM psoriasis; pemphigus vulgaris; Behcet's syndrome; lipid histiocytosis;  
KM ECR; PCR primer; ecdysone receptor; ss.



```
XX OS Drosophila sp.
XX PN WO200130843-A1.
XX PD 03-MAY-2001.
XX PF 23-OCT-2000; 2000WO-EP10430.
XX PR 25-OCT-1999; 99US-0433042.
XX PR 02-JUN-2000; 2000US-0586623.
XX PA (NOVS ) NOVARTIS AG.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Kadan M, Beerli R;
XX DR WPI; 2001-308618/32.
XX PT New fusion protein containing nucleotide-binding and ligand-binding
XX PT domains, useful e.g. in gene therapy of cancer, provides
XX PT ligand-activated control of gene expression -
XX PS Example 12; Page 110; 218pp; English.
XX CC The invention relates to fusion protein comprising a nucleotide-binding
XX CC domain (NBD), a ligand-binding domain (LBD) of an intracellular
XX CC receptor (ICR) and a transcription regulating domain (TRD). NBD is a
XX CC polypeptidyl zinc finger protein, or a modular part of it, that interacts
XX CC specifically with a contiguous sequence of at least 3 nucleotides. The
XX CC fusion protein functions as a ligand-activated transcriptional regulator.
XX CC The fusion protein and the nucleic acid encoding it, are used to regulate
XX CC gene expression, particularly in gene therapy for treating malignant
XX CC cell proliferative diseases (e.g. colon cancer, prostate cancer,
XX CC renal-cell carcinoma) and non-malignant cell proliferative
XX CC diseases (e.g. psoriasis, pemphigus vulgaris, Behcet's syndrome and
XX CC lipid histiocytosis). The fusion protein and its DNA are also useful for
XX CC treating diseases caused by viruses in humans/plants, genetic and/or
XX CC acquired diseases. The fusion protein can be designed to target any
XX CC selected gene (endogenous or exogenous), and can be made to have
XX CC different selectivity or specificity for endogenous or exogenous ligands.
XX CC The present sequence is Drosophila ecdysone receptor (EcR) coding region
XX CC amplifying primer, (Asci)-EcR. This primer is used to obtain LBD which
XX CC is used to construct fusion protein of the invention.
XX SQ Sequence 45 BP; 9 A; 14 C; 17 G; 5 T; 0 other;
XX
XX Query Match 71.0%; Score 14.2; DB 22; Length 45;
XX Best Local Similarity 84.2%; Pred. No. 5.6e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 GGACGAGGCGGACGACGCC 19
XX ||| ||||| || |||||
XX DB 3 GGAGAGGCGCGCCCGCCG 21
XX
XX RESULT 9
XX AA172470
XX ID AA172470 standard; DNA; 45 BP.
XX AC AA172470;
XX XX
XX DT 16-MAY-2002 (first entry)
XX XX
XX DE D. melanogaster ecdysone receptor LBD primer. ECRasc-B.
XX XX
XX KW Polymerase chain reaction; primer; amplify; PCR; reporter;
XX KW polypeptide gene switch; ligand binding domain; LBD; transcription;
XX KW nuclear hormone receptor; gene therapy; regulation; expression; ss.
XX OS Synthetic.
XX PN WO200206463-A2.
```

```
XX XX 24-JAN-2002.
XX XX
XX PF 16-JUL-2001; 2001WO-EP08190.
XX PR 18-JUL-2000; 2000US-0619063.
XX XX
XX PA (NOVS ) NOVARTIS AG.
XX PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Beerli R, Schopfer U, Barbas CF;
XX DR WPI; 2002-179793/23.
XX XX
XX PT Single chain, monomeric polypeptide gene switches for regulating gene
XX PT function, comprise two ligand binding domains derived from nuclear
XX PT hormone receptors operatively linked to one functional domain -
XX PS Example 1; Page 31; 63pp; English.
XX XX
XX CC The sequences given in AA172463-72 are primers which were used in the
XX CC generation of single chain switch which could be used in the
XX CC construction of a non-naturally occurring polypeptide gene switch
XX CC comprising two ligand binding domains (LBDs) derived from nuclear
XX CC hormone receptors operatively linked to a first functional domain. The
XX CC gene switch is useful for regulating the function of a target nucleotide
XX CC that contains a defined sequence, by exposing the target nucleotide to
XX CC the polypeptide gene switch in the presence of a ligand that binds one
XX CC of the LBDs of the polypeptide, where the DNA binding domain of the
XX CC polypeptide binds the defined sequence, or the functional domain of
XX CC the polypeptide alters the function of the target nucleotide. The gene
XX CC switch is also useful in the field of gene therapy and as a regulator
XX CC of gene expression or transcription. The advantage of the gene switches
XX CC of the invention over existing gene switches is the need for only a
XX CC single molecular switch and a single expression vector for production
XX CC of that switch.
XX SQ Sequence 45 BP; 9 A; 14 C; 17 G; 5 T; 0 other;
XX
XX Query Match 71.0%; Score 14.2; DB 24; Length 45;
XX Best Local Similarity 84.2%; Pred. No. 5.6e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 GGACGAGGCGGACGACGCC 19
XX ||| ||||| || |||||
XX DB 3 GGAGAGGCGCGCCCGCCG 21
XX
XX RESULT 10
XX AA298641
XX ID AA298641 standard; DNA; 50 BP.
XX AC AA298641;
XX XX
XX DT 05-JUN-2000 (first entry)
XX XX
XX DE E. coli K12 DNAB oligonucleotide used as a target in a homogeneous assay.
XX XX
XX KW Homogeneous specific binding assay; DNAJ gene; analyte determination;
XX KW antigen; hapten; drug; cancer marker; pesticide; pollutant;
XX KW photochemically activatable chemiluminescent compound; ss.
XX OS Escherichia coli.
XX PN EP984281-A2.
XX XX
XX PD 08-MAR-2000.
XX XX
XX PF 21-MAY-1992; 99EP-0121547.
XX XX
XX PR 22-MAY-1991; 91US-0704569.
XX PR 20-JUN-1991; 91US-0718490.
```

PR 21-MAY-1992; 92EP-0304630.  
XX  
XX (DADE-) DADE BEHRING MARBURG GMBH.  
XX  
PI Ullman EF, Kirakossian H, Pease JS, Wagner DB, Daniloff Y;  
XX WPI; 2000-197307/18.  
XX  
XX  
PT Homogeneous specific binding assay, e.g. for proteins or nucleic acids,  
PR uses photochemically activatable chemiluminescent compound -  
XX  
XX Example 5; Page 65; 78pp; English.  
XX  
XX This sequence represents a fragment of the Escherichia coli K12 DNA  
CC gene, used as an example of a target sequence in a homogeneous assay. The  
CC invention relates to a homogeneous assay for determining an analyte,  
CC comprising combining medium suspected of containing an analyte with a  
CC label reagent and intrinsically metastable species, and determining the  
CC reaction. The label reagent comprises a suspended particle and a  
CC specific binding pair (sbp) member associated with a photochemically  
CC activatable chemiluminescent compound (PAC), the sbp is capable of  
CC binding to a second sbp or to the analyte, the second sbp being capable  
CC of binding to the analyte. The metastable species is capable of diffusing  
CC into the medium and reacts preferentially with the PAC, when brought  
CC into close proximity by the presence or absence of the analyte. The  
CC method can be used to determine antigens or haptens, e.g. blood group or  
CC HLA antigens or bacterial, fungal, protozoal or viral antigens, other  
CC proteins e.g. immunoglobulins, cytokines, enzymes, hormones, cancer  
CC markers or nutritional markers, microorganisms, drugs, metabolites,  
CC pesticides, pollutants or polynucleotides. The method is a homogeneous  
CC assay and does not require a separation step.  
XX  
SQ Sequence 50 BP; 10 A; 12 C; 23 G; 5 T; 0 other;  
Query Match 71.0%; Score 14.2; DB 21; Length 50;  
Best Local Similarity 84.2%; Pred. No. 5.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GACGAGCGCGACGACGCGC 20  
DB 13 GAAGCGCGCGACGACGCGC 31  
RESULT 11  
ID AAZ98665  
XX AAZ98665 standard; DNA; 50 BP.  
XX  
AC AAZ98665;  
XX  
DT 05-JUN-2000 (first entry)  
XX  
XX  
DE Escherichia coli K12 DNAJ gene fragment nucleotide sequence.  
XX  
XX  
KM Specific binding assay; DNAJ; analyte determination; antigen;  
KM hapten; drug; cancer marker; pesticide; chemiluminescent compound;  
KM pollutant; ss.  
XX  
XX Escherichia coli.  
OS  
XX  
PN EP984282-A2.  
XX  
PD 08-MAR-2000.  
XX  
PF 21-MAY-1992; 99EP-0121551.  
XX  
XX  
PR 22-MAY-1991; 91US-0704569.  
PR 20-JUN-1991; 91US-0718490.  
PR 21-MAY-1992; 92EP-0304630.  
XX  
XX (DADE-) DADE BEHRING MARBURG GMBH.  
PA  
PI Ullman EF, Kirakossian H, Pease JS, Wagner DB, Daniloff Y;  
XX

DR WPI; 2000-225922/20.  
XX  
XX Particles containing a chemiluminescent donor and a fluorescent  
PR acceptor are useful in specific binding assays to determine antigens,  
PT haptens, enzymes, hormones, cancer markers or nutritional markers -  
XX  
XX Example 5; Page 66; 79pp; English.  
XX  
XX This sequence represents a fragment of the Escherichia coli DNAJ gene.  
CC The fragment is used as an example target sequence in a method for  
CC determining analyte in a sample using the particles of the invention. The  
CC invention relates to particles (I) containing a compound (II) and a  
CC fluorescent compound (III). Compound II reacts with singlet oxygen to  
CC form a metastable intermediate that can decompose with simultaneous or  
CC subsequent emission of light. The fluorescent compound (III) is excited  
CC by activated compound (II) and emits at a wavelength longer than the  
CC emission wavelength of compound (II). The particles are useful in  
CC specific binding assays. The assays can be used to determine antigens or  
CC haptens, e.g. blood group or HLA antigens or bacterial, fungal, protozoal  
CC or viral antigens, other proteins e.g. immunoglobulins, cytokines,  
CC enzymes, hormones, cancer markers or nutritional markers, microorganisms,  
CC drugs, metabolites, pesticides, pollutants or polynucleotides. The longer  
CC emission wavelength of (III) eliminates interference from serum  
CC components when the particles are used in specific binding assays in the  
CC presence of such components.  
XX  
SQ Sequence 50 BP; 10 A; 12 C; 23 G; 5 T; 0 other;  
Query Match 71.0%; Score 14.2; DB 21; Length 50;  
Best Local Similarity 84.2%; Pred. No. 5.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GACGAGCGCGACGACGCGC 20  
DB 13 GAAGCGCGCGACGACGCGC 31  
RESULT 12  
ID AAS48592/C  
XX AAS48592 standard; DNA; 60 BP.  
XX  
AC AAS48592;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
XX  
DE Pseudomonas aeruginosa cellular proliferation inhibitory sequence #78.  
XX  
XX  
KM Antisense; ss; prokaryotic cellular proliferation;  
KM antibiotic; antibacterial; drug design.  
XX  
XX Pseudomonas aeruginosa.  
OS  
XX  
PN WO200170955-A2.  
XX  
PD 27-SEP-2001.  
XX  
XX  
PF 21-MAR-2001; 2001WO-US09180.  
XX  
XX  
PR 21-MAR-2000; 2000US-191078P.  
PR 23-MAY-2000; 2000US-206848P.  
PR 26-MAY-2000; 2000US-207727P.  
PR 23-OCT-2000; 2000US-242578P.  
PR 27-NOV-2000; 2000US-253625P.  
PR 22-DEC-2000; 2000US-257931P.  
PR 16-FEB-2001; 2001US-269308P.  
XX  
XX (ELIT-) ELITRA PHARM INC.  
PA  
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
XX Yamamoto RT, Xu HH;  
XX WPI; 2001-611495/70.  
XX

PT New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids -  
PS Claim 1: Seq ID No 1169; 511pp; English.  
XX  
XX The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the  
CC genes, their use in the discovery of novel antibiotics, the essential  
CC genes themselves and the encoded proteins. The prokaryotes used are  
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella  
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The  
CC invention is also useful for the identification of potential new targets  
CC for antibiotic development. The antisense nucleic acids can also be used  
CC to identify proteins used in proliferation, to express these proteins,  
CC and to obtain antibodies capable of binding to the expressed proteins.  
CC The proteins can be used to screen compounds in rational drug discovery  
CC programmes. The antisense nucleic acid sequence is also useful to screen  
CC for homologous nucleic acids which are required for cell proliferation in  
CC a wide variety of organisms. The present sequence is an antisense  
CC oligonucleotide of the invention.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 60 BP; 3 A; 22 C; 23 G; 12 T; 0 other;  
Query Match 71.0%; Score 14.2; DB 23; Length 60;  
Best Local Similarity 84.2%; Pred. No. 5.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 GGACGAGGGCGACGCGC 19  
DB 47 GGACGAGGGCGACGCGC 29  
RESULT 13  
AAS48615/C  
ID AAS48615 standard; DNA; 60 BP.  
XX  
XX AAS48615;  
AC  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE Pseudomonas aeruginosa cellular proliferation inhibitory sequence #101.  
XX  
KW Antisense; ss; prokaryotic cellular proliferation;  
KW antibiotic; antibacterial; drug design.  
XX  
OS Pseudomonas aeruginosa.  
XX  
PN WO200170955-A2.  
XX  
PD 27-SEP-2001.  
XX  
PE 21-MAR-2001; 2001WO-US09180.  
XX  
PF 21-MAR-2000; 2000US-191078P.  
PR 23-MAY-2000; 2000US-206848P.  
PR 26-MAY-2000; 2000US-207272P.  
PR 23-OCT-2000; 2000US-242578P.  
PR 27-NOV-2000; 2000US-253625P.  
PR 22-DEC-2000; 2000US-257931P.  
PR 16-FEB-2001; 2001US-269308P.  
XX  
XX (ELITRA PHARM INC.  
PA  
XX  
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
XX  
DR WPI: 2001-611495/70.  
XX  
PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -  
XX  
XX Claim 1: Seq ID No 1192; 511pp; English.  
PS  
XX  
XX The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the  
CC genes, their use in the discovery of novel antibiotics, the essential  
CC genes themselves and the encoded proteins. The prokaryotes used are  
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella  
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The  
CC invention is also useful for the identification of potential new targets  
CC for antibiotic development. The antisense nucleic acids can also be used  
CC to identify proteins used in proliferation, to express these proteins,  
CC and to obtain antibodies capable of binding to the expressed proteins.  
CC The proteins can be used to screen compounds in rational drug discovery  
CC programmes. The antisense nucleic acid sequence is also useful to screen  
CC for homologous nucleic acids which are required for cell proliferation in  
CC a wide variety of organisms. The present sequence is an antisense  
CC oligonucleotide of the invention.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 60 BP; 3 A; 22 C; 23 G; 12 T; 0 other;  
Query Match 71.0%; Score 14.2; DB 23; Length 60;  
Best Local Similarity 84.2%; Pred. No. 5.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 GGACGAGGGCGACGCGC 19  
DB 47 GGACGAGGGCGACGCGC 29  
RESULT 14  
AA085876/C  
ID AA085876 standard; DNA; 66 BP.  
XX  
XX AA085876;  
AC  
XX  
DT 06-NOV-1995 (first entry)  
XX  
DE "CTAATC-30mer" modified tailed 30 mer oligonucleotide.  
XX  
KW CTAATC-30mer; nucleic acid detection method; probe; ss.  
XX  
OS Synthetic.  
XX  
PN WO9506877-A.  
XX  
PD 09-MAR-1995.  
XX  
PF 29-AUG-1994; 94WO-US09705.  
XX  
PR 03-SEP-1993; 93US-0117365.  
XX  
XX (SYNTEX USA INC.  
PA  
XX  
PI Davalian D, Singh R, Ullman EF;  
PI WPI: 1995-115552/15.  
XX  
DR  
XX  
PT Determ of specific binding analyte using photo-sensitiser to  
PT generate singlet oxygen - which converts precursor to  
PT photoactive indicator when irradiated, also new precursor cpds,  
PT useful in immunoassays and nucleic acid hybridisation assays  
XX  
XX Example 1; Page 50; 72pp; English.  
PS  
XX  
XX AA085874-085877 are modified oligonucleotide probes, used to  
CC demonstrate a new nucleic acid detection method.  
CC  
XX

SQ Sequence 66 BP; 14 A; 26 C; 8 G; 18 T; 0 other;

Query Match 71.0%; Score 14.2; DB 16; Length 66;  
 Best Local Similarity 84.2%; Pred. No. 5.5e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGCGCAGCAGCGC 20  
 ||| ||||| ||||| |||||  
 DB 28 GAAGCGGCGCAGCATGGCG 10

## RESULT 15

AAV60517  
 ID AAV60517 standard; DNA; 60 BP.

AC AAV60517;

DT 08-DEC-1998 (first entry)

DE Cloned Factor X-binding aptamer sequence.

KM Factor X; aptamer; therapeutic; diagnosis; secondary; ss.

OS Synthetic.

PN US5756291-A.

PD 26-MAY-1998.

PF 07-JUN-1995; 95US-0484192.

PR 21-AUG-1992; 92US-0934387.

PR 21-FEB-1992; 92WO-US01383.

PR 07-JUN-1995; 95US-0484192.

PA (GILE-) GILEAD SCI INC.

PI Albrecht G, Griffin L, Latham J, Leung L, Toole JJ;

PI Vermaas E;

DR WPI; 1998-321524/28.

PT Assay for thrombin and purification of thrombin - using DNA aptamer

PS Example 22; Fig 6; 115pp; English.

CC AAV60515-47 represent cloned Factor X-binding aptamers. The Factor

CC X-binding aptamers are identified using the method of the Factor

CC invention. The specification describes a method for identifying

CC oligomer sequences which specifically bind target molecules such

CC as serum proteins, kinins, eicosanoids and extracellular proteins.

CC The method involves complexation of the target molecule with a

CC mixture of oligonucleotides containing random sequences and sequences

CC which serve as primer for PCR amplification. A complex is only formed

CC with specifically binding oligonucleotide sequences. The complex is

CC isolated, and complexed members of the oligonucleotide mixture are

CC recovered by PCR. The method can be used to generate aptamers that can

CC be used for therapeutic and diagnostic purposes, and for generating

CC secondary aptamers.

SQ Sequence 60 BP; 13 A; 6 C; 32 G; 9 T; 0 other;

Query Match 69.0%; Score 13.8; DB 19; Length 60;

Best Local Similarity 88.2%; Pred. No. 8e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAAGAGGCGCAGCAGC 17  
 ||| ||||| ||||| |||||

DB 28 GGAAGAGGCGCAGCAGC 44

Search completed: November 23, 2002, 06:28:34  
 Job time : 102.6 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:53:51 : Search time 21.55 Seconds  
(Without alignments)  
284.619 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20

Sequence: 1 gagcagagcgagcagcagcg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued\_Patents\_NA:\*  
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2: /cgn2\_6/ptodata/1/1na/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/1na/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/1na/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/1na/PCBUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/1na/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	71.0	30	1	US-07-718-490-2
2	14.2	71.0	50	1	US-07-718-490-1
3	14.2	71.0	65	1	US-08-479-743-5
4	14.2	71.0	65	5	PCT-US94-09705-5
5	14.2	71.0	66	1	US-08-479-743-3
6	14.2	71.0	66	5	PCT-US94-09705-3
7	13.6	68.0	60	1	US-08-484-192-151
8	13.6	68.0	30	1	US-08-428-370A-12
9	13.6	68.0	30	2	US-08-600-764-12
10	13.2	66.0	21	2	US-08-816-105A-3
11	13.2	66.0	31	4	US-09-657-453A-6
12	13.2	66.0	60	1	US-08-484-192-150
13	13.2	66.0	37	4	US-09-344-888A-19
14	12.6	63.0	23	1	US-08-064-271-8
15	12.6	63.0	23	3	US-08-930-589A-8
16	12.6	63.0	23	4	US-09-599-781-8
17	12.6	63.0	24	4	US-09-182-450-15
18	12.6	63.0	25	4	US-09-323-873A-30
19	12.6	63.0	31	1	US-08-623-891-12
20	12.6	63.0	31	4	US-09-340-861-12
21	12.6	63.0	31	4	US-09-634-262-12
22	12.6	63.0	45	1	US-08-594-808B-3
23	12.6	63.0	45	1	US-08-718-504-50
24	12.6	63.0	45	5	PCT-US95-10973A-43
25	12.6	63.0	48	4	US-08-979-608A-36
26	12.6	63.0	51	1	US-08-594-808B-1
27	12.6	63.0	67	2	US-08-888-497-23

28	12.6	63.0	67	4	US-09-362-230-23	Sequence 23, Appl
29	12.6	63.0	67	5	PCT-US94-07926-23	Sequence 23, Appl
30	12.6	63.0	72	6	5198345-25	Patent No. 5198345
31	12.6	63.0	73	1	US-07-982-712-12	Sequence 12, Appl
32	12.6	63.0	75	3	US-08-718-904-49	Sequence 49, Appl
33	12.6	63.0	75	5	PCT-US95-10973A-42	Sequence 42, Appl
34	12.6	63.0	84	2	US-08-374-552C-93	Sequence 93, Appl
35	12.6	63.0	84	2	US-08-374-552C-94	Sequence 94, Appl
36	12.6	63.0	84	4	US-08-979-608A-37	Sequence 37, Appl
37	12.4	62.0	30	4	US-08-793-701-16	Sequence 16, Appl
38	12.4	62.0	63	5	PCT-US95-13975-49	Sequence 49, Appl
39	12.4	62.0	84	4	US-09-404-390-7	Sequence 7, Appl
40	12.2	61.0	18	3	US-09-106-038A-89	Sequence 89, Appl
41	12.2	61.0	25	1	US-08-211-430-5	Sequence 5, Appl
42	12.2	61.0	25	2	US-08-887-798-17	Sequence 17, Appl
43	12.2	61.0	37	1	US-08-640-304-1	Sequence 1, Appl
44	12.2	61.0	37	1	US-08-190-103-1	Sequence 1, Appl
45	12.2	61.0	37	1	US-08-256-966-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-07-718-490-2/c  
Sequence 2, Application US/07718490  
Patent No. 5340716  
GENERAL INFORMATION:  
APPLICANT: Ullman, Edwin F.  
APPLICANT: Kirakossian, Hrair  
APPLICANT: Pease, John S.  
APPLICANT: Danilo, Yuri  
APPLICANT: Wagner, Daniel B.  
TITLE OF INVENTION: Assay Method Utilizing Photoactivated  
TITLE OF INVENTION: Chemiluminescent Label  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syntex (U.S.A.) Inc.  
STREET: 3401 Hillview Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07718,490  
FILING DATE: 19910620  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Leterey, Theodore J.  
REGISTRATION NUMBER: 28,319  
TELEPHONE: (415) 852-1091  
TELEFAX: (415) 496-3529  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: Escherichia coli  
STRAIN: K12 DNAJ  
INDIVIDUAL ISOLATE: Synthetic

US-07-718-490-2

Query Match 71.0%; Score 14.2; DB 1; Length 30;  
Best Local Similarity 84.2%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGCGGCGAGCAGCGCG 20  
||| ||||| |||||  
Db 28 GAAGCGGCGGCGAGCATGCGC 10

RESULT 2

US-07-718-490-1  
; Sequence 1, Application US/07718490  
; Patent No. 5340716  
; GENERAL INFORMATION:  
; APPLICANT: Ullman, Edwin F.  
; APPLICANT: Kirakosian, Hrair  
; APPLICANT: Pease, John S.  
; APPLICANT: Daniloff, Yuri  
; APPLICANT: Wagner, Daniel B.  
; TITLE OF INVENTION: Assay Method Utilizing Photoactivated  
; TITLE OF INVENTION: Chemiluminescent Label  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Syntex (U.S.A.) Inc.  
; STREET: 3401 Hillview Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/718,490  
; FILING DATE: 19910620  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Leitner, Theodore J.  
; REGISTRATION NUMBER: 28,319  
; REFERENCE/DOCKET NUMBER: 27340/ DO-1557  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 852-1091  
; TELEFAX: (415) 496-3529  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)T  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: Internal  
; ORIGINAL SOURCE:  
; ORGANISM: Escherichia coli  
; STRAIN: K12 DNAJ  
; INDIVIDUAL ISOLATE: Synthetic  
; US-07-718-490-1

Query Match 71.0%; Score 14.2; DB 1; Length 50;  
Best Local Similarity 84.2%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGCGGCGAGCAGCGCG 20  
||| ||||| |||||  
Db 13 GAAGCGGCGGCGAGCATGCGC 31

RESULT 3  
US-08-479-743-5

; Sequence 5, Application US/08479743  
; Patent No. 5807675  
; GENERAL INFORMATION:  
; APPLICANT: Davallian, Dariush  
; APPLICANT: Singh, Rajendra  
; APPLICANT: Ullman, Edwin F.  
; TITLE OF INVENTION: Fluorescent Oxygen Channeling Assays  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Syntex (U.S.A.) Inc.  
; STREET: 3401 Hillview Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,743  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117,365  
; FILING DATE: 03-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Roth, Carol J.  
; REGISTRATION NUMBER: 32,783  
; REFERENCE/DOCKET NUMBER: 27870  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 852-1698  
; TELEFAX: (415) 496-3529  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 65 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: synthetic  
; US-08-479-743-5

Query Match 71.0%; Score 14.2; DB 1; Length 65;  
Best Local Similarity 84.2%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGCGGCGAGCAGCGCG 20  
||| ||||| |||||  
Db 3 GAAGCGGCGGCGAGCATGCGC 21

RESULT 4  
PCT-US94-09705-5

; Sequence 5, Application PC/TUS9409705  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: FLUORESCENT OXYGEN CHANNELING IMMUNOASSAYS  
; NUMBER OF SEQUENCES: 5  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/09705  
; FILING DATE: 29-AUG-1994  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 65 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: synthetic  
PCT-US94-09705-5

Query Match 71.0%; Score 14.2; DB 5; Length 65;  
Best Local Similarity 84.2%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACGAGGCGGACGACGCG 20  
Db 3 GAAGCGGCGGACATGCG 21

## RESULT 5

US-08-479-743-3/C  
Sequence 3, Application US/08479743  
Patent No. 5807675  
GENERAL INFORMATION:  
APPLICANT: Davallan, Darlush  
APPLICANT: Singh, Rajendra  
APPLICANT: Ullman, Edwin F.  
TITLE OF INVENTION: Fluorescent Oxygen Channeling Assays  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syntex (U.S.A.) Inc.  
STREET: 3401 Hillview Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,743  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117,365  
FILING DATE: 03-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Roth, Carol J.  
REGISTRATION NUMBER: 32,783  
REFERENCE/DOCKET NUMBER: 27870  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 852-1698  
TELEFAX: (415) 496-3529  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 66 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: synthetic  
US-08-479-743-3

Query Match 71.0%; Score 14.2; DB 1; Length 66;  
Best Local Similarity 84.2%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACGAGGCGGACGACGCG 20  
Db 28 GAAGCGGCGGACATGCG 10

## RESULT 6

PCT-US94-09705-3/C  
Sequence 3, Application PC/TUS94409705  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: FLUORESCENT OXYGEN CHANNELING IMMUNOASSAYS  
NUMBER OF SEQUENCES: 5  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09705  
FILING DATE: 29-AUG-1994  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 66 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: synthetic  
PCT-US94-09705-3

Query Match 71.0%; Score 14.2; DB 5; Length 66;  
Best Local Similarity 84.2%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACGAGGCGGACGACGCG 20  
Db 28 GAAGCGGCGGACATGCG 10

## RESULT 7

US-08-484-192-151  
Sequence 151, Application US/08484192  
Patent No. 5756291  
GENERAL INFORMATION:  
APPLICANT: GRIFFIN, LINDA C.  
APPLICANT: ALBRECHT, GLENN  
APPLICANT: LATHAM, JOHN  
APPLICANT: LEUNG, LAWRENCE  
APPLICANT: VERMAAS, ERIC  
APPLICANT: TOOLE, JOHN J.  
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND  
METHODS OF MAKING  
NUMBER OF SEQUENCES: 181  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,192  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-484-192-151

Query Match      69.0%; Score 13.8; DB 1; Length 60;
Best Local Similarity 88.2%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGACGAGGGGACGACG 17
DB      28 GGAGAGGGGACGACG 44

RESULT 8
US-08-428-370A-12
; Sequence 12, Application US/08428370A
; Patent No. 5569583
; GENERAL INFORMATION:
; APPLICANT: Greenberg, Steven J.
; APPLICANT: Evans, Mary Jo
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Herpesviruses
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One Mt Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,370A
; FILING DATE: 25/04/95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716)856-4000
; TELEFAX: 716-849-0349
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Herpes simplex virus 2
; FEATURE:
; LOCATION: Polymerase gene sequence bases 2268-2297
US-08-428-370A-12

Query Match      68.0%; Score 13.6; DB 1; Length 30;
```

```

; Best Local Similarity 80.0%; Pred. No. 2.1e+03;
; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGACGAGGGGACGACGGC 20
DB      1 GGACGGGGACGACGCGG 20

RESULT 9
US-08-600-764-12
; Sequence 12, Application US/08600764
; Patent No. 5846706
; GENERAL INFORMATION:
; APPLICANT: Greenberg, Steven J.
; APPLICANT: Evans, Mary Jo
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Herpesviruses
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One Mt Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,764
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,370
; FILING DATE: 25/04/95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716)856-4000
; TELEFAX: 716-849-0349
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Herpes simplex virus 2
; FEATURE:
; LOCATION: Polymerase gene sequence bases 2268-2297
US-08-600-764-12

Query Match      68.0%; Score 13.6; DB 2; Length 30;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGACGAGGGGACGACGGC 20
DB      1 GGACGGGGACGACGCGG 20

RESULT 10
US-08-816-105A-3
; Sequence 3, Application US/08816105A
; Patent No. 5989882
; GENERAL INFORMATION:
; APPLICANT: Crueger, Anneliese; Dellweg, Hans-Georg; Lenz,
; APPLICANT: Jurgen; Schroder, Werner; Pape, Hermann;
```



```

1  APPLICANT: Goeke, Klaus; Schaper, Beate; Hemker, Michael;
2  APPLICANT: Piepersberg, Wolfgang; Distler, Jürgen;
3  APPLICANT: Straumann, Ansgar
4  TITLE OF INVENTION: PROCESSES FOR PREPARING ACARYOSYL
5  TITLE OF INVENTION: TRANSFERASE AND FOR USING IT IN THE
6  TITLE OF INVENTION: CONVERSION OF ACAROSE HOMOLOGUES
7  TITLE OF INVENTION: INTO ACAROSE, FOR THE PREPARATION
8  TITLE OF INVENTION: OF ACAROSE HOMOLOGUES
9  NUMBER OF SEQUENCES: 16
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Sprung Kramer Schaefer & Briscoe
12 STREET: 660 White Plains Road
13 CITY: Tarrytown
14 STATE: New York
15 COUNTRY: USA
16 ZIP: 10591-5144
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Diskette, 3.50 Inch, 1.4 MB storage
19 COMPUTER: Apple Macintosh 6500
20 OPERATING SYSTEM: System 7.5
21 SOFTWARE: WordPerfect 3.5
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/816,105A
24 FILING DATE: 14-MAR-1997
25 CLASSIFICATION: 435
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: DE 19625269.5
28 FILING DATE: 25-JUN-1996
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: DE 19611252.4
31 FILING DATE: 22-MAR-1996
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Kurt G. Briscoe
34 REGISTRATION NUMBER: 33,141
35 REFERENCE/DOCKET NUMBER: Bayer 9814-KGB
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (914) 332-1700
38 TELEFAX: (914) 332-1844
39 INFORMATION FOR SEQ ID NO: 3:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 21 nucleotides
42 TYPE: nucleic acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45 US-08-816-105A-3
46
47 Query Match 66.0%; Score 13.2; DB 2; length 21;
48 Best Local Similarity 83.3%; Pred. No. 3.1e+03;
49 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
50
51 QY 3 ACGAGCGCAGCAGCGCG 20
52 ||||| ||||| |||||
53 Db 1 ACAGGCGCGAGCAGCGCG 18
54
55 RESULT 11
56 US-09-657-453A-6
57 Sequence 6, Application US/09657453A
58 Patent No. 6458591
59 GENERAL INFORMATION:
60 APPLICANT: Brett P. Monia
61 APPLICANT: Jacqueline Wyatt
62 TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHORYLASE KINASE ALPHA 2 EXPRESSION
63 FILE REFERENCE: RTS-0136
64 CURRENT APPLICATION NUMBER: US/09/657,453A
65 CURRENT FILING DATE: 2000-09-07
66 NUMBER OF SEQ ID NOS: 105
67 SEQ ID NO 6
68 LENGTH: 31
69 TYPE: DNA
70 ORGANISM: Artificial Sequence
71 FEATURE:
72 OTHER INFORMATION: PCR Probe

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US-09-657-453A-6
Query Match 66.0%; Score 13.2; DB 4; Length 31;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGCGACGACGCG 19
   |||||||
DB 2 GATGAGGTGAGACACTGC 19

RESULT 12
US-08-484-192-150
; Sequence 150, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; TITLE OF INVENTION: METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOENSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-484-192-150

Query Match 66.0%; Score 13.2; DB 1; Length 60;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGGCGACGACG 18
   |||
DB 28 GGAGAGGCGCGAGACG 45

RESULT 13
US-09-344-888A-19/c
; Sequence 19, Application US/09344888A
; Patent No. 6291245

```

```
; GENERAL INFORMATION:
; APPLICANT: Kopetzki, Erhard
; APPLICANT: Schantz, Christian
; TITLE OF INVENTION: New Host-Vector System
; FILE REFERENCE: CD20315
; CURRENT APPLICATION NUMBER: US/09/344,888A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: EP98113156.8
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EP98119078.8
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 19
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-344-888A-19

Query Match          65.0%; Score 13; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 GGCAGACACGGCG 20
        |||||
Db       30 GGCAGACACGGCG 18

RESULT 14
US-08-064-271-8/c
; Sequence 8, Application US/08064271
; Patent No. 5543297
; GENERAL INFORMATION:
; APPLICANT: Kennedy, Brian P.
; APPLICANT: Cromlish, Wanda A.
; APPLICANT: Mancini, Joseph A.
; APPLICANT: O'Neill, Gary
; APPLICANT: Vickers, Philip J.
; APPLICANT: Wong, Elizabeth
; TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-2 CDNA AND
; TITLE OF INVENTION: ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in, 1.4kb
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7
; SOFTWARE: Microsoft Word 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064,271
; FILING DATE: 19930506
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Panzer, Curtis C.
; REGISTRATION NUMBER: 33,752
; REFERENCE/DOCKET NUMBER: 189061A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3199
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: DNA (genomic)
US-08-064-271-8

Query Match          63.0%; Score 12.6; DB 1; Length 23;
Best Local Similarity 78.9%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGACGAGGGCGACGCGC 19
        |||||
Db       21 GGCAGCGGGCGACATCGC 3

RESULT 15
US-08-930-589A-8/c
; Sequence 8, Application US/08930589A
; Patent No. 6107087
; GENERAL INFORMATION:
; APPLICANT: MERCK FROSST CANADA & CO.
; APPLICANT: O'NEILL, GARY P.
; APPLICANT: MANCINI, JOSEPH A.
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
; TITLE OF INVENTION: CYCLOOXYGENASE-2
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,589A
; FILING DATE: 28-JUN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coppola, Joseph A.
; REGISTRATION NUMBER: 38,413
; REFERENCE/DOCKET NUMBER: 19029PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-6734
; TELEFAX: 732-594-4720
; TEXT:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-930-589A-8

Query Match          63.0%; Score 12.6; DB 3; Length 23;
Best Local Similarity 78.9%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGACGAGGGCGACGCGC 19
        |||||
Db       21 GGCAGCGGGCGACATCGC 3

Search completed: November 23, 2002, 06:35:59
Job time : 22.55 secs
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:54:41 : Search time 17.25 Seconds  
(Without alignments)  
439.108 Million cell updates/sec

Title: US-09-296-264-3  
Perfect score: 20  
Sequence: 1 ggcagggcgagcagcgcg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 195614

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	40	9	US-10-015-536-13
2	14.2	71.0	45	9	US-09-908-1538-26
3	14.2	71.0	60	10	US-09-815-242-1169
4	14.2	71.0	60	10	US-09-815-242-1192
5	13.6	68.0	37	10	US-09-894-633A-29
6	13.4	67.0	50	9	US-09-905-291A-89
7	13.4	67.0	50	10	US-09-909-320-89
8	13.4	67.0	50	10	US-09-909-320-89
9	13.4	67.0	50	10	US-09-909-320-89
10	12.8	64.0	27	10	US-09-772-655-4
11	12.6	63.0	25	10	US-09-969-373-679
12	12.6	63.0	25	10	US-09-780-308-15
13	12.6	63.0	34	10	US-09-852-922-6
14	12.6	63.0	34	10	US-09-852-922-7
15	12.6	63.0	48	10	US-09-962-055-36
16	12.6	63.0	48	12	US-10-023-523-36
17	12.6	63.0	48	12	US-10-023-523-36
18	12.6	63.0	84	10	US-09-962-055-37
19	12.6	63.0	84	12	US-10-023-523-37

20	12.6	63.0	84	12	US-10-023-523-37	Sequence 37, Appl
21	12.6	63.0	90	9	US-09-971-980-17	Sequence 17, Appl
22	12.4	62.0	59	9	US-08-933-797-527	Sequence 527, Appl
23	12.2	61.0	31	10	US-09-801-274-1524	Sequence 1524, Ap
24	12.2	61.0	46	10	US-09-972-331-6	Sequence 6, Appl1
25	12.2	61.0	46	10	US-09-972-331-20	Sequence 20, Appl
26	12.2	61.0	51	9	US-09-908-1538-16	Sequence 16, Appl
27	12.2	61.0	88	10	US-09-923-876-1505	Sequence 1505, Ap
28	12.2	61.0	94	10	US-09-294-0938-4852	Sequence 4852, Ap
29	12.2	61.0	98	10	US-09-969-373-1435	Sequence 1435, Ap
30	12	60.0	18	10	US-09-962-055-35	Sequence 35, Appl
31	12	60.0	18	12	US-10-023-523-35	Sequence 35, Appl
32	12	60.0	18	12	US-10-023-523-35	Sequence 35, Appl
33	12	60.0	59	10	US-09-923-217-976	Sequence 976, App
34	12	60.0	59	10	US-09-833-263-976	Sequence 976, App
35	12	60.0	60	10	US-09-862-055-18	Sequence 18, Appl
36	12	60.0	60	12	US-10-023-523-18	Sequence 18, Appl
37	12	60.0	60	12	US-10-023-523-18	Sequence 18, Appl
38	12	60.0	86	10	US-09-867-701-3669	Sequence 3669, Ap
39	12	60.0	90	12	US-10-023-523-34	Sequence 34, Appl
40	12	60.0	90	12	US-10-023-523-34	Sequence 34, Appl
41	12	60.0	90	12	US-10-023-523-34	Sequence 34, Appl
42	12	60.0	93	10	US-09-998-598-2578	Sequence 2578, Ap
43	12	60.0	99	10	US-09-969-373-880	Sequence 880, App
44	11.8	59.0	45	10	US-09-742-693-2	Sequence 2, Appl1
45	11.8	59.0	85	10	US-09-062-104A-10	Sequence 10, Appl

## ALIGNMENTS

RESULT 1  
US-10-015-536-13/c  
Sequence 13, Application US/10015536  
Patent No. US20020165149A1  
GENERAL INFORMATION:  
APPLICANT: Krantz, David M.  
APPLICANT: Starwalt, Scott  
TITLE OF INVENTION: Mutated Class II Major Histocompatibility Proteins  
FILE REFERENCE: 103-00  
CURRENT APPLICATION NUMBER: US/10/015,536  
CURRENT FILING DATE: 2001-12-10  
PRIOR APPLICATION NUMBER: 60/254,248  
PRIOR FILING DATE: 2000-12-08  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 13  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-015-536-13

Query Match 71.0%; Score 14.2; DB 9; Length 40;  
Best Local Similarity 84.2%; Pred. No. 5.9e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Caps 0;

QY 2 GACGAGGCGGCGCGCG 20  
DB 39 GACGTGGCGGATCCGCG 21

RESULT 2  
US-09-908-1538-26  
Sequence 26, Application US/099081538  
Patent No. US20020168714A1  
GENERAL INFORMATION:  
APPLICANT: Barbas, Carlos F.  
APPLICANT: Beerli, Roger  
APPLICANT: Schopfer, Ulrich

```

; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING
; TITLE OF INVENTION: SINGLE-CHAIN, MONOMERIC, LIGAND DEPENDENT POLYPEPTIDE
; TITLE OF INVENTION: SWITCHES
; FILE REFERENCE: TSRI 725.1
; CURRENT APPLICATION NUMBER: US/09/908,153B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 09/619,063
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 45
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: Synthesized
; US-09-908-153B-26

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Query Match          71.0%; Score 14.2; DB 9; Length 45;
Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```
QY 1 GGACGAGGGCGACGCGC 19
    ||| ||||| || |||
DB 3 GGAGGAGGGCGGCGCGC 21

```

```

RESULT 3
; US-09-815-242-1169/c
; Sequence 1169, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1169
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-815-242-1169

```

```

Query Match          71.0%; Score 14.2; DB 10; Length 60;
Best Local Similarity 84.2%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```
QY 1 GGACGAGGGCGACGCGC 19
    ||| ||||| ||||| |

```

```
DB 47 GGACGAGGGCGGCGCGCC 29

```

## RESULT 4

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; US-09-815-242-1192/c
; Sequence 1192, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1192
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-815-242-1192

```

```

Query Match          71.0%; Score 14.2; DB 10; Length 60;
Best Local Similarity 84.2%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```
QY 1 GGACGAGGGCGGCGCGCC 19
    ||| ||||| ||||| |
DB 47 GGACGAGGGCGGCGCGCC 29

```

## RESULT 5

```

; US-09-894-633A-29
; Sequence 29, Application US/09894633A
; Patent No. US20020124285A1
; GENERAL INFORMATION:
; APPLICANT: Comer, Timothy
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRE
; FILE REFERENCE: 38-21(15856)B
; CURRENT APPLICATION NUMBER: US/09/894,633A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/214,357
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 09/894,633
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 37

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;; TYPE: DNA  
;; ORGANISM: artificial sequence  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)..(37)  
;; OTHER INFORMATION: synthetic primer sequence  
US-09-894-633A-29

Query Match 68.0%; Score 13.6; DB 10; Length 37;  
Best Local Similarity 80.0%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGACGAGGCGACGACGCG 20  
||||| ||| |||||  
DB 14 GGACGAGGAGGAGCGCGCG 33

RESULT 6  
US-09-905-291A-89  
; Sequence 89, Application US/09905291A  
; Patent No. US20020160374A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/905,291A  
; CURRENT FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313

;; PRIOR FILING DATE: 1999-11-30  
;; PRIOR APPLICATION NUMBER: PCT/US99/28564  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/28565  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: PCT/US99/30911  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
;; PRIOR FILING DATE: 2000-01-05  
;; NUMBER OF SEQ ID NOS: 423  
;; SEQ ID NO 89  
;; LENGTH: 50  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-905-291A-89

Query Match 67.0%; Score 13.4; DB 9; Length 50;  
Best Local Similarity 93.3%; Pred. No. 1.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GACGAGGCGACGAC 16  
||||| ||| |||||  
DB 10 GACGAGGCGGACTAC 24

RESULT 7  
US-09-909-320-89  
; Sequence 89, Application US/09909320  
; Patent No. US2002013240A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/909,320  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 89  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-909-920-89

Query Match 67.0%; Score 13.4; DB 10; Length 50;  
Best Local Similarity 93.3%; Pred. No. 1.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GACGAGGCGAGCAGC 16  
|||||  
Db 10 GACGAGGCGAGGATAC 24

RESULT 8  
US-09-909-088B-89  
Sequence 89, Application US/0909088B  
Patent No. US20020146709A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Gueney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/909, 088B  
CURRENT FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 89  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-909-088B-89

Query Match 67.0%; Score 13.4; DB 10; Length 50;  
Best Local Similarity 93.3%; Pred. No. 1.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GACGAGGCGAGCAGC 16  
|||||  
Db 10 GACGAGGCGAGGATAC 24

RESULT 9  
US-09-772-656-4  
Sequence 4, Application US/09772656  
Patent No. US20010049832A1  
GENERAL INFORMATION:  
APPLICANT: Bruce, Wesley B.  
TITLE OF INVENTION: Root Transcriptional Factor  
FILE REFERENCE: 1167R  
CURRENT APPLICATION NUMBER: US/09/772,656  
CURRENT FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/178,916

; PRIOR FILING DATE: 2000-02-01  
; PRIOR APPLICATION NUMBER: US Unknown  
; PRIOR FILING DATE: 2001-01-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-772-656-4

Query Match  
Best Local Similarity 83.3%; Score 13.2; DB 10; Length 27;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACGAGGCGCAGCAGCGC 19  
Db 5 GCGGAGCGCGCAGCAAGCG 22

RESULT 10  
US-09-969-373-679/c  
; Sequence 679, Application US/09969373  
; Patent No. US20020133852A1  
; GENERAL INFORMATION:  
; APPLICANT: Effertz, Roger J.  
; APPLICANT: Hauge, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 679  
; LENGTH: 96  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-679

Query Match  
Best Local Similarity 87.5%; Score 12.8; DB 10; Length 96;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GACGAGGCGCAGCAGC 17  
Db 71 GACGAGCGCAGCAGCAGC 56

RESULT 11  
US-09-780-053-15/c  
; Sequence 15, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eld  
; APPLICANT: Mary Paris  
; APPLICANT: Eliana Levin  
; APPLICANT: Steve Chappell Mitchell  
; TITLE OF INVENTION: 83P564: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.5US01  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-780-053-15

Query Match  
Best Local Similarity 78.9%; Score 12.6; DB 10; Length 25;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GACGAGGCGCAGCAGCGC 20  
Db 23 GTCGAGCAGCAGCGCGCG 5

RESULT 12  
US-09-779-308-15/c  
; Sequence 15, Application US/09779308  
; Patent No. US20020150972A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Paris  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eld  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Eliana Levin  
; APPLICANT: Steve Chappell Mitchell  
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.4US01  
; CURRENT APPLICATION NUMBER: US/09/779,308  
; CURRENT FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 60/181,020  
; PRIOR FILING DATE: 2000-02-08  
; NUMBER OF SEQ ID NOS: 718  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-779-308-15

Query Match  
Best Local Similarity 78.9%; Score 12.6; DB 10; Length 25;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GACGAGGCGCAGCAGCGC 20  
Db 23 GTCGAGCAGCAGCGCGCG 5

RESULT 13  
US-09-852-922-6  
; Sequence 6, Application US/09852922  
; Patent No. US20020076768A1  
; GENERAL INFORMATION:  
; APPLICANT: TOYO BOSEKI KABUSHIKI KAISHA  
; TITLE OF INVENTION: MODIFIED THERMOSTABLE DNA POLYMERASE  
; FILE REFERENCE: 000053  
; CURRENT APPLICATION NUMBER: US/09/852,922  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 2000-138796  
; PRIOR FILING DATE: 2000-05-11  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 34  
; TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-852-922-6  
Query Match 63.0%; Score 12.6; DB 10; Length 34;  
Best Local Similarity 78.9%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 GACGAGGGCGAGCAGCGCG 20  
DB 13 GACGAGGGCGAGGAGTTTCG 31  
RESULT 14  
US-09-852-922-7/c  
Sequence 7, Application US/09852922  
Patent No. US20020076768A1  
GENERAL INFORMATION:  
APPLICANT: TOYO BOSEKI KABUSHIKI KAISHA  
TITLE OF INVENTION: MODIFIED THERMOSTABLE DNA POLYMERASE  
FILE REFERENCE: 000053  
CURRENT APPLICATION NUMBER: US/09/852,922  
PRIOR APPLICATION NUMBER: 2001-05-10  
PRIOR FILING DATE: 2000-05-11  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 34  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-852-922-7  
Query Match 63.0%; Score 12.6; DB 10; Length 34;  
Best Local Similarity 78.9%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 GACGAGGGCGAGCAGCGCG 20  
DB 22 GACGAGGGCGAGGAGTTTCG 4  
RESULT 15  
US-09-962-055-36  
Sequence 36, Application US/09962055  
Patent No. US20020052033A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Law, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/962,055  
FILING DATE: 24-Sep-2001

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...48  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-962-055-36  
Query Match 63.0%; Score 12.6; DB 10; Length 48;  
Best Local Similarity 78.9%; Pred. No. 2.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 GACGAGGGCGAGCAGCGCG 20  
DB 28 GACGAGGAGCAGCAGCAGC 46

Search completed: November 23, 2002, 06:42:02  
Job time : 18.25 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2002, 09:10:06 ; Search time 755.55 Seconds  
(without alignments)  
428.707 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20  
Sequence: 1 ggaagagagagagagagagcg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

EST:\*  
1: em\_estdb:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlun:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: gb\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_alter:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.2	76.0	79	9	AI0000040
2	14.8	74.0	87	10	AW064096
3	14.8	74.0	91	17	AZ919805
4	14.8	74.0	91	17	BH218633
5	14.4	72.0	64	9	AI900558
6	14.4	72.0	84	17	BH226921

Result No.	Score	Query Match	Length	ID	Description
7	14.2	71.0	80	10	AV920979
8	14.2	71.0	83	9	AI430740
9	14.2	71.0	89	10	BE264581
10	14.2	71.0	90	17	TA178C01P
11	13.8	69.0	79	17	BH407770
12	13.8	69.0	80	12	BF022188
13	13.8	69.0	85	13	BI855354
14	13.8	69.0	93	17	AZ848413
15	13.8	69.0	96	17	BH416254
16	13.6	68.0	43	9	AA663711
17	13.6	68.0	49	17	BH802890
18	13.6	68.0	50	9	AI03161
19	13.6	68.0	50	9	AI03162
20	13.6	68.0	50	9	AI03170
21	13.6	68.0	50	9	AI03171
22	13.6	68.0	50	9	AI03175
23	13.6	68.0	50	9	AI03176
24	13.6	68.0	50	9	AI03180
25	13.6	68.0	61	13	BI109390
26	13.6	68.0	67	10	AW246906
27	13.6	68.0	74	13	BM978652
28	13.6	68.0	77	14	BQ760479
29	13.6	68.0	79	14	BQ167594
30	13.6	68.0	82	9	AI682177
31	13.6	68.0	82	13	BI755472
32	13.6	68.0	87	14	F37066
33	13.6	68.0	89	17	BH414941
34	13.6	68.0	95	10	AV913999
35	13.6	68.0	95	10	BE470627
36	13.6	68.0	95	17	BH215460
37	13.6	68.0	97	17	AZ771502
38	13.6	68.0	100	14	BM872271
39	13.6	68.0	100	14	BQ759154
40	13.4	67.0	66	17	BH641036
41	13.2	66.0	69	17	AZ820652
42	13.2	66.0	77	13	BI963211
43	13.2	66.0	79	14	R87701
44	13.2	66.0	85	17	BH621101
45	13.2	66.0	88	9	AA467645

## ALIGNMENTS

RESULT 1  
LOCUS AI0000040  
DEFINITION os46c07.s1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1608396 3'  
similar to TR:015551 015551 RAT VENTRAL PROSTATE.1 HOMOLOG.  
;contains TARI.b1 MSRI repetitive element ;, mRNA sequence.

ACCESSION AI0000040  
VERSION AI0000040.1 GI:3190594  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bdrp/image/image.html



Db 34 GCACGAGCGCAGTACGG 17

RESULT 4  
LOCUS BH218633/c  
DEFINITION 1006080D10.x1 1006 - RescuenMu Grid G Zea mays genomic, DNA  
SEQUENCE.  
ACCESSION BH218633  
VERSION BH218633.1 GI:16811673  
KEYWORDS GSS.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
REFERENCE Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; PACC  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 91)  
WALBOT.V.  
Maize genomic sequences found using engineered RescuenMu transposon  
Unpublished (2001)  
AUTHORS Walbot V.  
JOURNAL  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Very probable ligation site found so sequence was trimmed.  
Post-ligation sequence submitted separately.  
Plate: 1006080 row: 28  
Class: transposon-tagged.

FEATURES  
source Location/Qualifiers  
1..91  
/organism="Zea mays"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/clone\_lib="1006 - RescuenMu Grid G"  
/issue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: leaf; Vector: RescuenMu (engineered from pluescript backbone); Site\_1: BamHI; Site\_2: BglII; RescuenMu is a 4.9 Kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuenMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescuenMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 7 a 22 c 33 g 29 t  
ORIGIN

Query Match 74.0%; Score 14.8; DB 17; Length 91;  
Best Local Similarity 88.9%; Pred. No. 3e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACGAGCGCAGCAGCGC 19  
|||||  
Db 77 GACGAGCGCAGCAGCGC 60

RESULT 5  
LOCUS A1900558/c  
DEFINITION 64 bp mRNA linear EST 30-NOV-2001  
SC07g10.y1 Gm-cl012 glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
Gm-cl012-1531 5' similar to SW:PSAF-FLATR P46486 PHOTOSYSTEM I  
REACTION CENTRE SUBUNIT III PRECURSOR ; mRNA sequence.  
ACCESSION A1900558  
VERSION A1900558.1 GI:5606404  
KEYWORDS EST.

SOURCE soybean.  
ORGANISM Glycine max  
Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
1 (bases 1 to 64)  
Shoemaker R., Kelm P., Vodkin L., Erpelting J., Corvett V., Khanna A., Bolla B., Marra M., Hillier L., Kueba T., Martin J., Beck C., Wylie T., Underwood K., Steptoe M., Theising B., Allen M., Bowers Y., Person B., Swaller T., Gidbons M., Pape D., Harvey N., Schurr R., Ritzer E., Kohn S., Shun T., Jackson Y., Cardenas M., McCann R., Waterston R. and Willson R.  
Public Soybean EST Project  
Unpublished (1999)  
CONTACT: Shoemaker R./Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand this clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800 )-533-4363 or contact via email: cout@resgen.com  
Seq primer: -40RP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1..64  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl012-1531"  
/clone\_lib="Gm-cl012"  
/issue\_type="Apical shoot tips, 9-10 day old etiolated seedlings"  
/lab\_host="X110-Gold"  
/note="Vector: pluescript II XR; Site\_1: EcoRI; Site\_2: XhoI; This cDNA library was constructed from mRNA isolated from the apical shoots of 9 to 10 day old etiolated seedlings. The shoot tips including any emerged leaves were harvested for mRNA isolation. The cDNA library was prepared using the Stratagene pluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pluescript vector. The ligated cDNA fragments were transformed into X110-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."

BASE COUNT 4 a 34 c 11 g 15 t  
ORIGIN

Query Match 72.0%; Score 14.4; DB 9; Length 64;  
Best Local Similarity 93.8%; Pred. No. 4.2e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GAGGCGCAGCAGCGCG 20  
|||||  
Db 34 GAGGCGCAGCAGCGCG 19

RESULT 6  
LOCUS BH226921/c  
DEFINITION 84 bp DNA linear GSS 08-NOV-2001  
1006135608.2EL.y1 1006 - RescuenMu Grid G Zea mays genomic, DNA  
sequence.  
ACCESSION BH226921  
VERSION BH226921.1 GI:16826390  
KEYWORDS

KEYWORDS GSS.  
SOURCE Zea mays.  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
Clade: Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 84)  
AUTHORS Walbot,V.  
TITLE Maize genomic sequences found using engineered Rescemu transposon  
JOURNAL Unpublished (2001)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1006135 column: 32  
Class: transposon-tagged.  
Location/Qualifiers  
1..84  
/organism="Zea mays"  
/cultivar="mixed background W23/Al8/B73"  
/db\_xref="taxon:4577"  
/clone\_id="1006 - Rescemu Grid G"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: leaf; Vector: Rescemu (engineered from  
pBluescript backbone); Site\_1: BamHI; Site\_2: BglII;  
Rescemu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on Rescemu, go to the web  
site 'www.zmdb.lastate.edu and follow the links for  
'Rescemu'. Grid G was grown at Stanford in 2000. DNA was  
extracted from leaf punches, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."

BASE COUNT 11 a 33 c 20 g 20 t  
ORIGIN

Query Match 72.0%; Score 14.4; DB 17; Length 84;  
Best Local Similarity 93.8%; Pred. No. 4.2e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GACGAGGCGACGACG 17  
|||||  
Db 69 GACGAGGCGACGACG 54

RESULT 7  
AV920979/c 80 bp mRNA linear EST 18-JAN-2002  
LOCUS AV920979 K. Sato unpublished cDNA library, cv. Haruna Nijo  
DEFINITION germination shoots Hordeum vulgare subsp. vulgare cDNA clone  
bags16f09 3', mRNA sequence.  
ACCESSION AV920979  
VERSION AV920979.1 GI:18216758  
KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare.  
ORGANISM Hordeum vulgare subsp. vulgare.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
; Triticeae; Hordeum.  
REFERENCE 1 (bases 1 to 80)  
AUTHORS Sato,K., Saitoh,D. and Takeda,K.  
TITLE Barley EST sequencing project in NIG and Okayama Univ  
JOURNAL Unpublished (2002)  
COMMENT Contact: Tadasu Shin-1

Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.  
REFERENCE 1 (bases 1 to 80)  
AUTHORS  
TITLE Location/Qualifiers  
JOURNAL  
COMMENT

BASE COUNT 12 a 31 c 15 g 22 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 10; Length 80;  
Best Local Similarity 84.2%; Pred. No. 5.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACGAGGCGACGACGCG 20  
|||||  
Db 48 GACGAGGCGACGACGCG 30

RESULT 8  
A1430740/c 83 bp mRNA linear EST 09-MAR-1999  
LOCUS m516e05.x1 Soares mouse placenta 4NDMP13.5 14.5 Mus musculus cDNA  
DEFINITION clone IMAGE:446048 3', mRNA sequence.  
ACCESSION A1430740  
VERSION A1430740.1 GI:4276576  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murine; Mus.  
REFERENCE 1 (bases 1 to 83)  
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
Underwood,K., Steptoe,M., Theisling,B., Allen,M., Bowers,Y., Person  
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Riltter  
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
Waterston,R. and Willson,R.  
TITLE The WashU-NCI Mouse EST Project 1999  
JOURNAL Unpublished (1999)  
COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
This clone was previously sequenced on the 5' end only, this new  
data is from the 3' end  
Possible reversed clone: polyT not found.  
Location/Qualifiers  
1..83  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_image="IMAGE:446048"  
/clone\_id="Soares mouse placenta 4NDMP13.5 14.5"  
/sex="unknown"  
/tissue\_type="placenta"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: placenta; Vector: pT73D-Pac (Pharmacia)  
with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
1st strand cDNA was primed with a Not I - oligo(dT) primer

```

15'
TCGTACCAATCTGAAGTGGAGCGCCGGGAATTTTTTTTTTTTTTTTTTTTTT
T 3': double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT      9 a      38 c      23 g      13 t
ORIGIN

Query Match      71.0%; Score 14.2; DB 9; Length 83;
Best Local Similarity 84.2%; Pred. No. 5.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGAGCGC 19
      ||| ||||| ||||| |||||
Db 26 GGACGAGGCGGACGAGCGC 8

RESULT 9
BE264581      89 bp      mRNA      1linear      EST 13-JUL-2000
LOCUS      601192351F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536245 5',
DEFINITION      mRNA sequence.
ACCESSION      BE264581
VERSION      BE264581.1 GI:9138138
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 89)
REFERENCE      NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgarbs-femail.nih.gov
      Plate: LHC218 row: e column: 14
      High quality sequence stop: 89.
      Location/Qualifiers
      1..89
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:3536245"
      /clone_1lb="NIH_MGC_7"
      /tissue_type="small cell carcinoma"
      /cell_line="MGC3"
      /lab_host="DH10B (phage-resistant)"
      /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
      EcoRI; cDNA made by oligo-dT priming. Directionally
      cloned into EcoRI/XhoI sites using the following 5'
      adaptor: GGACGAGCG. Size-selected >500bp for average
      insert size 1.8kb. Library constructed by Ling Hong in
      the laboratory of Gerald M. Rubin (University of
      California, Berkeley) using ZAP-cDNA synthesis kit
      (Stratagene) and Superscript II RT (Life Technologies)."
```

```

AL474684
VERSION      AL474684.1 GI:11839870
KEYWORDS      GSS.
SOURCE      Trypanosoma brucei.
ORGANISM      Trypanosoma brucei
Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 90)
REFERENCE      Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
AUTHORS      Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
      Melville,S.E., Rajadream,M.A. and Barrell,B.G.
      Direct Submision
      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
      project, Sanger Centre, The Wellcome Trust Genome Campuss, Hinxton,
      Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
      nh@sanger.ac.uk
      Constructed at the Institute for Genomic Research (TIGR),
      Rockville, MD: Genomic DNA isolated from a cloned population of
      Trypanosoma brucei (TREP927/4 GUTat 10.1) was mechanically sheared
      to give a tight size distribution (
      4 kb). The v + i method used for the library construction is
      described in detail in Smith, H. and Venter, J.C. (Making small
      insert libraries for whole genome shotgun sequencing projects. In
      Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
      Barrell, Oxford University Press, 1999).
      Email: nelsayed@tigr.org
      Details of T. brucei sequencing at the Sanger Centre are available
      at http://www.sanger.ac.uk/Projects/T-brucei/.
      Location/Qualifiers
      1..90
      /organism="Trypanosoma brucei"
      /strain="TREP927"
      /db_xref="taxon:5691"
      /clone="178c01"

BASE COUNT      36 a      22 c      23 g      9 t
ORIGIN

Query Match      71.0%; Score 14.2; DB 17; Length 90;
Best Local Similarity 84.2%; Pred. No. 5.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGCGGACGAGCGC 20
      ||||| ||| ||||| |||||
Db 38 GACGAGGCGGACGAGCGC 56

RESULT 11
BH407770      79 bp      DNA      1linear      GSS 12-DEC-2001
LOCUS      1007050E04.1EL_Y1 1007 - Rescuenku Grid H Zea mays genomic, DNA
DEFINITION      sequence.
ACCESSION      BH407770
VERSION      BH407770.1 GI:17572739
KEYWORDS      GSS.
SOURCE      Zea mays.
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 79)
REFERENCE      Walbot,V.
AUTHORS      Maize genomic sequences found using engineered Rescuenku transposon
TITLE      Unpublished (2001)
JOURNAL      Contact: Walbot V
      Department of Biological Sciences
      Stanford University
      855 California Ave, Palo Alto, CA 94304, USA
      Tel: 650 723 2227
      Fax: 650 725 8221
      Email: walbot@stanford.edu
      Very probable ligation site of ends cut by single endonuclease.
      Reverse complemented post-ligation sequence from source sequence.
      Plate: 1007050 column: 25
```

```
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone="IMAGE:3662737"  
/tissue_type="NCI_CGAP L130"  
/tissue_type="tumor, metastatic to mammary  
lab_host="DH10B"
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RESULT 14  
AZ848413/C

LOCUS AZ848413 93 bp DNA linear GSS 21-FEB-2001  
 DEFINITION 2M019F24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M019F24 F, DNA sequence.  
 ACCESSION AZ848413  
 VERSION AZ848413.1 GI:13031481  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 93)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.  
 and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 JOURNAL Contact: Robert B. Weis  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0149 Row: F Column: 24  
 Seq primer: CGTTGTAAACGACGCGCACT  
 Class: Plasmid ends  
 High quality sequence stop: 93.  
 Location/Qualifiers  
 1..93  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M019F24"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: pMD42uv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g114732114[gb|AF129072.1]), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 14 a 35 c 28 g 16 t  
 ORIGIN  
 Query Match 69.0%; Score 13.8; DB 17; Length 93;  
 Best Local Similarity 88.2%; Pred. No. 7.2e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 ACGAGGCGGACGACGC 19  
 ||| ||||| |||||  
 Db 28 ACGGCGGCGGCGCACGC 12

RESULT 15  
 BH416254/c

LOCUS BH416254 96 bp DNA linear GSS 12-DEC-2001  
 DEFINITION 1007047B09.xl 1007 - Rescuemu Grid H Zea mays genomic, DNA  
 sequence.  
 ACCESSION BH416254  
 VERSION BH416254.1 GI:17598453  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 96)  
 Walbot,V.  
 Maize genomic sequences found using engineered Rescuemu transposon  
 Unpublished (2001)  
 JOURNAL Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Possible ligation site of ends cut by 2 different endonucleases.  
 Reverse complemented post-ligation sequence from source sequence.  
 Plate: 1007047 Column: 14  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1..96  
 /organism="Zea mays"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 /clone\_1lb="1007 Rescuemu Grid H"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: leaf; Vector: Rescuemu (engineered from  
 pluescript backbone); Site.1: BamHI; Site.2: BglII;  
 Rescuemu is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on Rescuemu, go to the web  
 site 'www.zmdb.lastate.edu' and follow the links for  
 'Rescuemu.' Grid H was grown at Berkeley in 2001. DNA  
 was extracted from leaf punches, double digested using  
 BamHI and BglII, and ligated to form circular plasmids.  
 DH10B cells were transformed and then screened on LB  
 plates with ampicillin."

BASE COUNT 14 a 41 c 25 g 16 t  
 ORIGIN  
 Query Match 69.0%; Score 13.8; DB 17; Length 96;  
 Best Local Similarity 88.2%; Pred. No. 7.2e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GGACGAGGCGGACGACG 17  
 ||| ||||| ||||| |||  
 Db 17 GGACGAGGCGGACGACG 1

Search completed: November 26, 2002, 04:06:38  
 Job time : 766.8 secs

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GenCore version 5.1.3  
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## OM nucleic - nucleic search, using sw model

Run on: December 3, 2002, 14:46:40 ; Search time 302.2 Seconds

(without alignments)  
1926.063 Million cell updates/sec

Title: US-09-296-264-4

Perfect score: 20  
Sequence: 1 tgggtcgcgagcctgatca 20Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0  
Maximum DB seq length: 100Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenBank:\*

1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_sts:\*  
27: em\_vl:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_in:\*  
32: em\_htg\_liv:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rnd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_hgtgo\_hum:\*  
40: em\_hgtgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.2	76.0	82	6 104095	104095 Sequence 10
2	14.2	71.0	42	6 AR194079	AR194079 Sequence
3	14.2	71.0	66	6 AX112901	AX112901 Sequence
4	14.2	71.0	77	12 AF401224	AF401224 Synthetic
5	13.8	69.0	20	6 186696	186696 Sequence 22
6	13.6	68.0	24	6 E13049	E13049 Primer 4/1
7	13.6	68.0	26	6 AX049355	AX049355 Sequence
8	13.4	67.0	21	6 AX034723	AX034723 Sequence
9	13.2	66.0	23	6 AX251733	AX251733 Sequence
10	13.2	66.0	74	6 AX478566	AX478566 Sequence
11	13.2	66.0	82	6 AX478567	AX478567 Sequence
12	13.2	66.0	84	8 PVTBRL2	X08010 Phaseolus v
13	12.8	64.0	17	6 AX017782	AX017782 Sequence
14	12.8	64.0	19	6 AX132324	AX132324 Sequence
15	12.8	64.0	38	6 121500	121500 Sequence 47
16	12.8	64.0	66	6 A07506	A07506 Nucleotide
17	12.8	64.0	91	9 HUMCP2106	M23225 Human mutan
18	12.6	63.0	19	6 AR148676	AR148676 Sequence
19	12.6	63.0	23	6 AX306373	AX306373 Sequence
20	12.6	63.0	23	6 AX320086	AX320086 Sequence
21	12.6	63.0	23	6 AX352397	AX352397 Sequence
22	12.6	63.0	23	6 AX419617	AX419617 Sequence
23	12.6	63.0	24	6 E26146	E26146 Novel brain
24	12.6	63.0	25	6 AX127099	AX127099 Sequence
25	12.6	63.0	32	6 E34282	E34282 Environment
26	12.6	63.0	32	6 E34338	E34338 Environment
27	12.6	63.0	33	6 AX326729	AX326729 Sequence
28	12.6	63.0	33	6 AX326730	AX326730 Sequence
29	12.6	63.0	40	6 AX456208	AX456208 Sequence
30	12.6	63.0	40	6 AX456258	AX456258 Sequence
31	12.6	63.0	41	6 AX268538	AX268538 Sequence
32	12.6	63.0	49	6 AX279731	AX279731 Sequence
33	12.6	63.0	51	6 AX161788	AX161788 Sequence
34	12.6	63.0	63	6 AX468790	AX468790 Sequence
35	12.6	63.0	63	6 AX468800	AX468800 Sequence
36	12.6	63.0	69	6 AR081748	AR081748 Sequence
37	12.6	63.0	69	6 AR167980	AR167980 Sequence
38	12.6	63.0	76	1 MCTKX2	X16757 Mycoplasma
39	12.6	63.0	78	10 U96708	U96708 Mus musculi
40	12.6	63.0	94	6 AX088803	AX088803 Sequence
41	12.6	63.0	97	6 AX106283	AX106283 Sequence
42	12.6	63.0	97	6 AX140574	AX140574 Sequence
43	12.6	63.0	97	6 AX200434	AX200434 Sequence
44	12.6	63.0	97	6 AX267090	AX267090 Sequence
45	12.4	62.0	21	6 AX034726	AX034726 Sequence

## ALIGNMENTS

RESULT 1

LOCUS 104095

DEFINITION Sequence 10 from Patent EP 0128733.

ACCESSION 104095

VERSION 104095.1 GI:591892

KEYWORDS

SOURCE .

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 82)

AUTHORS Lee,J.M. and Ullrich,A.

TITLE Human insulin-like growth factor (IGF) and human epidermal growth factor (EGF) produced from a recombinant host. process, expression vector and recombinant host therefor, and IGF-containing

pharmaceutical composition  
JOURNAL Patent: EP 0128733-A1 10 19-DEC-1984;  
FEATURES Location/Qualifiers  
source 1..82  
/organism="unknown"  
BASE COUNT 20 a 19 c 19 g 24 t  
ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 82;  
Best Local Similarity 85.0%; Pred. No. 6.9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGGGTCGGAGCCTGAATCA 20  
Db 58 TGGGTACGATCCTCAATCA 77

RESULT 2  
LOCUS AR194079/c 42 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 8 from patent US 6348333.  
ACCESSION AR194079  
VERSION AR194079.1 GI:20240671  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 42)  
AUTHORS Niva M., Okamoto M., Matsumoto T. and Segawa T.  
TITLE VEGF-binding KDR polypeptide  
JOURNAL Patent: US 6348333-A 8 19-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..42  
/organism="unknown"

BASE COUNT 12 a 11 c 8 g 11 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 42;  
Best Local Similarity 84.2%; Pred. No. 2.3e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGGGTCGGAGCCTGAATC 19  
Db 29 TGGATCCGAGCCCAATC 11

RESULT 3  
LOCUS AX112901 66 bp DNA linear PAT 01-MAY-2001  
DEFINITION Sequence 3 from Patent WO0127294.  
ACCESSION AX112901  
VERSION AX112901.1 GI:13939380  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 66)  
AUTHORS Devico A.L., Fouts T.R. and Tuskan R.G.  
TITLE Virus coat protein/receptor chimeras and methods of use  
JOURNAL Patent: WO 0127294-A 3 19-APR-2001;  
FEATURES Location/Qualifiers  
source 1..66  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Artificial Sequence - primer"

BASE COUNT 10 a 28 c 20 g 8 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 66;  
Best Local Similarity 84.2%; Pred. No. 2.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGTCGGAGCCTGAATCA 20  
Db 1 GGGTCGGAGCCGAGCA 19

RESULT 4  
LOCUS AF401224/c 77 bp DNA linear SYN 26-AUG-2001  
DEFINITION Synthetic construct GCN4F cis element sequence.  
ACCESSION AF401224  
VERSION AF401224.1 GI:15290628  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 77)  
AUTHORS Xian L., Quanhong Y., Rihe P., Aisheng X. and Huiqin F.  
TITLE Direct Submission  
JOURNAL Submitted (23-JUL-2001) Shanghai Yong Ye Agro-Bioengineering Co., Ltd, Shanghai Academy of Agricultural Sciences, Beid Road 2901, Shanghai 201106, China

FEATURES Location/Qualifiers  
source 1..77  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="cis element containing five copies of the GCN4F element; can be inserted into lacZ reporter plasmid for yeast one-hybrid system"

BASE COUNT 21 a 19 c 21 g 16 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 12; Length 77;  
Best Local Similarity 84.2%; Pred. No. 2.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGTCGGAGCCTGAATCA 20  
Db 77 GGGCCCGATCCTGACTCA 59

RESULT 5  
LOCUS I86696 20 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 22 from patent US 5702895.  
ACCESSION I86696  
VERSION I86696.1 GI:3206414  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Matsunaga H., Tsukuno K., Wakisaka S. and Yamane A.  
TITLE Method and kit for detecting methicillin-resistant Staphylococcus aureus  
JOURNAL Patent: US 5702895-A 22 30-DEC-1997;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"

BASE COUNT 5 a 6 c 4 g 5 t  
ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 20;  
Best Local Similarity 88.2%; Pred. No. 3.8e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTCCGAGCCTGAATCA 20  
Db 2 GTCCGTAACCTGAATCA 18

RESULT 6  
LOCUS EI3049 24 bp DNA linear PAT 27-APR-1998  
LOCUS EI3049

DEFINITION Primer.  
ACCESSION E13049  
VERSION E13049.1 GI:3251861  
KEYWORDS JP 1997121869-A/6.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Kondo, M. and Sudou, S.  
TITLE MEA-2 GENE  
JOURNAL Patent: JP 1997121869-A 6 13-MAY-1997;  
ITO HAM KK  
COMMENT OS None  
OC Artificial sequences.  
PN JP 1997121869-A/6  
PD 13-MAY-1997  
PF 07-NOV-1995 JP 1995311638  
PI KONDO MASAKI, SUDOU SHIZUYO  
PC C12N15/09.C07H21/02.C07H21/04.C07K14/47.C07K16/18.C12N1/21, PC  
C1201/68,  
PC G01N33/53.G01N33/53.G01N33/531.(C12N1/21,C12R1:19); CC  
strandedness: Single;  
CC topology: Linear;  
CC hypothetical: No;  
FH Key Location/Qualifiers  
FH FT source 1..24  
FT /organism='Artificial sequences'.  
FEATURES  
source 1..24  
/organism='unidentified'  
/db\_xref='taxon:32644'  
BASE COUNT 5 a 5 c 9 g 5 t  
ORIGIN  
Query Match 68.0%; Score 13.6; DB 6; Length 24;  
Best Local Similarity 80.0%; Pred. No. 4.7e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 1 TTGGTCGGAGCGCTGAATCA 20  
||| ||||| ||||| |||||  
Db 1 TTGGCGCCGAGACCGGAATCA 20  
||| ||||| ||||| |||||  
RESULT 7  
AX049355/c 96 bp DNA linear PAT 12-JAN-2001  
LOCUS  
DEFINITION Sequence 25 from Patent WO0071709.  
ACCESSION AX049355  
VERSION AX049355.1 GI:12226111  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 96)  
AUTHORS Gltos, B., Gassier, B., Sagne, C., el Westikawy, S. and Hamon, M.  
TITLE Polypeptides, vesicular carriers of glutamate and gaba  
JOURNAL Patent: WO 0071709-A 25 30-NOV-2000;  
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE; (INSERM)  
(FR)  
FEATURES  
source 1..96  
Location/Qualifiers  
/organism='Homo sapiens'  
/db\_xref='taxon:9606'  
BASE COUNT 23 a 23 c 26 g 24 t  
ORIGIN  
Query Match 68.0%; Score 13.6; DB 6; Length 96;  
Best Local Similarity 80.0%; Pred. No. 4.3e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 1 TTGGTCGGAGCGCTGAATCA 20

Db 81 TTGGTCGGAGCGAGGAGCA 62  
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RESULT 8  
AX034723 21 bp DNA linear PAT 15-NOV-2000  
LOCUS  
DEFINITION Sequence 5 from Patent WO0052203.  
ACCESSION AX034723  
VERSION AX034723.1 GI:11190682  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial construct.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Anthony, R.M., Brown, T.J. and French, G.L.  
TITLE Identification of bacteria  
JOURNAL Patent: WO 0052203-A 5 08-SEP-2000;  
ANTHONY RICHARD MICHAEL (GB) ; BROWN TIMOTHY JAMES (GB) ; KING S  
COLLEGE LONDON (GB) ; FRENCH GARY LAWRENCE (GB) ; GUY S & ST THOMAS  
S NATIONAL H (GB)  
FEATURES  
source 1..21  
Location/Qualifiers  
/organism='synthetic construct'  
/db\_xref='taxon:32630'  
/note='OLIGO'  
BASE COUNT 5 a 5 c 6 g 5 t  
ORIGIN  
Query Match 67.0%; Score 13.4; DB 6; Length 21;  
Best Local Similarity 93.3%; Pred. No. 6e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 6 CCGAGCGCTGAATCA 20  
||| ||||| ||||| |||||  
Db 1 CCAGAGCGCTGAATCA 15  
||| ||||| ||||| |||||  
RESULT 9  
AX251733/c 23 bp DNA linear PAT 05-OCT-2001  
LOCUS  
DEFINITION Sequence 11 from Patent WO016859.  
ACCESSION AX251733  
VERSION AX251733.1 GI:15985090  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Jing, S.  
TITLE IL-17 receptor like molecules and uses thereof  
JOURNAL Patent: WO 016859-A 11 20-SEP-2001;  
Amgen Inc. (US)  
FEATURES  
source 1..23  
Location/Qualifiers  
/organism='synthetic construct'  
/db\_xref='taxon:32630'  
/note='Primer 2432-36'  
BASE COUNT 4 a 10 c 5 g 4 t  
ORIGIN  
Query Match 66.0%; Score 13.2; DB 6; Length 23;  
Best Local Similarity 83.3%; Pred. No. 7.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2 GGGTCGGAGCGCTGAATC 19  
||| ||||| ||||| |||||  
Db 20 GAGTCGGAGCGCTGAATC 3  
||| ||||| ||||| |||||  
RESULT 10  
AX478566 74 bp DNA linear PAT 12-AUG-2002  
LOCUS  
AX478566

DEFINITION Sequence 16 from Patent WO0216645.  
 ACCESSION AX478566  
 VERSION AX478566.1 GI:22217335  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 REFERENCE 1  
 AUTHORS Brenner, S.  
 TITLE Polymorphic dna fragments and uses thereof  
 JOURNAL Patent: WO 0216645-A 16 28-FEB-2002;  
 LYNX THERAPEUTICS, INC. (US)  
 FEATURES  
 source Location/Qualifiers  
 1..74  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="synthesized oligonucleotide"  
 BASE COUNT 19 a 18 c 20 g 17 t  
 ORIGIN  
 Query Match 66.0%; Score 13.2; DB 6; Length 74;  
 Best Local Similarity 83.3%; Pred. No. 7e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 2 GGGTCGGAGCCTGAATC 19  
 ||| ||||| ||||| ||  
 Db 48 GGGCCCGAGTCTGACTC 65  
 RESULT 11  
 AX478567/c 82 bp DNA linear PAT 12-AUG-2002  
 LOCUS AX478567  
 DEFINITION Sequence 17 from Patent WO0216645.  
 ACCESSION AX478567  
 VERSION AX478567.1 GI:22217336  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 REFERENCE 1  
 AUTHORS Brenner, S.  
 TITLE Polymorphic dna fragments and uses thereof  
 JOURNAL Patent: WO 0216645-A 17 28-FEB-2002;  
 LYNX THERAPEUTICS, INC. (US)  
 FEATURES  
 source Location/Qualifiers  
 1..82  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="synthesized oligonucleotide"  
 BASE COUNT 19 a 22 c 20 g 21 t  
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 Best Local Similarity 83.3%; Pred. No. 7e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 2 GGGTCGGAGCCTGAATC 19  
 ||| ||||| ||||| ||  
 Db 31 GGGCCCGAGTCTGACTC 14  
 RESULT 12  
 PYTRNL2 84 bp tRNA linear PLN 02-AUG-1994  
 LOCUS PYTRNL2/c  
 DEFINITION Phaseolus vulgaris mitochondrial tRNA-Leu(2).  
 ACCESSION X08010  
 VERSION X08010.1 GI:21056  
 KEYWORDS mitochondrial import; transfer RNA-Leu.  
 SOURCE Phaseolus vulgaris.  
 ORGANISM Phaseolus vulgaris  
 Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Phaseolus.  
 REFERENCE 1 (bases 1 to 84)  
 AUTHORS Marechal-Drouard, L., Weil, J.H. and Guillemaut, P.  
 TITLE Import of several tRNAs from the cytoplasm into the mitochondria in  
 bean Phaseolus vulgaris  
 JOURNAL Nucleic Acids Res. 16 (11), 4777-4788 (1988)  
 MEDLINE 88262475  
 PUBMED 3387208  
 COMMENT sequence corresponds to mt tRNA-Leu2 and its cytoplasmic  
 counterpart  
 Data kindly reviewed (23-AUG-1988) by GUILLEMAUT P.  
 FEATURES  
 source Location/Qualifiers  
 1..84  
 /organism="Phaseolus vulgaris"  
 /db\_xref="taxon:3885"  
 1..84  
 /product="tRNA-Leu"  
 /note="tRNA-Leu(2)"  
 10  
 /note="2-methylguanosine"  
 /mod\_base=m2g  
 12  
 /note="4-acetylcytidine"  
 /mod\_base=ac4c  
 16  
 /note="dihydrouridine"  
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 /note="unmodified in cyt tRNA-Leu"  
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 /note="2'-O-methylguanosine"  
 /mod\_base=gm  
 19  
 /note="dihydrouridine"  
 /mod\_base=d  
 21  
 /note="acp3u"  
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 27  
 /note="2,2-dimethylguanosine"  
 /mod\_base=m22g  
 33  
 /note="pseudouridine"  
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 35  
 /note="unidentified modified nucleotide"  
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 38  
 /note="1-methylguanosine"  
 /mod\_base=m1g  
 40  
 /note="pseudouridine"  
 /mod\_base=p  
 45  
 /note="2'-O-methyluridine"  
 /mod\_base=um  
 52  
 /note="unidentified modified nucleotide"  
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 56  
 /note="5-methylcytidine"  
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 66  
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 BASE COUNT 18 a 20 c 26 g 18 t 2 others  
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Query Match 66.0%; Score 13.2; DB 8; Length 84;  
Best Local Similarity 78.9%; Pred. No. 7e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TGGGTCGAGAGCCTGAATC 19  
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Db 49 TCGGACGAGAGCCTGATC 31

RESULT 13  
AX017782

LOCUS AX017782 17 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 11 from patent WO9946404.  
ACCESSION AX017782  
VERSION AX017782.1 GI:10042389

KEYWORDS  
SOURCE

Hordeum vulgare.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 17)  
Ramsey, L.D., Powell, W., Waugh, R., Swanson, J.S. and Thomas, W.T.  
DNA sequences and their use for the selection of cereals

PATENT: WO 9946404-A 11 16-SEP-1999;  
RAMSEY LUKE DOUGLAS (GB); SCOTTISH CROP RESEARCH INST (GB); POWELL  
WAYNE (GB); WAUGH ROBERT (GB); SWANSTON JOHN STUART (GB); THOMAS  
WILLIAM THEODORE BLAYNE (GB)

FEATURES  
source location/Qualifiers

1..17  
/organism="Hordeum vulgare"  
/db\_xref="taxon:4513" 3 t

BASE COUNT 4 a 4 c 6 g 3 t

ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 17;  
Best Local Similarity 87.5%; Pred. No. 1.2e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GGGTCGAGAGCCTGAATC 17  
|||||  
Db 1 GGGTCGAGAGCCTGAATC 16

RESULT 14  
AX132324/c

LOCUS AX132324 19 bp DNA linear PAT 15-MAY-2001  
DEFINITION Sequence 3542 from patent WO0130362.  
ACCESSION AX132324  
VERSION AX132324.1 GI:14138629

KEYWORDS  
SOURCE

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 19)  
Robbins, J.M. and Tritz, R.  
Ribozyme therapy for the treatment of proliferative skin and eye  
diseases

PATENT: WO 0130362-A 3542 03-MAY-2001;  
JOURNAL IMMUSOL, INC. (US)  
location/Qualifiers

1..19  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/note="CGc25 hs ribozyme binding site"  
BASE COUNT 3 a 7 c 6 g 3 t

ORIGIN  
Query Match 64.0%; Score 12.8; DB 6; Length 19;  
Best Local Similarity 87.5%; Pred. No. 1.2e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TGGGTCGAGAGCCTGA 16  
|||||  
Db 18 TGGGTCCTGAGACGAGA 3

RESULT 15  
I21500

LOCUS I21500 38 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 47 from patent US 5521300.  
ACCESSION I21500  
VERSION I21500.1 GI:1601854

KEYWORDS  
SOURCE

Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 38)  
Shah, J.S., Nleupski, R.M. and Liu, J.

Oligonucleotides complementary to mycobacterial nucleic acids  
PATENT: US 5521300-A 47 28-MAY-1996;  
JOURNAL Location/Qualifiers

1..38  
/organism="unknown"  
BASE COUNT 10 a 11 c 15 g 2 t

ORIGIN  
Query Match 64.0%; Score 12.8; DB 6; Length 38;  
Best Local Similarity 87.5%; Pred. No. 1.2e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GTCCGAGAGCCTGAATC 19  
|||||  
Db 23 GCCCGAGAGCCTGAATC 38

Search completed: December 3, 2002, 18:12:18  
Job time : 311.2 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:52:31 : Search time 98.55 Seconds  
(Without alignments) 457.027 Million cell updates/sec

Title: US-09-296-264-4

Perfect score: 20

Sequence: 1 tgggtcgcgagcctgaatca 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2290332

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*  
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	20	100.0	20	AA231434 Human neutrophilin m
2	14.8	74.0	30	AA268645 A 3' primer for th
3	14.2	71.0	42	AAV50375 PCR primer for KDR
4	14.2	71.0	66	AAH19643 Human immunodefict
5	13.8	69.0	51	AA127594 Human SNP oligonuc
6	13.8	69.0	60	ABN35552 Human spliced tran
7	13.6	68.0	24	AA74039 Male-enhanced anti
8	13.6	68.0	28	AAK01737 Rat GDNFR-beta cDN
9	13.6	68.0	65	ABN5425 Mouse spliced tran

C	10	13.6	68.0	65	24	ABN56524	Mouse spliced tran
C	11	13.6	68.0	96	23	ABL57923	Human VEGF1 exon 4.
C	12	13.4	67.0	21	21	AAH94347	Oligonucleotide 1c
C	13	13.2	66.0	23	22	AAH28284	Oligonucleotide 1c
C	14	13.2	66.0	23	23	AAH53534	pcMV/SPORT vector
C	15	13.2	66.0	47	21	AA269457	Human map-related
C	16	13.2	66.0	50	22	AA130919	Human SNP oligonuc
C	17	13.2	66.0	50	22	AA130919	Human SNP oligonuc
C	18	13.2	66.0	50	22	AA130919	Human SNP oligonuc
C	19	13.2	66.0	60	24	ABN6396	Human SNP oligonuc
C	20	13.2	66.0	74	21	AAH64280	Human spliced tran
C	21	13.2	66.0	74	21	AAH57120	Oligonucleotide S-
C	22	13.2	66.0	74	21	AAH14490	Sequence tag plasm
C	23	13.2	66.0	74	21	ABH53615	Oligonucleotide S-
C	24	13.2	66.0	82	21	AAH4281	Oligonucleotide S-
C	25	13.2	66.0	82	21	AAH57121	Sequence tag plasm
C	26	13.2	66.0	82	21	AAH4491	Oligonucleotide S-
C	27	13.2	66.0	82	22	ABH69723	Human foetal liver
C	28	13.2	66.0	82	22	ABH35254	Probe #13720 for g
C	29	13.2	66.0	82	22	AAH16622	Human brain expres
C	30	13.2	66.0	82	22	AAH3784	Human bone marrow
C	31	13.2	66.0	82	22	AAH4561	Human FADD primer
C	32	13.2	66.0	82	22	AAH48460	Probe #14494 for g
C	33	13.2	66.0	82	24	ABH16436	Human genome-deriv
C	34	13.2	66.0	82	24	ABH53616	Oligonucleotide S-
C	35	12.8	64.0	17	20	AAH20451	PCR primer Bmac399
C	36	12.8	64.0	18	21	AAH44752	Human FADD primer
C	37	12.8	64.0	19	21	AAH85956	Cdc25 hs ribozyme
C	38	12.8	64.0	19	22	AAH61118	Olfactory receptor
C	39	12.8	64.0	23	24	ABH37920	Human very low den
C	40	12.8	64.0	24	24	ABH52448	Human olfactory re
C	41	12.8	64.0	25	21	AAH51171	Primer for olfacto
C	42	12.8	64.0	25	21	AAH51172	Primer for olfacto
C	43	12.8	64.0	25	22	AAH51319	Human olfactory re
C	44	12.8	64.0	25	22	AAH51321	Human olfactory re
C	45	12.8	64.0	25	24	ABH37918	Olfactory receptor

#### ALIGNMENTS

RESULT 1	AA231434	AA231434 standard; DNA; 20 BP.
ID	AA231434	
XX	AA231434	
AC	AA231434	
XX	07-FEB-2000 (first entry)	
DT		
XX		
DE	Human neutrophilin mRNA specific antisense oligo GTT3604.	
XX		
KW	Neutrophilin; human; growth; metastasis; tumor; neovascularisation;	
KW	cancer; papilloma; diabetic retinopathy; antisense; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
PN	W09955855-A2.	
PD		
PD	04-NOV-1999.	
PF	23-APR-1999; 99WO-CA00324.	
XX		
PR	23-APR-1998; 98US-0082791.	
XX		
PA	(GENE-) GENESENSE TECHNOLOGIES INC.	
PI	Wright JA, Young AH, Lee YS:	
XX	WPI: 2000-023357/02.	
DR		
XX	Antisense oligonucleotides that inhibit neutrophilin expression, useful	
PT	for treating cancer -	

xx Claim 4; Page 16; 57pp; English.  
xx  
ps  
cc Sequences AA31431-460 represent antisense oligonucleotides which  
cc inhibit human neuropilin expression. The antisense oligonucleotides can  
cc be used to inhibit the growth or metastasis of a mammalian tumor and  
cc inhibit neovascularisation. The oligonucleotides may be used to treat  
cc various forms of cancers or tumors, such as sarcomas, melanomas,  
cc adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell  
cc carcinomas of the mouth, throat, larynx and lung, genitourinary cancers  
cc such as cervical and bladder cancer, hematopoietic cancers, colon cancer,  
cc breast cancer, pancreatic cancer, renal cancer, brain cancer, skin  
cc cancer, liver cancer, head and neck cancers, and nervous system cancers,  
cc as well as benign lesions such as papillomas. The methods may be used to  
cc treat neovascularisation disorders such as diabetic retinopathy, and  
cc retinopathy of prematurity and age related macular degeneration.  
cc  
xx  
SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 other;  
  
Query Match 100.0%; Score 20; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 TGGTCCGAGCCTGAATCA 20  
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Db 1 TGGTCCGAGCCTGAATCA 20  
  
RESULT 2  
AA68645/c  
ID AA68645 standard; DNA: 30 BP.  
xx  
AC AA68645;  
xx  
DT 14-AUG-1997 (first entry)  
xx  
DE A 3' primer for the reverse tetracycline repressor gene.  
xx  
KM DNA integration; LexA; gene therapy; oncogene inactivation;  
KM retrovirus; HIV-1; integrase; reverse tetracycline repressor;  
KM rtel gene; primer; PCR; polymerase chain reaction; ss.  
xx  
OS Synthetic.  
xx  
PN WO9720038-A1.  
xx  
PD 05-JUN-1997.  
xx  
PF 27-NOV-1996; 96WO-US19277.  
xx  
PR 01-DEC-1995; 95US-0008263.  
xx  
PA (REGC ) UNIV CALIFORNIA.  
xx  
PI Chow SA, Goulaouic H;  
xx  
DR WPI; 1997-310594/28.  
xx  
PT Fusion protein comprising retroviral integrase and DNA binding  
PT regions - useful for integrating donor DNA into specific sites on  
PT target DNA, especially for inactivating oncogene(s) or inserting  
PT therapeutic genes  
xx  
PS Example 10; Page 56; 92pp; English.  
xx  
cc A 3' primer (AA68645) containing a BamHI site and a 5' primer  
cc (AA68644) containing a KpnI site were used in the PCR amplification  
cc of the E. coli reverse tetracycline repressor (rTET) gene. The  
cc PCR product was used to prepare a construct coding for an HIV-1  
cc integrase-rTET fusion. The activities of this fusion protein  
cc confirmed the generality of a method of fusing integrases from  
cc different sources, e.g. HIV-1 and FIV, with different DNA  
cc binding proteins, e.g. LexA and rTet, to achieve site-directed

CC integration into a target DNA molecule (see also AAW1781-84).  
xx  
SQ Sequence 30 BP; 7 A; 10 C; 5 G; 8 T; 0 other;  
  
Query Match 74.0%; Score 14.8; DB 18; Length 30;  
Best Local Similarity 88.9%; Pred. No. 6.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
OY 1 TGGTCCGAGCCTGAAT 18  
|||  
Db 19 TGGTCCGAGCCTGAATC 2  
  
RESULT 3  
AAV50375/c  
ID AAV50375 standard; DNA: 42 BP.  
xx  
AC AAV50375;  
xx  
DT 11-NOV-1998 (first entry)  
xx  
DE PCR primer for KDR coding sequence.  
xx  
KM KDR; VEGF receptor; vascular endothelial growth factor; inhibitor;  
KM neovascularisation suppressor; solid tumour; therapy; PCR primer; ss.  
xx  
OS Synthetic.  
xx  
PN WO9831794-A1.  
xx  
PD 23-JUL-1998.  
xx  
PF 16-JAN-1998; 98WO-JP00140.  
xx  
PR 17-JAN-1997; 97JP-0019706.  
xx  
PA (TOAG ) TOA GOSHI KK.  
xx  
PI Matsumoto T, Niwa M, Okamoto M, Segawa T;  
xx  
DR WPI; 1998-414094/35.  
xx  
XX Low-molecular vascular endothelial growth factor inhibiting peptide  
PT - for suppression of neovascularisation contains first and second  
PT immunoglobulin-like domains of KDR VEGF receptor  
xx  
PS Example 3; Page 22; 53pp; Japanese.  
xx  
CC This sequence is a PCR primer for DNA encoding the KDR protein, which is  
CC a vascular endothelial growth factor (VEGF) receptor. The polypeptide of  
CC the invention has a relatively low molecular weight and which inhibits  
CC the activity of VEGF. The polypeptide contains the first and second  
CC immunoglobulin-like (Ig) domains (and optionally the third) of the  
CC extracellular part of the KDR VEGF receptor but does not contain at least  
CC part of the sixth Ig domain. The peptide is used for the suppression of  
CC neovascularisation and thus treatment of diseases involving this, such as  
CC solid tumours. Because of its low molecular weight, the polypeptide  
CC readily infiltrates into the affected tissues.  
xx  
SQ Sequence 42 BP; 12 A; 11 C; 8 G; 11 T; 0 other;  
  
Query Match 71.0%; Score 14.2; DB 19; Length 42;  
Best Local Similarity 84.2%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
OY 1 TGGTCCGAGCCTGAATC 19  
|||  
Db 29 TGGTCCGAGCCTGAATC 11  
  
RESULT 4  
AAH19643



ID AAH19643 standard; DNA: 66 BP.  
 XX AAH19643:  
 AC  
 XX  
 DT 20-JUL-2001 (first entry)  
 XX  
 DE Human immunodeficiency virus gp120 reverse primer.  
 XX  
 KW Human immunodeficiency virus; HIV; gp120; glycoprotein 120; antiviral:  
 KW vaccine; CD4; chimeric polypeptide; FLSC; viral infection;  
 KW PCR primer; ss.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 PN WO200127294-A1.  
 XX  
 PD 19-APR-2001.  
 XX  
 PF 06-OCT-2000; 2000MO-US27546.  
 XX  
 PR 08-OCT-1999; 99US-0158321.  
 XX  
 PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.  
 XX  
 PI Device AL, Fouts TR, Tuskan RG;  
 XX  
 DR WPI; 2001-290724/30.  
 XX  
 PT Chimeric polypeptide comprising a virus coat polypeptide linked to a  
 PT viral receptor polypeptide where the coat and receptor polypeptides can  
 PT bind to each other, useful for preventing, inhibiting, or ameliorating  
 PT a viral infection -  
 XX  
 PS Example 1; Page 40; 80pp; English.  
 XX  
 CC The present sequence was used in the construction of a polynucleotide  
 CC encoding a single chain gp120-CD4 chimeric polypeptide FLSC. This  
 CC procedure was described in an example illustrating an invention  
 CC relating to a new chimeric polypeptide comprising a virus coat  
 CC protein and a viral receptor protein linked by a spacer. The coat  
 CC protein sequence and the viral receptor sequence interact with each  
 CC other to form a complex that is capable of binding a co-receptor.  
 CC The chimeric polypeptide is useful for preventing, inhibiting, or  
 CC ameliorating a viral infection by passive protection against virus  
 CC infection or by producing an immune response. Antibodies against the  
 CC chimeric polypeptide and polynucleotides encoding the chimeric  
 CC polypeptide are also useful for treating or preventing a viral  
 CC infection. The chimeric polypeptide, polynucleotide and antibodies  
 CC are also useful for diagnosing subjects at risk of a viral infection.  
 CC The polypeptide is useful for identifying novel co-receptors and for  
 CC characterizing proteins as co-receptors.  
 CC  
 XX  
 SQ Sequence 66 BP; 10 A; 28 C; 20 G; 8 T; 0 other;  
 OY  
 Query Match 71.0%; Score 14.2; DB 22; Length 66;  
 Best Local Similarity 84.2%; Pred. No. 1.3e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Db 2 GGTCCGAGCGCTGAATCA 20  
 1 GGTCCGAGCGCGCGACCA 19  
 RESULT 5  
 ID AAL27594/c  
 XX AAL27594 standard; DNA: 51 BP.  
 AC AAL27594:  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Human SNP oligonucleotide #802.  
 XX

KW Immunosuppressive; immunostimulatory; antiinflammatory; cyostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
 KW amyloid protein; oncoprotein; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200147944-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000MO-US35498.  
 XX  
 PR 28-DEC-1999; 99US-0173419.  
 XX  
 PR 27-DEC-2000; 2000US-0173419.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shimkets RA, Leach M;  
 XX  
 DR WPI; 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 XX  
 PS Claim 1; Page 1613; 4143pp; English.  
 XX  
 CC The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
 CC G-protein coupled receptors and thioesterases. The present sequence is  
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
 CC by them may be used in the prevention, diagnosis and treatment of  
 CC diseases associated with inappropriate expression of the proteins listed  
 CC above. Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukaemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms.  
 CC  
 XX  
 SQ Sequence 51 BP; 7 A; 18 C; 10 G; 16 T; 0 other;  
 OY  
 Query Match 69.0%; Score 13.8; DB 22; Length 51;  
 Best Local Similarity 88.2%; Pred. No. 2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Db 1 TGGGTCGAGCGCTGAA 17  
 48 TTGGTCGAGCGCTGAA 32  
 RESULT 6  
 ID ABN35552/c  
 XX ABN35552 standard; DNA: 60 BP.  
 AC ABN35552:  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:8300.  
 XX  
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX

OS Homo sapiens.  
 PN WO200210449-A2.  
 XX  
 XX 07-FEB-2002.  
 PD  
 XX 20-JUL-2001; 2001WO-IB01903.  
 PF  
 XX 28-JUL-2000; 2000US-221607P.  
 PR 02-MAY-2001; 2001US-287724P.  
 XX  
 XX (COMP-) COMPUGEN INC.  
 PA  
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX  
 DR WPI: 2002-257383/30.  
 XX  
 XX New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of  
 PT a genome, useful for detecting tissue-, pathology-, and  
 PT developmental-specific genes -  
 XX  
 XX Example 1; SEQ ID 8300; 47bp; English.  
 PS  
 XX The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the  
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises  
 CC several oligonucleotides, each capable of hybridizing selectively to a  
 CC set of messenger RNAs transcribed from a given transcription unit of  
 CC the genome, which encodes one or more messenger RNA splice variants.  
 CC The oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a  
 CC particular biological or pathological state, and so allowing the  
 CC detection of tissue- and pathology-specific genes such as those genes  
 CC only expressed in specific tissue under a specific pathological  
 CC condition; to detect developmental specific genes; and to detect RNA  
 CC transcripts and splice variants of a transcriptome of a patient suffering  
 CC from a particular disorder. ABN27253 to ABN59589 represent  
 CC oligonucleotide sequences from rats, humans and mice, which are used in  
 CC the exemplification of the present invention.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SO Sequence 60 BP; 12 A; 18 C; 12 G; 18 T; 0 other:  
 Query Match 69.0%; Score 13.8; DB 24; Length 60;  
 Best Local Similarity 88.2%; Pred. No. 2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TGGGTCGAGCCTGAA 17  
 |||||  
 DB 59 TGGGTCGAGCCTGAA 43

RESULT 7  
 AAT74039  
 ID AAT74039 standard; cDNA; 24 BP.  
 XX  
 AC AAT74039;  
 XX  
 DT 16-SEP-1997 (first entry)  
 XX  
 DE Male-enhanced antigen-2 structural gene PCR primer.  
 XX  
 KW Mouse; MEA-2; detecting mutation; polymerase chain reaction; ss.  
 XX  
 OS Synthetic.

XX JP09121869-A.  
 PN  
 XX 13-MAY-1997.  
 PD  
 XX 07-NOV-1995; 95JP-0311638.  
 PF  
 XX 07-NOV-1995; 95JP-0311638.  
 PR  
 XX (ITOH-) ITO HAM KK.  
 PA  
 DR WPI: 1997-314229/29.  
 XX  
 XX Male-enhanced antigen Mea-2 gene - especially from mouse, useful for  
 PT detecting mutation(s)  
 PT  
 PS Claim 9; Page 6; 13pp; Japanese.  
 XX  
 XX The present sequence represents a PCR primer corresponding to part  
 CC of the base sequence encoding male-enhanced antigen-2 (MEA-2). The  
 CC primer was used to amplify part of the structural gene of mouse MEA-2.  
 CC The polynucleotide encoding the whole MEA-2 sequence can be used for  
 CC the detection of mutations affecting the MEA-2 gene.  
 CC  
 XX  
 SO Sequence 24 BP; 5 A; 5 C; 9 G; 5 T; 0 other:  
 Query Match 68.0%; Score 13.6; DB 18; Length 24;  
 Best Local Similarity 80.0%; Pred. No. 2.4e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TGGGTCGAGCCTGAATCA 20  
 |||||  
 DB 1 TGGGTCGAGCCTGAATCA 20

RESULT 8  
 AAX01737  
 ID AAX01737 standard; DNA; 28 BP.  
 XX  
 AC AAX01737;  
 XX  
 DT 07-JUN-1999 (first entry)  
 XX  
 DE Rat GDNFR-beta cDNA cloning upstream primer.  
 XX  
 KW Glial Cell Line-Derived Neurotrophic Factor; GDNF; GDNF receptor; GDNFR;  
 KW tyrosine phosphorylation; motoneuronal; neurodegenerative; human; rat;  
 KW Parkinson's disease; GDNFR-beta; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9852591-A1.  
 XX  
 PD 26-NOV-1998.  
 XX  
 PF 04-MAY-1998; 98WO-US09056.  
 XX  
 PR 22-MAY-1997; 97US-0861990.  
 XX  
 PA (CEPH-) CEPHALON INC.  
 XX  
 PI Arumae U, Ibanez CF, Saarma M, Sariola H, Suvanto P;  
 PI Trump M;  
 XX  
 DR WPI: 1999-070126/06.  
 XX  
 XX Newly isolated and characterised GDNFR - used to further understand  
 PT its biological action and the signalling events that occur when  
 PT GDNFs bind to responsive cells  
 XX  
 PS Example 24; Page 54; 113pp; English.  
 XX  
 CC The invention relates to isolated Glial Cell Line-Derived Neurotrophic

CC Factor Receptor (GDNFR) polypeptides. Isolated nucleic acid sequences  
 CC encoding rat and human GDNFR-beta polypeptides are disclosed. GDNFR can  
 CC be used in methods of identifying and isolating receptors. They can also  
 CC be used for determining compounds/compositions that bind GDNFR receptors.  
 CC Similarly, the receptor is used to identify GDNFR homologues by screening  
 CC compounds/compositions exhibiting similar biological effects including  
 CC tyrosine phosphorylation, and increases in c-fos mRNA and cell survival.  
 CC GDNFR analogues can be identified by screening compounds/compositions,  
 CC which are antagonistic for the above biological effects. GDNFR may have  
 CC potential therapeutic use against motorneuronal and neurodegenerative  
 CC diseases, especially Parkinson's disease. The isolation and  
 CC characterisation of GDNFR receptors will enable better understanding of  
 CC its biological actions and the signalling events occurring when GDNFR  
 CC binds to responsive cells, which had previously been hindered by the  
 CC lack of cell lines comprising GDNFR receptors. Sequences AAX01737-38  
 CC represent PCR primers used for cloning the cDNA encoding a rat  
 CC GDNFR-beta polypeptide.

SQ Sequence 28 BP; 9 A; 8 C; 6 G; 5 T; 0 other;

Query Match 68.0%; Score 13.6; DB 20; Length 28;  
 Best Local Similarity 80.0%; Pred. No. 2.4e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TGGGTCCGAGCCTGAATCA 20  
 Db 2 TGGATCCGACACCTGAATGA 21  
 ||| ||||| ||||| ||||| |||||

RESULT 9  
 ABNS5425  
 ID ABNS5425 standard; DNA; 65 BP.

AC ABNS5425;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:28173.  
 XX  
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200210449-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 20-JUL-2001; 2001WO-1B01903.  
 XX  
 PR 28-JUL-2000; 2000US-221607P.  
 PR 02-MAY-2001; 2001US-287724P.  
 XX  
 PA (COMP-) COMPUGEN INC.  
 XX  
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX  
 DR WPI: 2002-257383/30.  
 XX  
 PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of  
 PT a genome, useful for detecting tissue-, pathology-, and  
 PT developmental-specific genes -  
 XX  
 PS Example 1; SEQ ID 28173; 47pp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the  
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises  
 CC several oligonucleotides, each capable of hybridising selectively to a  
 CC set of messenger RNAs transcribed from a given transcription unit of  
 CC the genome, which encodes one or more messenger RNA splice variants.

CC The oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a  
 CC particular biological or pathological state, and so allowing the  
 CC detection of tissue- and pathology-specific genes such as those genes  
 CC only expressed in specific tissue under a specific pathological  
 CC condition; to detect developmental specific genes; and to detect RNA  
 CC transcripts and splice variants of a transcriptome of a patient suffering  
 CC from a particular disorder. ABN27253 to ABNS9589 represent  
 CC oligonucleotide sequences from rats, humans and mice, which are used in  
 CC the exemplification of the present invention.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 65 BP; 16 A; 12 C; 23 G; 14 T; 0 other;

Query Match 68.0%; Score 13.6; DB 24; Length 65;  
 Best Local Similarity 80.0%; Pred. No. 2.6e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TGGGTCCGAGCCTGAATCA 20  
 Db 3 TGGGTCCAGAGGGGAATCA 22  
 ||||| ||| ||||| ||||| |||||

RESULT 10  
 ABNS6524/C  
 ID ABNS6524 standard; DNA; 65 BP.

AC ABNS6524;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:29272.  
 XX  
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200210449-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 20-JUL-2001; 2001WO-1B01903.  
 XX  
 PR 28-JUL-2000; 2000US-221607P.  
 PR 02-MAY-2001; 2001US-287724P.  
 XX  
 PA (COMP-) COMPUGEN INC.  
 XX  
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX  
 DR WPI: 2002-257383/30.  
 XX  
 PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of  
 PT a genome, useful for detecting tissue-, pathology-, and  
 PT developmental-specific genes -  
 XX  
 PS Example 1; SEQ ID 29272; 47pp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the  
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises  
 CC several oligonucleotides, each capable of hybridising selectively to a  
 CC set of messenger RNAs transcribed from a given transcription unit of  
 CC the genome, which encodes one or more messenger RNA splice variants.

CC The oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a  
 CC particular biological or pathological state, and so allowing the  
 CC detection of tissue- and pathology-specific genes such as those genes  
 CC only expressed in specific tissue under a specific pathological  
 CC condition: to detect developmental specific genes; and to detect RNA  
 CC transcripts and splice variants of a transcriptome of a patient suffering  
 CC from a particular disorder. ABN27253 to ABN59589 represent  
 CC oligonucleotide sequences from rats, humans and mice, which are used in  
 CC the exemplification of the present invention.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 65 BP; 21 A; 16 C; 13 G; 15 T; 0 other;

Query Match Score 13.6; DB 24; Length 65;

Best Local Similarity 80.0%; Pred. No. 2.6e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TGGGTCGAGACCTGAATCA 20  
 1 ||||| 1 ||||| 1  
 DB 42 TTGGTCGGGTCTGATTA 23

RESULT 11

ABL57923/c

ID ABL57923 standard; cDNA; 96 BP.

XX ABL57923;

DE 22-JUL-2002 (first entry)

XX Human VG51 exon 4.

XX Antiasthmatic; anxiolytic; antiepileptic; antihypertensive; human;

KW psychotropic; glutamate transporter; transporter; GABA;

KW gamma-aminobutyric acid transporter; GABA transporter; neurotransmitter;

KW asthma; anxiety; epilepsy; hypertension; psychiatric disorder;

XX neurotic disorder; VG51; ss.

OS Homo sapiens.

XX WO200071709-A1.

XX 19-MAY-2000; 2000WO-FR01383.

XX 21-MAY-1999; 99FR-0006525.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

XX Giros B, Gasnier B, Sagne C, El Westikawy S, Hamon M;

XX WPI. 2001-025160/03.

XX New mammalian amino acid transporter, used e.g. to screen for

XX gamma-aminobutyric acid (GABA) transporter. GABA and glutamate are

XX neurotransmitters. The transporter can be used to produce specific

XX antibodies, to screen for binding agents. Modulators of the transporter

XX glutamate/GABA transport, e.g. asthma, anxiety, epilepsy, hypertension

CC and other psychiatric and neurotic disorders, while determining levels of  
 CC the transporter and its coding sequence can be used for diagnosis of such  
 CC disorders. The full length coding sequence is given in ABL57930.

XX Sequence 96 BP; 23 A; 23 C; 26 G; 24 T; 0 other;

Query Match Score 13.6; DB 23; Length 96;

Best Local Similarity 80.0%; Pred. No. 2.6e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TGGGTCGAGACCTGAATCA 20  
 1 ||||| 1 ||||| 1  
 DB 81 TTGGTCGGGTCTGATTA 62

RESULT 12

AAA94347

XX AAA94347 standard; DNA; 21 BP.

XX AAA94347;

DE 10-JAN-2001 (first entry)

XX Oligonucleotide 1c for bacterial species identification.

KW Large ribosomal subunit; 23S rDNA; bacterial species identification;

XX oligonucleotide probe; ss.

XX Escherichia coli.

XX WO200052203-A2.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-GB00740.

XX 02-MAR-1999; 99GB-0004804.

XX (UNLO ) KINGS COLLEGE LONDON.

XX (GUYS-) GUY'S & ST THOMAS'S NAT HEALTH TRUST.

XX French GL, Anthony RM, Brown TJ;

XX WPI. 2000-587320/55.

XX Claim 6; Page 5; 39pp; English.

XX The present sequence is one of a number of oligonucleotide used in a

XX method for identifying bacteria in a sample. PCR primers were used to

XX amplify the large ribosomal subunit (23S rDNA) from bacteria in the

XX sample. The resulting amplicon was then used to probe oligonucleotides,

XX including the present sequence, which were designed to hybridise to only

XX one bacterial species. This method is useful for detecting at least one

XX of Escherichia coli, Staphylococcus aureus, Pseudomonas aeruginosa,

XX Enterococcus spp. preferably Enterococcus faecium or Enterococcus

XX faecalis, Klebsiella spp., Enterobacter spp., Proteus spp. preferably

XX Listeria sp., Stenotrophomonas maltophilia and Burkholderia cepacia. The

XX oligonucleotide probes can be used singly for the identification of

XX certain individual species or in a panel or array for the identification

XX of many different species. The assay can be easily extended to identify a

XX wider range of bacterial species with the addition of oligonucleotides

XX without increasing the complexity of performing the assay. Unlike prior

XX art techniques, the detection method rapidly identifies large numbers of

XX bacteria without prior knowledge of the causative agents.

XX Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 other;



Job time : 102.6 secs

RESULT 15

AAZ69457 standard; DNA; 47 BP.

AC AAZ69457;

DT 10-SEP-2001 (first entry)

DE Human map-related biallelic marker SRQ ID NO:3813.

KW Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW diagnosis; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

Key Location/Qualifiers  
FT variation replace(24,G)  
FT /\*tag=a

FT /standard\_name="single nucleotide polymorphism"

PN W09954500-A2.

PD 28-OCT-1999.

PF 21-APR-1999; 99W0-1B00822.

PR 21-APR-1998; 98US-0082614.

PR 23-NOV-1998; 98US-0109732.

PA (GEST ) GENSET.

PI Cohen D, Blumenfeld M, Chumakov I;

WPI: 2000-013267/01.

PT Novel biallelic markers used to construct a high density disequilibrium  
map of the human genome -

PS Claim 3; Page 1044; 2745pp; English.

CC AAZ65654 to AAZ69578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the  
CC invention have a variety of uses: they can be used for high density  
CC mapping of the human genome, and in complex association studies and  
CC haplotyping studies which are useful in determining the genetic basis  
CC for disease states. Compositions and methods of the invention can also  
CC be useful for the identification of the targets for the development of  
CC pharmaceutical agents and diagnostic methods, as well as the  
CC characterisation of the differential efficacious responses to and side  
CC effects from pharmaceutical agents acting on a disease as well as other  
CC treatment.  
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297  
CC and 3367, are not actually given a sequence in the Sequence Listing  
CC from the present invention.

CC Sequence 47 BP; 17 A; 10 C; 11 G; 9 T; 0 other;

Query Match 66.0%; Score 13.2; DB 21; Length 47;

Best Local Similarity 83.3%; Pred. No. 4e+03; Mismatches 3; Indels 0; Gaps 0;

0Y 3 GGTCGAGAGCTGAATCA 20  
||||| ||| ||||| |  
DB 19 GGTCGAGAGCTGAATCA 36

Search completed: November 23, 2002, 06:28:38

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:53:51 ; Search time 21.55 Seconds  
(Without alignments) 284.619 Million cell updates/sec

Title: US-09-296-264-4

Perfect score: 20  
Sequence: 1 tgggtccgagcctgaatca 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/1na/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/1na/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/1na/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/1na/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/1na/PCrus\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/1na/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	71.0	42	4	US-09-142-956B-8
2	13.8	69.0	20	1	US-08-586-274-22
3	12.8	64.0	18	3	US-09-357-072-8
4	12.8	64.0	38	1	US-07-744-282C-47
5	12.8	64.0	38	5	PCT-US92-06821A-90
6	12.8	64.0	47	4	US-09-641-638-591
7	12.8	64.0	50	2	US-08-244-548-5
8	12.8	64.0	50	2	US-08-244-548-6
9	12.6	63.0	19	4	US-09-262-773-33
10	12.6	63.0	49	4	US-09-538-709-1064
11	12.6	63.0	69	2	US-08-598-455B-20
12	12.6	63.0	69	4	US-09-069-781B-20
13	12.6	63.0	69	4	US-09-137-132-20
14	12.6	63.0	69	4	US-08-864-564A-20
15	12.6	63.0	69	4	US-09-094-410-20
16	12.6	63.0	97	4	US-09-020-956-64
17	12.6	63.0	97	4	US-09-030-607-64
18	12.6	63.0	97	4	US-09-605-785-64
19	12.6	63.0	97	4	US-09-439-313-64
20	12.6	63.0	97	4	US-09-352-616A-64
21	12.6	63.0	97	4	US-09-232-149A-64
22	12.4	62.0	24	5	PCT-US93-02457-11
23	12.4	62.0	24	5	PCT-US93-11458-12
24	12.4	62.0	28	5	PCT-US93-11458-13
25	12.2	61.0	20	2	US-09-166-203-50
26	12.2	61.0	20	4	US-09-377-309-50
27	12.2	61.0	24	4	US-09-600-031-9

c	28	12.2	61.0	28	4	US-08-460-269C-15	Sequence 15, Appl
c	29	12.2	61.0	36	1	US-08-244-492A-9	Sequence 9, Appl
c	30	12.2	61.0	36	1	US-08-709-915-12	Sequence 12, Appl
	31	12.2	61.0	60	4	US-08-264-578-4	Sequence 4, Appl
	32	12.2	61.0	60	4	US-08-264-578-5	Sequence 5, Appl
	33	12.2	61.0	65	1	US-08-484-686B-34	Sequence 34, Appl
	34	12.2	61.0	65	1	US-08-484-686B-37	Sequence 37, Appl
	35	12.2	61.0	65	4	US-08-463-160B-34	Sequence 34, Appl
	36	12.2	61.0	65	4	US-08-463-160B-37	Sequence 37, Appl
	37	12.2	61.0	65	5	PCT-US91-02368-38	Sequence 38, Appl
	38	12.2	61.0	68	2	US-08-790-963-87	Sequence 87, Appl
	39	12.2	61.0	68	4	US-09-371-774-87	Sequence 87, Appl
c	40	12.2	61.0	69	3	US-08-812-121-13	Sequence 13, Appl
c	41	12.2	61.0	69	4	US-09-403-672-13	Sequence 13, Appl
	42	12.2	60.0	26	4	US-08-463-691-17	Sequence 17, Appl
	43	12.2	60.0	26	4	US-08-255-236-5	Sequence 5, Appl
	44	12.2	60.0	30	3	US-08-961-083-327	Sequence 327, App
	45	12.2	60.0	78	4	US-09-357-487B-33	Sequence 33, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-142-956B-8/c
; Sequence 8, Application US/09142956B
; Patent No. 6348333
; GENERAL INFORMATION:
; APPLICANT: Niwa, Mikio
; APPLICANT: Okamoto, Masaji
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Segawa, Toshiaki
; TITLE OF INVENTION: YEGF-BINDING POLYPEPTIDES
; FILE REFERENCE: 06501-021001
; CURRENT FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US/09/142, 956B
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: PCT/JP98/00140
; PRIOR FILING DATE: 1997-01-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-142-956B-8
Query Match          71.0%; Score 14.2; DB 4; Length 42;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy      1 TGGGTCGAGCGCTGAATC 19
Db      29 TGAGTCGAGCGCCCAATC 11
RESULT 2
US-08-586-274-22
; Sequence 22, Application US/08586274
; Patent No. 5702895
; GENERAL INFORMATION:
; APPLICANT: MATSUMAGA, HIROMARI
; APPLICANT: TSUKUMO, KENICHI
; APPLICANT: WAKISAKA, SHINJI
; APPLICANT: YAMANE, AKIO
; TITLE OF INVENTION: METHOD AND KIT FOR DETECTING
; TITLE OF INVENTION: METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
```

ADDRESSEE: P. C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/586,274  
FILING DATE: 16-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-006390  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OHLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 209-038-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-586-274-22

Query Match 69.0%; Score 13.8; DB 1; Length 20;  
Best Local Similarity 88.2%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTCCGAGCCTGATCA 20  
|||||  
DB 2 GTCCGTAACCTGATCA 18

RESULT 3  
US-09-357-072-8  
Sequence 8, Application US/09357072  
Patent No. 6015712  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
APPLICANT: Brenda F. Baker  
APPLICANT: Hong Zhang  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF FADD EXPRESSION  
FILE REFERENCE: RTS-0027  
CURRENT APPLICATION NUMBER: US/09/357,072  
CURRENT FILING DATE: 1999-07-19  
NUMBER OF SEQ ID NOS: 87  
SEQ ID NO 8  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-357-072-8

Query Match 64.0%; Score 12.8; DB 3; Length 18;  
Best Local Similarity 87.5%; Pred. No. 7.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TCCGAGCCGATCA 20  
|||||  
DB 2 TCCGGTCCGATCA 17

RESULT 4  
US-07-744-282C-47  
Sequence 47, Application US/07744282C  
Patent No. 5521300  
GENERAL INFORMATION:  
APPLICANT: Shah, Jyotsna S.  
APPLICANT: Nietupski, Raymond M.  
APPLICANT: Liu, Jing  
TITLE OF INVENTION: Oligonucleotides Complementary to  
TITLE OF INVENTION: Mycobacterial Nucleic Acids  
NUMBER OF SEQUENCES: 127  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kevin M. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/744,282C  
FILING DATE: August 13, 1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kevin M. Farrell  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: GTR90-05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
US-07-744-282C-47

Query Match 64.0%; Score 12.8; DB 1; Length 38;  
Best Local Similarity 75.0%; Pred. No. 7.7e+02;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTCCGAGCCTGATC 19  
|||||  
DB 23 GCCCAGAGCCUGAUC 38

RESULT 5  
PCR-US92-06821A-90  
Sequence 90, Application PC/TUS9206821A  
GENERAL INFORMATION:  
APPLICANT: Shah, Jyotsna S.  
APPLICANT: Nietupski, Raymond M.  
APPLICANT: Liu, Jing  
TITLE OF INVENTION: Oligonucleotides Complementary to  
TITLE OF INVENTION: Mycobacterial Nucleic Acids  
NUMBER OF SEQUENCES: 133  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amoco Corporation  
STREET: 200 East Randolph Drive, P.O. Box 87703  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60680  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/06821A  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/744,282  
FILING DATE: 13-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, Norval B.  
REGISTRATION NUMBER: 33,595  
REFERENCE/DOCKET NUMBER: CN 5851  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-856-7180  
TELEFAX: 312-856-4972  
INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
PCT-US92-06821A-90

Query Match 64.0%: Score 12.8; DB 5; length 38;  
Best Local Similarity 75.0%: Pred. No. 7.7e+02;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTCCGAGCCTGAATC 19  
||| |||||:|||||  
DB 23 GCCCAGACCUGAATC 38

RESULT 6  
US-09-641-638-691/C  
Sequence 691, Application US/09641638  
Patent No. 6432648  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bouquelerec, Lydie  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
FILE REFERENCE: GENSET.051CPI  
CURRENT APPLICATION NUMBER: US/09/641,638  
CURRENT FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent.pm  
SEQ ID NO 691  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 10-349-97 : polymorphic base A or G  
US-09-641-638-691

Query Match 64.0%: Score 12.8; DB 4; length 47;  
Best Local Similarity 77.8%: Pred. No. 7.9e+02;  
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGATCGAGCCTGAATC 19  
||| ||||| |||||  
DB 27 GGATCGAGCCTGAATC 10

RESULT 7  
US-08-244-548-5  
Sequence 5, Application US/08244548  
Patent No. 5874556  
GENERAL INFORMATION:  
APPLICANT: LUTON, STEPHEN D.  
APPLICANT: ALLEN, JAMES M.  
TITLE OF INVENTION: HYBRID GENES FOR USE IN THE PRODUCTION  
TITLE OF INVENTION: OF TH-INDEPENDENT CYTOTOXIC T CELLS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,548  
FILING DATE: 06-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: DYLAN, TYLER M.  
REGISTRATION NUMBER: 37,612  
REFERENCE/DOCKET NUMBER: 22627-20005.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-244-548-5

Query Match 64.0%: Score 12.8; DB 2; length 50;  
Best Local Similarity 87.5%: Pred. No. 7.9e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTCCGAGCCTGAATC 19  
||| ||||| |||||  
DB 23 GTCCGAGCCTGAATC 38

RESULT 8  
US-08-244-548-6/C  
Sequence 6, Application US/08244548  
Patent No. 5874556  
GENERAL INFORMATION:  
APPLICANT: LUTON, STEPHEN D.  
APPLICANT: ALLEN, JAMES M.  
TITLE OF INVENTION: HYBRID GENES FOR USE IN THE PRODUCTION  
TITLE OF INVENTION: OF TH-INDEPENDENT CYTOTOXIC T CELLS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,548  
FILING DATE: 06-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: DYLAN, TYLER M.  
REGISTRATION NUMBER: 37,612  
REFERENCE/DOCKET NUMBER: 22627-20005.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-244-548-6

Query Match 64.0%; Score 12.6; DB 2; Length 50;  
Best Local Similarity 87.5%; Pred. No. 7.9e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTCCGAGCCTGAATC 19  
DB 32 GTCCGAGCCTGAATC 17

RESULT 9  
US-09-262-773-33/C  
Sequence 33, Application US/09262773  
Patent No. 6225451  
GENERAL INFORMATION:  
APPLICANT: Ballinger, Dennis G.  
APPLICANT: Ding, Wei  
APPLICANT: Wagner, Susanne  
APPLICANT: Hess, Mark A.  
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE  
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1  
FILE REFERENCE: Myriad 3  
CURRENT APPLICATION NUMBER: US/09/262,773  
CURRENT FILING DATE: 1999-03-04  
NUMBER OF SEQ ID NOS: 210  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 33  
LENGTH: 19  
TYPE: DNA  
ORGANISM: primer  
US-09-262-773-33

Query Match 63.0%; Score 12.6; DB 4; Length 19;  
Best Local Similarity 78.9%; Pred. No. 9.2e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TGGGTCGAGCCTGAATC 19  
DB 19 TAGGACGAGCCTGAATC 1

RESULT 10  
US-09-538-709-1064  
Sequence 1064, Application US/09538709  
Patent No. 6468749  
GENERAL INFORMATION:  
APPLICANT: Ulanovsky, et al  
TITLE OF INVENTION: SEQUENCE-DEPENDENT GENE SORTING TECHNIQUES  
FILE REFERENCE: 540579-2006  
CURRENT APPLICATION NUMBER: US/09/538,709  
CURRENT FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 1311

SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1064  
LENGTH: 49  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Adaptor  
US-09-538-709-1064

Query Match 63.0%; Score 12.6; DB 4; Length 49;  
Best Local Similarity 78.9%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGTCGAGCCTGAATCA 20  
DB 23 GGGTCGAGCCTGAATCA 41

RESULT 11  
US-08-599-455B-20/C  
Sequence 20, Application US/08599455B  
Patent No. 5972621  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT  
MODULATE BODY WEIGHT USING THE OB RECEPTOR  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: PASTESQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/599,455B  
FILING DATE: 22-JAN-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejoh, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/017001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-599-455B-20

Query Match 63.0%; Score 12.6; DB 2; Length 69;

Best Local Similarity 78.9%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GCGCCGAGCCGATCA 20  
Db 25 GCGTTGGAGCCGTAACA 7

## RESULT 12

US-09-069-781B-20/C

; Sequence 20, Application US/09069781B

; Patent No. 6287782

; GENERAL INFORMATION:

; APPLICANT: Tartaglia, Louis A.

; APPLICANT: Tepper, Robert I.

; APPLICANT: Culpepper, Janice A.

; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,

; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/069,781B

; FILING DATE: 29-APRIL-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/864,564

; FILING DATE: 28-MAY-1997

; APPLICATION NUMBER: US 08/708,123

; FILING DATE: 03-SEP-1996

; APPLICATION NUMBER: US 08/638,524

; FILING DATE: 26-APR-1996

; APPLICATION NUMBER: US 08/599,455

; FILING DATE: 22-JAN-1996

; APPLICATION NUMBER: US 08/583,153

; FILING DATE: 28-DEC-1995

; APPLICATION NUMBER: US 08/570,142

; FILING DATE: 11-DEC-1995

; APPLICATION NUMBER: US 08/569,485

; FILING DATE: 08-DEC-1995

; APPLICATION NUMBER: US 08/566,622

; FILING DATE: 04-DEC-1995

; APPLICATION NUMBER: US 08/562,663

; FILING DATE: 27-NOV-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Melkielejohn, Ph.D., Anita L.

; REGISTRATION NUMBER: 35,283

; REFERENCE/DOCKET NUMBER: 07334/082001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 69 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: RNA

; US-09-069-781B-20

Query Match 63.0%; Score 12.6; DB 4; Length 69;

Best Local Similarity 78.9%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GCGCCGAGCCGATCA 20  
Db 25 GCGTTGGAGCCGTAACA 7

## RESULT 13

US-09-137-132-20/C

; Sequence 20, Application US/09137132

; Patent No. 6380363

; GENERAL INFORMATION:

; APPLICANT: Tartaglia, Louis A.

; APPLICANT: Tepper, Robert I.

; APPLICANT: Culpepper, Janice A.

; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,

; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/137,132

; FILING DATE: 18-AUG-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/864,564

; FILING DATE: 28-MAY-1997

; APPLICATION NUMBER: 08/708,123

; FILING DATE: 03-SEP-1996

; APPLICATION NUMBER: 08/638,524

; FILING DATE: 26-APR-1996

; APPLICATION NUMBER: 08/599,455

; FILING DATE: 22-JAN-1996

; APPLICATION NUMBER: 08/583,153

; FILING DATE: 28-DEC-1995

; APPLICATION NUMBER: 08/570,142

; FILING DATE: 11-DEC-1995

; APPLICATION NUMBER: 08/569,485

; FILING DATE: 08-DEC-1995

; APPLICATION NUMBER: 08/566,622

; FILING DATE: 04-DEC-1995

; APPLICATION NUMBER: 08/562,663

; FILING DATE: 27-NOV-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Melkielejohn, Ph.D., Anita L.

; REGISTRATION NUMBER: 35,283

; REFERENCE/DOCKET NUMBER: 07334/019004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 69 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: RNA

; US-09-137-132-20

Query Match 63.0%; Score 12.6; DB 4; Length 69;



QY 2 GGGTCGAGCCTGAATCA 20  
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Db 25 GGCTTTCGAGCCTGAACA 7

Search completed: November 23, 2002, 06:36:01  
Job time : 23.55 secs

**THIS PAGE BLANK (USE 79)**

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:54:41 : Search time 17.25 Seconds  
(without alignments)  
439.108 Million cell updates/sec

Title: US-09-296-264-4

Perfect score: 20

Sequence: 1 tgggtccgagcctgataca 20

Scoring table: IDENTITY\_NUC

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 195614

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published\_Applications\_NA:\*

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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
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12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	66	9	US-09-934-060A-8
2	13.2	66.0	23	10	US-09-809-567-11
3	13.2	66.0	82	10	US-09-864-761-20574
4	12.8	64.0	25	10	US-09-886-053-519
5	12.8	64.0	25	10	US-09-886-053-519
6	12.6	63.0	33	10	US-09-780-668A-25
7	12.6	63.0	33	10	US-09-780-668A-26
8	12.6	63.0	41	10	US-09-821-821-17
9	12.6	63.0	97	10	US-09-759-143-64
10	12.6	63.0	97	10	US-09-780-669-64
11	12.6	63.0	97	10	US-09-030-606-64
12	12.6	63.0	97	10	US-09-822-827-64
13	12.6	63.0	97	10	US-09-115-453-64
14	12.4	62.0	39	12	US-10-081-281-16
15	12.4	62.0	66	10	US-09-969-708-357
16	12.4	62.0	69	10	US-09-775-743A-10
17	12.4	62.0	81	8	US-08-790-540A-17
18	12.4	62.0	81	8	US-08-791-391A-17
19	12.4	62.0	81	8	US-08-791-391A-26

20	12.2	61.0	21	10	US-09-726-774-64	Sequence 64, Appl
21	12.2	61.0	32	10	US-09-814-777A-51	Sequence 51, Appl
22	12.2	60.0	18	10	US-09-809-867-1	Sequence 1, Appl
23	12.2	60.0	30	10	US-09-765-272-327	Sequence 327, App
24	12.2	60.0	30	10	US-09-051-034A-5	Sequence 5, Appl1
25	12.2	60.0	98	10	US-09-864-761-27818	Sequence 27818, A
26	12.2	60.0	98	10	US-09-969-708-151	Sequence 151, App
27	11.8	59.0	18	10	US-09-780-668A-22	Sequence 22, Appl
28	11.8	59.0	18	10	US-09-780-668A-23	Sequence 23, Appl
29	11.8	59.0	31	10	US-09-801-274-570	Sequence 570, App
30	11.8	59.0	82	10	US-09-908-853-3	Sequence 3, Appl1
31	11.6	58.0	20	10	US-09-733-294A-107	Sequence 107, App
32	11.6	58.0	24	9	US-09-978-295A-99	Sequence 99, Appl
33	11.6	58.0	24	9	US-09-978-697-99	Sequence 932, App
34	11.6	58.0	27	10	US-09-780-669-832	Sequence 832, App
35	11.6	58.0	27	10	US-09-822-827-832	Sequence 6, Appl1
36	11.6	58.0	30	10	US-09-872-820-6	Sequence 1, Appl1
37	11.6	58.0	54	12	US-10-113-573-1	Sequence 3530, Ap
38	11.6	58.0	82	10	US-09-923-876-3530	Sequence 3, Appl1
39	11.6	58.0	86	10	US-09-384-472-3	Sequence 31748, A
40	11.6	58.0	97	10	US-09-864-761-31748	Sequence 5, Appl1
41	11.6	58.0	97	10	US-09-051-034A-5	Sequence 46, Appl
42	11.4	57.0	60	10	US-09-559-671A-46	Sequence 201, App
43	11.4	57.0	18	9	US-09-978-295A-201	Sequence 201, App
44	11.2	56.0	18	9	US-09-978-697-201	
45	11.2	56.0				

## ALIGNMENTS

RESULT 1  
US-09-934-060A-8  
Sequence 8, Application US/09934060A  
Patent No. US2002015121A1.  
GENERAL INFORMATION:  
APPLICANT: Devlico, Anthony L.  
APPLICANT: Fouts, Timothy R.  
APPLICANT: Tuskat, Robert G.  
TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE  
FILE REFERENCE: 4115-144 CIP  
CURRENT APPLICATION NUMBER: US/09/934,060A  
PRIOR FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: US 09/684,026  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: US 60/158,321  
PRIOR FILING DATE: 1999-10-08  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 66  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthesized construct  
US-09-934-060A-8

Query Match 71.0%; Score 14.2; DB 9; Length 66;  
Best Local Similarity 84.2%; Pred. No. 2.5e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTCCGAGCCTGATCA 20  
DB 1 GGGTCCGAGCCTGATCA 19

RESULT 2  
US-09-809-567-11/C  
Sequence 11, Application US/09809567  
Patent No. US20020045213A1  
GENERAL INFORMATION:  
APPLICANT: Jinq, Shuqian  
TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof

```
FILE REFERENCE: 01017/36916A
CURRENT APPLICATION NUMBER: US/09/809,567
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/724,460
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/189,816
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer 2432-36
US-09-809-567-11

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 10; Length 23;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTCGGAGCCTGAATC 19
1 ||||| ||| |||
DB 20 GAGTCGGAGCCTGATC 3

RESULT 3
US-09-864-761-20574/c
Sequence 20574, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20574
LENGTH: 82
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AB016897.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.97
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.83
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.85
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3
OTHER INFORMATION: NT HIT: AL161501.2, EVALUATE 5.60e-01
OTHER INFORMATION: EST_HUMAN HIT: AW992151.1, EVALUATE 2.60e+00
US-09-864-761-20574

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 10; Length 82;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGGTCCGAGCCTGAAT 18
||||| | ||||| |||
DB 63 TGGGTAGCGAGCCTGAAT 46

RESULT 4
US-09-886-055-519
Sequence 519, Application US/09886055
Patent No. US2002013273A1
GENERAL INFORMATION:
APPLICANT: STRYER, LOBERT
APPLICANT: ZOZULYA, SERGEY
TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
FILE REFERENCE: 078003-0277150
CURRENT APPLICATION NUMBER: US/09/886,055
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,812
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 522
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 519
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Degenerate
OTHER INFORMATION: primer
NAME/KEY: modified_base
LOCATION: (20)
OTHER INFORMATION: A, T, C or G
NAME/KEY: modified_base
LOCATION: (22)-(23)
OTHER INFORMATION: A, T, C or G
US-09-886-055-519

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 10; Length 25;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGTCGGAGCCTGAA 17
||||| ||| :|||
DB 2 GGGTCGGAGRSTRAD 17

RESULT 5
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US-09-886-055-521  
; Sequence 521, Application US/09886055  
; Patent No. US20020132273A1  
; GENERAL INFORMATION:  
; APPLICANT: STRYER, LUBERT  
; APPLICANT: ZOZULYA, SERGEY  
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSOR PERCEPTION, AND  
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS  
; FILE REFERENCE: 078003-0277150  
; CURRENT APPLICATION NUMBER: US/09/886,055  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/213,812  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 522  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 521  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Degenerate  
; NAME/KEY: modified\_base  
; LOCATION: (20)  
; OTHER INFORMATION: A, T, C or G  
; NAME/KEY: modified\_base  
; LOCATION: (22)-(23)  
; OTHER INFORMATION: A, T, C or G  
US-09-886-053-521

Query Match 64.0%; Score 12.8; DB 10; Length 25;  
Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGTCGCGAGCCTGAATC 17  
Db 2 GGGTCGCGAGCCTGAATC 17

RESULT 6  
US-09-780-668A-25/C  
; Sequence 25, Application US/09780668A  
; Patent No. US20020147311A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Burger, Christa  
; APPLICANT: Lo, Kin-Ming  
; TITLE OF INVENTION: Enhancing the Circulating Half-Life of Antibody-Based Fusion  
; FILE REFERENCE: Lex-011  
; CURRENT APPLICATION NUMBER: US/09/780,668A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,768  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 5' oligonucleotide with linker  
US-09-780-668A-25

Query Match 63.0%; Score 12.6; DB 10; Length 33;  
Best Local Similarity 78.9%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGTCGCGAGCCTGAATC 20  
Db 31 GGATCCGCGAGCCTGAATCA 13

RESULT 7  
US-09-780-668A-26  
; Sequence 26, Application US/09780668A  
; Patent No. US20020147311A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Burger, Christa  
; APPLICANT: Lo, Kin-Ming  
; TITLE OF INVENTION: Enhancing the Circulating Half-Life of Antibody-Based Fusion  
; FILE REFERENCE: Lex-011  
; CURRENT APPLICATION NUMBER: US/09/780,668A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,768  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 3' oligonucleotide with linker  
US-09-780-668A-26

Query Match 63.0%; Score 12.6; DB 10; Length 33;  
Best Local Similarity 78.9%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGTCGCGAGCCTGAATC 20  
Db 3 GGATCCGCGAGCCTGAATCA 21

RESULT 8  
US-09-821-821-17/C  
; Sequence 17, Application US/09821821  
; Patent No. US20020064823A1  
; GENERAL INFORMATION:  
; APPLICANT: Weicher, Andrew A.  
; APPLICANT: Calzone, Frank J.  
; TITLE OF INVENTION: CD20/IgE-Receptor Like Molecules and Uses Thereof  
; FILE REFERENCE: 01017/36938A  
; CURRENT APPLICATION NUMBER: US/09/821,821  
; CURRENT FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: US 09/723,258  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: US 60/193,728  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer 2289-26  
US-09-821-821-17

Query Match 63.0%; Score 12.6; DB 10; Length 41;  
Best Local Similarity 78.9%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TGGGTCCGAGCCTGAATC 19  
Db 39 TGTGTCCGGGTGCTGAATC 21

RESULT 9  
US-09-759-143-64  
; Sequence 64, Application US/09759143  
; Patent No. US20020022248A1  
; GENERAL INFORMATION:

```
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedicik, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Wang, Aljun
; APPLICANT: Li, Samuel
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-64
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Query Match 63.0%; Score 12.6; DB 10; Length 97;
Best Local Similarity 78.9%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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OY 1 TGGGTCGGAGCGCTGAATC 19
DB 12 TGAGTCGGAGCGCTGAATC 30
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RESULT 10
US-09-780-669-64
; Sequence 64, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedicik, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 97
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-64
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Query Match 63.0%; Score 12.6; DB 10; Length 97;
Best Local Similarity 78.9%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 1 TGGGTCGGAGCGCTGAATC 19
DB 12 TGAGTCGGAGCGCTGAATC 30
```

```
RESULT 11
US-09-030-606-64
; Sequence 64, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHOD
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESS: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/030,606
; APPLICATION NUMBER: 25-FEB-1998
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-606-64
```

```
Query Match 63.0%; Score 12.6; DB 10; Length 97;
Best Local Similarity 78.9%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
OY 1 TGGGTCGGAGCGCTGAATC 19
DB 12 TGAGTCGGAGCGCTGAATC 30
```

```
RESULT 12
US-09-822-827-64
; Sequence 64, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 97
```

FILE REFERENCE: 210121.534C1  
CURRENT APPLICATION NUMBER: US/09/822, 827  
CURRENT FILING DATE: 2001-03-28  
NUMBER OF SEQ ID NOS: 982  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO: 64  
LENGTH: 97  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-822-827-64

Query Match 63.0%; Score 12.6; DB 10; Length 97;  
Best Local Similarity 78.9%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TGGGTCCGAGCCTGAATC 19  
DB 12 TGAGTCGGAGCCTGAATC 30

RESULT 13  
US-09-115-453-64  
Sequence 64, Application US/09115453B  
Patent NO. US20020090372A1  
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND  
TITLE OF INVENTION: METHODS FOR THEIR USE  
FILE REFERENCE: 210121.427C4  
CURRENT APPLICATION NUMBER: US/09/115, 453B  
CURRENT FILING DATE: 1998-07-14  
NUMBER OF SEQ ID NOS: 228  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO: 64  
LENGTH: 97  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-115-453-64

Query Match 63.0%; Score 12.6; DB 10; Length 97;  
Best Local Similarity 78.9%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TGGGTCCGAGCCTGAATC 19  
DB 12 TGAGTCGGAGCCTGAATC 30

RESULT 14  
US-10-081-281-16  
Sequence 16, Application US/10081281  
Patent NO. US20020151707A1  
GENERAL INFORMATION:

APPLICANT: Kindvogel, Wayne  
Gross, Jane A  
Sheppard, Paul  
TITLE OF INVENTION: Immune Mediators and Related Methods  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/081,281

FILING DATE: 20-Feb-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/261,811A  
FILING DATE: 03-Mar-1999  
APPLICATION NUMBER: US 08/480,002  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/482,133  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/483,241  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 60/005,964  
FILING DATE: 27-OCT-1995  
APPLICATION NUMBER: US 08/557,581  
FILING DATE: 07-JUN-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Parent, Annette S.  
REGISTRATION NUMBER: 42,058  
REFERENCE/DOCKET NUMBER: 014058-005630US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-10-081-281-16

Query Match 62.0%; Score 12.4; DB 12; Length 39;  
Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TGGGTCCGAGCCT 14  
DB 18 TGAGTCGGAGACT 31

RESULT 15  
US-09-969-708-357/C  
Sequence 357, Application US/09969708  
Patent NO. US20020102532A1  
GENERAL INFORMATION:

APPLICANT: Augustus, Meena  
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign  
TITLE OF INVENTION: Sets  
FILE REFERENCE: 689290-70  
CURRENT APPLICATION NUMBER: US/09/969,708  
CURRENT FILING DATE: 2001-10-03  
PRIOR APPLICATION NUMBER: US/60/237,606  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: US/60/237,608  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: US/60/237,425  
PRIOR FILING DATE: 2000-10-03  
NUMBER OF SEQ ID NOS: 658  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 357  
LENGTH: 66  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-969-708-357

Query Match 62.0%; Score 12.4; DB 10; Length 66;  
Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGGTCCGAGCCTG 15  
DB 61 GGGTCCGAGCCTG 48

Search completed: November 23, 2002, 06:42:03  
Job time : 18.25 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 25, 2002, 09:10:06 ; Search time 755.55 Seconds  
(without alignments)  
428.707 Million cell updates/sec

Title: US-09-296-264-4

Perfect score: 20  
Sequence: 1 tgggtccgagacgtatcata 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estdb:\*  
2: em\_estdb:\*  
3: em\_estdb:\*  
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11: em\_estdb:\*  
12: em\_estdb:\*  
13: em\_estdb:\*  
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27: em\_estdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	88	12	BF117110 u205c06.y
2	13.8	69.0	30	12	BE735559 601304856
3	13.8	69.0	55	9	AA498823 v432h02.r
4	13.8	69.0	58	9	AA869727 v415h03.r
5	13.8	69.0	60	9	AA080195 mm33e01.r
6	13.8	69.0	82	14	W17669 mb76c07.r1

7	13.8	69.0	90	9	AJ239904	AJ239904 AJ239904
8	13.6	68.0	94	9	AA725453	AA725453 a115h08.s
9	13.4	67.0	77	14	NA4726	NA4726 y37c09.r1
10	13.4	67.0	77	17	BH891526	BH891526 3526_1_18
11	13.2	66.0	65	9	AA096874	AA096874 m002a03.r
12	13.2	66.0	68	13	Bj076607	Bj076607 B076607
13	13.2	66.0	75	9	A1902463	A1902463 CM-BT006-
14	12.8	64.0	45	13	B1519819	B1519819 603062250
15	12.8	64.0	58	9	AA906833	AA906833 ok73f04.s
16	12.8	64.0	58	17	BH889500	BH889500 3526_1_10
17	12.8	64.0	85	9	AA980524	AA980524 u442c10.r
18	12.8	64.0	92	17	BH895490	BH895490 3526_1_34
19	12.8	64.0	97	17	AG024646	AG024646 Oryza sat
20	12.8	64.0	100	14	BM820025	BM820025 K-EST0088
21	12.6	63.0	60	14	BM954016	BM954016 sm69a01.
22	12.6	63.0	78	9	AA836634	AA836634 odf6b10.s
23	12.6	63.0	81	10	AV742234	AV742234 AV742234
24	12.6	63.0	88	14	W16240	W16240 mb64b04.r1
25	12.6	63.0	91	9	AA710526	AA710526 v550f09.r
26	12.6	63.0	92	17	BH852872	BH852872 SALK_0757
27	12.6	63.0	93	17	BH862040	BH862040 SALK_0885
28	12.6	63.0	95	9	AA225611	AA225611 nc08e12.9
29	12.6	63.0	100	12	BG114826	BG114826 602315273
30	12.4	62.0	59	9	AL798042	AL798042 AL798042
31	12.4	62.0	66	9	AA410714	AA410714 zv35h07.s
32	12.4	62.0	71	17	A2816914	A2816914 2M085C21
33	12.4	62.0	83	9	AA869319	AA869319 vq50e04.r
34	12.4	62.0	83	12	BG345720	BG345720 dg40d05.y
35	12.4	62.0	84	9	AA836964	AA836964 o697g08.s
36	12.4	62.0	85	13	B1906423	B1906423 603063464
37	12.4	62.0	87	9	AA723245	AA723245 z984c08.s
38	12.4	62.0	91	9	AA621438	AA621438 af35g08.s
39	12.2	61.0	70	9	A1544943	A1544943 fb59f02.y
40	12.2	61.0	75	14	H94092	H94092 yw58d11.r1
41	12.2	61.0	76	9	A1793479	A1793479 fc48c01.x
42	12.2	61.0	76	9	AA229247	AA229247 nc46g09.r
43	12.2	61.0	80	12	BF129926	BF129926 601817752
44	12.2	61.0	90	17	BH852734	BH852734 SALK_0755
45	12.2	61.0	94	14	H55585	H55585 CHR220524 C

## ALIGNMENTS

RESULT 1  
LOCUS BF117110 88 bp mRNA linear EST 29-DEC-2000  
DEFINITION u205c06.y1 NCI-CGAP Mam5 Mus musculus cDNA clone IMAGE:366170 5' similar to SW:HY45\_MOUSE P01821 IG HEAVY CHAIN V REGION MCI01  
PRECUSOR: , mRNA sequence.

ACCESSION BF117110 GI:10986586  
VERSION BF117110.1  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.  
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL  
COMMENT Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Iotchar Hennighausen Ph.D., Robin Humphreys  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:  
image.liml.gov/image/html/resources.shtml

MGI:1428938





Thiesing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
On Sep 12, 1996 this sequence version replaced gi:1292054.  
Contact: Marra M/Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LINDA; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:216740

Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 1.

## FEATURES

source

1. 82  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:335340"  
/clone\_lib="Soares mouse p3M19.5"  
/dev\_stage="19.5 dpc total fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Vector: pT73p (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAAGTGGAGCGCGCATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

BASE COUNT 23 a 15 c 28 g 16 t  
ORIGIN

Query Match 69.0%; Score 13.8; DB 14; Length 82;  
Best Local Similarity 88.2%; Pred. NO. 6.1e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTCCGAGCCTGATC 19  
|||||  
Db 20 GGTCCGAGCCTATC 4

RESULT 7 90 bp mRNA linear EST 10-AUG-1999  
AJ239904  
LOCUS  
DEFINITION AJ239904 Aspergillus niger ATCC6275 Aspergillus niger cDNA clone  
AN06A08, mRNA sequence.  
ACCESSION AJ239904  
VERSION AJ239904.1 GI:5443895  
KEYWORDS EST.  
SOURCE Aspergillus niger.  
ORGANISM Aspergillus niger.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eutotiales; Trichocommataceae; mitosporic Trichocommataceae; Aspergillus.

REFERENCE  
AUTHORS Choi, J.Y., Lee, D.W., Koh, J.S., Kim, J.H., Yang, M.S., and Chae, K.S.  
TITLE Identification of expressed sequence tags (ESTs) of the highly transcribed genes in Aspergillus niger  
JOURNAL Biotechnol. Lett. 21, 381-384 (1999)  
COMMENT Contact: Chae KS  
Faculty of Biological Sciences  
Chonbuk National University  
Chonju 561-756, Republic of Korea.

## FEATURES

source

1. 90

/organism="Aspergillus niger"  
/strain="ATCC6275"  
/db\_xref="taxon:5061"  
/clone="AN06A08"  
/clone\_lib="Aspergillus niger ATCC6275"  
BASE COUNT 26 a 19 c 25 g 19 t 1 others  
ORIGIN

Query Match 69.0%; Score 13.8; DB 9; Length 90;  
Best Local Similarity 83.3%; Pred. NO. 6.2e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGTCCGAGCCTGATC 19  
|||||  
Db 26 GGTCCGAGCCTGATC 43

RESULT 8 94 bp mRNA linear EST 31-DEC-1998  
AA725453  
LOCUS

DEFINITION AA725453 Soares\_papillary\_tumor\_NbHPA Homo sapiens cDNA clone  
1342911 3', similar to SM:NM\_03886 NADH-UBIQUINONE  
OXIDOREDUCTASE CHAIN 1; mRNA sequence.

ACCESSION AA725453  
VERSION AA725453.1 GI:2743160  
KEYWORDS EST.  
SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE NCI-CGAP National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@nci.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/dbtrp/image/image.html

Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Insert Length: 644 Std Error: 0.00  
Seq primer: -40M13 fwd. ET from Amersham  
High quality sequence stop: 1.

## FEATURES

source

1. 94  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="1342911"  
/clone\_lib="Soares\_papillary\_tumor\_NbHPA"  
/tissue\_type="papillary\_tumor"  
/dev\_stage="adult"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: papillary gland; Vector: pT73p (Pharmacia)  
with a modified polylinker. Site 1: Not I; Site 2: Eco  
RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer  
[5'-TGTTACCAATCTGAAAGTGGAGCGCGCATTTTCTTTTCTTTT  
TTTTT-3'], double-stranded cDNA was size selected, ligated  
to Eco RI adapters (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of a modified pT73  
vector (Pharmacia). Library went through one round of  
normalization to a cot = 5. Library constructed by Bento  
Soares and M. Fatima Bonaldo. RNA from sporadic papillary  
adenomas was kindly provided by Dr. Stephen Marx, National  
Institute of Diabetes and Digestive and Kidney Diseases,  
NIH."



[illegible]

REFERENCE 1 (bases 1 to 65)  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theising,B., Wylie,T., Lennan,G., Soares,B., Wilson,R. and  
 Waterston,R.  
 The WashU-HMT Mouse EST Project  
 Unpublished (1996)  
 CONTACT: Marra M/Mouse EST Project  
 WashU-HMT Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:333156  
 Seq primer: -28m13 rev1 ET from Amerham  
 High quality sequence stop: 62.  
 Location/Qualifiers  
 1. 65  
 /organism="Mus musculus"  
 /strain="C57BL/6 x CBA"  
 /db\_xref="taxon:10090"  
 /clone\_image="IMAGE:552364"  
 /clone\_lib="Stratagene mouse lung 937302"  
 /sex="female"  
 /tissue\_type="lung"  
 /dev\_stage="6-8 month old"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /note="Organ: lung; Vector: pBluescript SK-; Site.1: EcoRI  
 ; Site.2: XhoI; Cloned unidirectionally. Primer: oligo  
 dt. 6-8 month old female lung and 1.5 year old male lung  
 were source of mRNA. Average insert size: 1.5 Kb; Uni-ZAP  
 XR Vector; -5' adaptor sequence: 5' GAATTCGGGACGAG 3' -3'  
 adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."  
 7 a 31 c 23 g 4 t

BASE COUNT  
 ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 65;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGTCGGAGCGCTGATC 19  
 ||| ||||| ||| |||  
 Db 59 GGGCCGGAGCTGCATC 42

RESULT 12  
 BJ076607/c 68 bp mRNA linear EST 11-DEC-2001  
 LOCUS BJ076607 NIBB Mochil normalized Xenopus tailbud library Xenopus  
 DEFINITION laevis cDNA clone XL058603 3', mRNA sequence.  
 ACCESSION BJ076607  
 VERSION BJ076607.1 GI:17521523  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM  
 Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 Xenopodinae; Xenopus.  
 1 (bases 1 to 68)  
 Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara  
 Y.  
 Expressed genes in X. laevis embryo  
 Unpublished (2001)  
 CONTACT: Tadasu Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856

TITLE  
 JOURNAL  
 COMMENT

REFERENCE  
 AUTHORS

Fax: 81-559-81-6855  
 Email: tshin@genes.nig.ac.jp.  
 Location/Qualifiers  
 1. 68  
 /organism="Xenopus laevis"  
 /db\_xref="taxon:8355"  
 /clone\_image="XL058603"  
 /clone\_lib="NIBB Mochil normalized Xenopus tailbud  
 library"  
 /tissue\_type="whole embryo"  
 /dev\_stage="stage 25"  
 /note="Vector: pBSRN3; Site.1: NotI; Site.2: EcoRI; CDNAS  
 were oligo-dT primed and directionally cloned. Staging  
 according to Nieuwkoop and Faber. Library is subtracted  
 and was constructed by N. Garrett and A.M. Zorn,  
 (Wellcome/CRC Institute)."  
 28 a 13 c 11 g 16 t

BASE COUNT  
 ORIGIN

Query Match 66.0%; Score 13.2; DB 13; Length 68;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGTCGGAGCGCTGATCA 20  
 ||| ||||| |||||  
 Db 40 GTTTCAGAGCTGATCA 23

RESULT 13  
 AI902463/c 75 bp mRNA linear EST 30-MAR-2000  
 LOCUS AI902463 CM-BT006-170299-218 BT006 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION AI902463  
 ACCESSION AI902463  
 VERSION AI902463.1 GI:6492850  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM  
 human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 75)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 CONTACT: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/seq/gethtml.pl?l=CMat2-CM-BT006-218.html  
 &t3=170299&t4=1)  
 Seq primer: puc 18 forward.  
 Location/Qualifiers  
 1. 75  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="BT006"  
 /sex="female"  
 /dev\_stage="Adult"  
 /note="Organ: breast; Vector: puc18; Site.1: SmaI; Site.2:  
 SmaI; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No. 196

TITLE  
 JOURNAL  
 COMMENT

REFERENCE  
 MEDLINE  
 COMMENT

,716 - Ludwig Institute for Cancer Research) profiles into the pUC18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

BASE COUNT 17 a 19 c 21 g 12 t 6 others

Query Match 66.0%; Score 13.2; DB 9; Length 75;  
Best Local Similarity 83.3%; Pred. No. 1.1e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGGGTCGAGCCTGAT 18  
||||| ||||| |||||  
Db 72 TGGGTCCCGAGCTGAT 55

RESULT 14  
B1519819 45 bp mRNA linear EST 29-AUG-2001  
LOCUS 603062250T1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5211228 3',  
DEFINITION mRNA sequence.

ACCESSION B1519819  
VERSION B1519819  
KEYWORDS GI:15344611  
SOURCE EST.  
ORGANISM human.

REFERENCE 1 (bases 1 to 45)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapds-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L14M1530 row: d column: 13  
High quality sequence stop: 45.

FEATURES  
source location/Qualifiers

1.45  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="5211228"  
/clone\_id="NIH\_MGC\_118"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"  
/note="Vector: PCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH\_MGC Library."  
BASE COUNT 8 a 11 c 17 g 9 t

ORIGIN

Query Match 64.0%; Score 12.8; DB 13; Length 45;  
Best Local Similarity 87.5%; Pred. No. 1.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TCCGAGCCTGATCA 20  
||||| ||||| |||||  
Db 28 TCCAGAGCCTGATCA 13

RESULT 15

AA906833 58 bp mRNA linear EST 09-JUN-1998  
LOCUS OK73104.S1 NCI-CGAP\_GC4 Homo sapiens cDNA clone IMAGE:1519615 3'  
DEFINITION Similar to SW:NPX\_HUMAN P55769 NHP2/RS6 FAMILY PROTEIN YEL026W  
HOMOLOGY: mRNA sequence.

ACCESSION AA906833  
VERSION AA906833.1  
KEYWORDS GI:3042077  
SOURCE EST.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 58)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapds-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.llnl.gov/bdrp/image/image.html

Trace considered overall poor quality  
Insert Length: 599 Std Error: 0.00  
Seq primer: -40ml3 fwd. RT from Amersham  
High quality sequence stop: 1.

FEATURES  
source location/Qualifiers

1.58  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="1519615"  
/clone\_id="NCI-CGAP\_GC4"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 10 a 13 c 24 t

ORIGIN

Query Match 64.0%; Score 12.8; DB 9; Length 58;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TCCGAGCCTGATCA 20  
||||| ||||| |||||  
Db 37 TCCGAGCCTGATCA 52

Search completed: November 26, 2002, 04:06:50  
Job time : 767.8 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2002, 14:46:40 ; Search time 302.2 Seconds

(Without alignments)  
1926.063 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20  
Sequence: 1 ttttcagggaatccggggg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Geneml:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_lys:\*  
12: gb\_lys:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: gb\_vl:\*  
16: em\_fun:\*  
17: em\_fun:\*  
18: em\_fun:\*  
19: em\_mu:\*  
20: em\_mu:\*  
21: em\_mu:\*  
22: em\_mu:\*  
23: em\_mu:\*  
24: em\_mu:\*  
25: em\_mu:\*  
26: em\_mu:\*  
27: em\_mu:\*  
28: em\_mu:\*  
29: em\_mu:\*  
30: em\_mu:\*  
31: em\_mu:\*  
32: em\_mu:\*  
33: em\_mu:\*  
34: em\_mu:\*  
35: em\_mu:\*  
36: em\_mu:\*  
37: em\_mu:\*  
38: em\_mu:\*  
39: em\_mu:\*  
40: em\_mu:\*  
41: em\_mu:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	52	5	TCUMIT03
2	14.2	71.0	75	9	AB00468546
3	13.8	69.0	53	5	TCUMIT03
4	13.6	68.0	51	6	AX160046
5	13.6	68.0	51	6	AX160045
6	13.6	68.0	54	5	TOLMIT03
7	13.6	68.0	97	11	AL772837
8	13.4	67.0	21	6	AR020977
9	13.4	67.0	21	6	AR020978
10	13.4	67.0	21	6	AR043392
11	13.4	67.0	21	6	AR043393
12	13.4	67.0	21	6	AR062307
13	13.4	67.0	21	6	AR062308
14	13.4	67.0	21	6	AR183766
15	13.4	67.0	21	6	AR183767
16	13.2	66.0	36	6	AR061022
17	13.2	66.0	36	6	AX018732
18	13.2	66.0	53	5	TREMIT03
19	13.2	66.0	53	5	TREMIT03
20	13.2	66.0	53	5	TREMIT03
21	13.2	66.0	59	9	HUMACX1XC2
22	12.8	64.0	22	6	AX365220
23	12.8	64.0	28	6	AX229851
24	12.8	64.0	51	6	AX162296
25	12.8	64.0	66	9	AF189424
26	12.8	64.0	91	1	AF087267
27	12.6	63.0	24	6	AX445637
28	12.6	63.0	28	6	AX252923
29	12.6	63.0	28	6	AX342689
30	12.6	63.0	28	6	AX374942
31	12.6	63.0	80	9	HUMIGHZCJ
32	12.6	63.0	84	9	AB00468530
33	12.6	63.0	88	14	PVXANPTII
34	12.4	62.0	76	3	TA28SRNAB
35	12.4	62.0	78	3	HA28SRNAC
36	12.4	62.0	78	3	TV28SRNAC
37	12.4	62.0	79	3	PH28SRNAC
38	12.4	62.0	81	6	ARI56804
39	12.4	62.0	85	10	MUSPCD02
40	12.2	61.0	19	6	A38742
41	12.2	61.0	19	6	ARI02156
42	12.2	61.0	19	6	AX131000
43	12.2	61.0	20	4	DOGPA4301
44	12.2	61.0	20	6	AX023313
45	12.2	61.0	21	6	AX058986

## ALIGNMENTS

RESULT 1  
TCUMIT03/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SEGMENT  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

TCUMIT03 52 bp DNA linear VRT 23-SEP-1999  
Toxostoma curvirostre isolate CBH67X tRNA-Glu gene, partial  
sequence; mitochondrial gene for mitochondrial product.  
AF154453  
AF154453.1 GI:5918791

3 of 6  
Toxostoma curvirostre.  
Mitochondrion Toxostoma curvirostre.  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Passeriformes; Sturnidae; Toxostoma.  
1 (bases 1 to 52)  
Zink, R.M., Dittmann, D.L., Klicka, J. and Blackwell, R.C.

Pred. No. 18 the number of results predicted by chance to have a

TITLE	Evolutionary patterns of morphometrics, allozymes and mitochondrial DNA in thrashers (Toxostoma)
JOURNAL	The Auk (1999) In press
REFERENCE	2 (bases 1 to 52)
AUTHORS	Zink, R.M., Dittmann, D.L., Klicka, J. and Blackwell-Rago, R.C.
TITLE	Direct Submission
JOURNAL	Submitted (26-MAY-1999) Bell Museum, University of Minnesota, 100 Ecology Bldg, 1987 Upper Buford Circle, St Paul, MN 55108, USA
FEATURES	Location/Qualifiers
Source	1..52
	/organism="Toxostoma curvirostre"
	/organella="mitochondrion"
	/isolate="CBTH67X"
	/specimen_voucher="RMZ 2951, LSU Museum of Zoology"
	/db_xref="taxon:99878"
	/sex="male"
	/country="USA:Texas, 10 miles SSE of Charlotte"
	/note="Isolated May 26, 1992"
	<1..>52
trna	/product="trna-glu"
BASE COUNT	12 a 12 c 9 g 19 t
ORIGIN	
Query Match	71.0%, Score 14.2; DB 5; Length 52;
Best Local Similarity	84.2%; Pred. No. 1.6e+04;
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY	2 TTTTCAGGGAATCCGGGG 20
Db	32 TTTTCAGGAATCCGGAG 14
RESULT 2	
AB00468546	
LOCUS	AB00468546 75 bp DNA linear PRI 14-APR-2000
DEFINITION	Human gene for Type XIX collagen a1 chain, exon 46.
ACCESSION	AB004622
VERSION	AB004622.1 GI:2598711
KEYWORDS	Type XIX collagen a1 chain.
SEGMENT	46 of 52
SOURCE	Homo sapiens DNA, clone:KIG12.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1
AUTHORS	Khaleduzaman, M., Sumiyoshi, H., Ueki, Y., Inoguchi, K., Niomiya, Y.
TITLE	and Yoshioaka, H.
JOURNAL	Structure of the human type XIX collagen (COL19A1) gene, which
MEDLINE	suggests it has arisen from an ancestor gene of the FACIT family
REFERENCE	Genomics 45 (2), 304-312 (1997)
AUTHORS	2 (bases 1 to 75)
TITLE	Yoshioaka, H.
JOURNAL	Direct Submission
	Submitted (05-JUN-1997) Hidekatsu Yoshioaka, Okayama University
	Medical School, Molecular Biology and Biochemistry; 2-5-1
	Shikata-cho, Okayama, Okayama 700, Japan
	(E-mail:mbb@ccs.cc.okayama-u.ac.jp, Tel:086-235-7128,
	Fax:086-222-7768)
FEATURES	Location/Qualifiers
Source	1..75
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="KIG12"
	16..60
	/gene="COL19A1"
	/number=46
BASE COUNT	22 a 14 c 20 g 19 t
ORIGIN	
Query Match	71.0%, Score 14.2; DB 9; Length 75;
Best Local Similarity	84.2%; Pred. No. 1.6e+04;
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY	1	TTTTTCAGGGAATCCGGG	19
DB	8	TTTTTCAGGGAATCATCGG	26
RESULT 3			
TCIMT03/c			
LOCUS		TCIMT03	53 bp DNA linear VRT 23-SEP-1999
DEFINITION		Toxostoma cinereum isolate GRH4BN tRNA-Glu gene, partial sequence.	
ACCESSION		AF154459	
VERSION		AF154459.1	GI:5918797
KEYWORDS			
SEGMENT			
SOURCE			
ORGANISM			
			3 of 6
			Toxostoma cinereum.
			Mitochondrion Toxostoma cinereum
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			Archosauria; Aves; Neognathae; Passeriformes; Sturnidae; Toxostoma.
REFERENCE			1 (bases 1 to 53)
AUTHORS			Zink,R.M., Dittmann,D.L., Klicka,J. and Blackwell-Rago,R.C.
TITLE			Evolutionary patterns of morphometrics, allozymes and mitochondrial DNA in thrashers (Toxostoma)
JOURNAL			The Auk (1999) In press
REFERENCE			2 (bases 1 to 53)
AUTHORS			Zink,R.M., Dittmann,D.L., Klicka,J. and Blackwell-Rago,R.C.
TITLE			Direct Submission
JOURNAL			Submitted (26-MAY-1999) Bell Museum, University of Minnesota, 100 Ecology Bldg, 1987 Upper Buford Circle, St Paul, MN 55108, USA
FEATURES			location/Qualifiers
SOURCE			1..53
			/organism="Toxostoma cinereum"
			/organelle="mitochondrion"
			/isolate="GRH4BN"
			/specimen_voucher="B16587, LSU Museum of Zoology"
			/specimen_voucher="RMZ 2165, American Museum, New York"
			/db_xref="taxon:99877"
			/sex="female"
			/country="Mexico:Baja California, 3 km. west of Camalu"
			/note="Isolated November 10, 1983"
			<1..>53
tRNA			/product="tRNA-Glu"
BASE COUNT			13 a 14 c 9 g 17 t
ORIGIN			
			Query Match 69.0%; Score 13.8; DB 5; Length 53;
			Best Local Similarity 88.2%; Pred. No. 2.6e+04;
			Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	2	TTTTCAGGGAATCCGGG	18
DB	33	TTTTTCAGGAATCTCGG	17
RESULT 4			
LOCUS		AX160046	50 bp DNA linear PAT 22-JUN-2001
DEFINITION		Sequence 3374 from Patent WO0140521.	
ACCESSION		AX160046	
VERSION		AX160046.1	GI:14541377
KEYWORDS			
SOURCE			.
ORGANISM			human.
			Homo sapiens
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE			1 (bases 1 to 50)
AUTHORS			Shmukets,R.A. and Leach,M.
TITLE			Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL			Patent: WO 0140521-A 3374 07-JUN-2001;
Curagen Corporation (US)			Location/Qualifiers
FEATURES			1..50
SOURCE			

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
misc\_feature  
25..26  
/note="Nucleotide deleted between bases 25 and 26  
Accession number cg43253001"  
misc\_feature  
26  
/note="2 of 2 allelic variants (3373 is other entry)"  
BASE COUNT 10 a 12 c 19 g 9 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 50;  
Best Local Similarity 80.0%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTTTCAGGGAATCCGGGG 20  
DB 4 TGTCTCGGGAGACCGGGG 23

RESULT 5  
AX160045  
LOCUS AX160045 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 3373 from Patent WO0140521.  
ACCESSION AX160045  
VERSION AX160045.1 GI:14541376  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 51)  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0140521-A 3373 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES  
source location/Qualifiers  
1..51  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
misc\_feature  
26  
/note="1 of 2 allelic variants (3374 is other entry)  
Accession number cg43253001"  
BASE COUNT 10 a 12 c 20 g 9 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 51;  
Best Local Similarity 80.0%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTTTCAGGGAATCCGGGG 20  
DB 4 TGTCTCGGGAGACCGGGG 23

RESULT 6  
TO1MIT03/c  
LOCUS TO1MIT03 54 bp DNA linear VRT 23-SEP-1999  
DEFINITION Toxostoma ocellatum isolate OCTH2MX tRNA-Glu gene, partial  
sequence; mitochondrial gene for mitochondrial product.  
ACCESSION AF154447  
VERSION AF154447.1 GI:5918785  
KEYWORDS  
SEGMENT 3 of 6  
SOURCE Toxostoma ocellatum.  
ORGANISM Mitochondrion Toxostoma ocellatum  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Passeriformes; Sturnidae; Toxostoma.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Zink,R.M., Dittmann,D.L., Klicka,J. and Blackwell-Rago,R.C.  
TITLE Evolutionary patterns of morphometrics, allozymes and mitochondrial  
DNA in thrashers (Toxostoma)  
JOURNAL The Auk (1999) In press

REFERENCE 2 (bases 1 to 54)  
AUTHORS Zink,R.M., Dittmann,D.L., Klicka,J. and Blackwell-Rago,R.C.  
TITLE Direct Submission  
JOURNAL Submitted (26-MAY-1999) Bell Museum, University of Minnesota, 100  
Ecology Bldg, 1967 Upper Buford Circle, St Paul, MN 55108, USA  
FEATURES  
source location/Qualifiers  
1..54  
/organism="Toxostoma ocellatum"  
/organella="mitochondrion"  
/isolate="OCTH2MX"  
/specimen\_voucher="RMZ 2190, American Museum, New York"  
/specimen\_voucher="BJ6570, LSU Museum of Zoology"  
/db\_xref="taxon:99881"  
/sex="male"  
/country="Mexico:Oaxaca, 5 km SE of Matatlan"  
/note="Isolated November 18, 1993"  
<1..>54  
/product="tRNA-Glu"  
BASE COUNT 15 a 15 c 7 g 17 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 5; Length 54;  
Best Local Similarity 80.0%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTTTCAGGGAATCCGGGG 20  
DB 34 TTTTCAGGGAATCCGGAG 15

RESULT 7  
AL772837/c  
LOCUS AL772837 97 bp DNA linear STS 19-JUN-2002  
DEFINITION Arabidopsis thaliana transposon insertion STS SM\_3.805, sequence  
tagged site.  
ACCESSION AL772837  
VERSION AL772837.1 GI:21535024  
KEYWORDS STS; STS, sequence tagged site.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE 1  
AUTHORS Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B.,  
Murphy,G., Langham,S., Legrys,C., Jones,J.D.G. and Bevan,M.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 97)  
AUTHORS Clarke,J.H.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUN-2002) Clarke J.H., John Innes Centre, Colney  
Lane, Norwich, NR4 7UJ, UK  
COMMENT AT denotes an activation tag dissociation transposon within a  
single line. ET an enhancer trap dissociation transposon. GT a gene  
trap dissociation transposon. MT a mis-expression enhancer trap  
dissociation transposon. SM a defective suppressor mutator  
transposon. \_3 denotes a sequence derived from the 3' end of the  
transposon. \_5 denotes a sequence derived from the 5' end of the  
transposon. BBSRC GARNET, ARIS project  
On-line seed stock requests: [http://nasc.nott.ac.uk/NASC\\_stock\\_code](http://nasc.nott.ac.uk/NASC_stock_code): N55688.  
FEATURES  
source location/Qualifiers  
1..97  
/organism="Arabidopsis thaliana"  
/variety="Landsberg erecta"  
/db\_xref="taxon:3702"  
/clone="AC006223"  
1..97  
/standard\_name="SM\_3.805"  
BASE COUNT 43 a 17 c 13 g 24 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 11; Length 97;

Best Local Similarity 80.0%, Pred. No. 3.2e+04; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 4;

RESULT 8	LOCUS	DEFINITION	ACCESSION	VERSION	GI:3975592
AR020977	AR020977	Sequence 9 from patent US 5789245.	AR020977	AR020977.1	GI:3975592
		21 bp	DNA	linear	PAT 05-DEC-1998

REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 21) Dubensky,T.W.Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W., Jolly,D.J. and Driver,D.A..
TITLE	Alphavirus structural protein expression cassettes
JOURNAL	Patent: US 5789245-A 9 04-Aug-1998;
FEATURES	Location/Qualifiers

BASE COUNT	ORIGIN
3 a	5 t
8 c	5 g

Query Match	67.0%	(Score 13.4)	DB 6	Length 21
Best Local Similarity	93.3%	Pred. No. 4.6e+04		
Matches 14	Conservative 0	Mismatches 1	Indels 0	Gaps 0

Qy	2	TTTTCAGGGATCCG	16
Db	3	TTTTCAGGGATCCG	17

RESULT	9			
LOCUS	AR020978/c			
DEFINITION	Sequence from patent US 5789245.	21 bp	DNA	linear
ACCESSION	AR020978			PAT 05-DEC-1998
VERSION	AR020978.1			
KEYWORDS	GI:3975593			
SOURCE	Unknown.			
ORGANISM	Unknown.			

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 21)	Dubensky, T.W., Jr., Polo, J.M., Ibanez, C.E., Chang, S.M.W., Jolly, D.J. and Driver, D.A.	Alphavirus structural protein expression cassettes	Patent: US 5789245-A 10 04-AUG-1998;

BASE COUNT	/organism="unknown"			
ORIGIN	5 a	5 c	8 g	3 t

Query Match	67.0%	Score 13.4	DB 6	Length 21
Best Local Similarity	93.3%	Pred. No. 4.6e+04		
Matches 14	Conservative 0	Mismatches 1	Indels 0	Gaps 0

Oy	2	TTTTCAGGGATCCG	16
Db	19	TTTTCAGGGATCCG	5

RESULT 10			
AR043392			
LOCUS	AR043392	21 bp	DNA
DEFINITION	Sequence 9 from patent US 5814462.		linear
ACCESSION	AR043392		PAT 29-SEP-1999

VERSION	AR043392.1	GI:5964400
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	GI:5964400

REFERENCE	1 (bases 1 to 21)
AUTHORS	Dubensky, T.W. Jr., Polo, J.M., Jolly, D.J. and Driver, D.A.
TITLE	Eukaryotic layered vector initiation systems
JOURNAL	Patent: US 5614482-A 9 29-SEP-1998;
FEATURES	Location/Qualifiers
Source	1 21

BASE COUNT	3	a	8	c	5	g	5	t
ORIGIN	/organism="unknown"							

Query Match	67.0%	Score 13.4	DB 6	Length 21
Best Local Similarity	93.3%	Pred. Nc. 4.6e+04		
Matches 14	Conservative 0	Mismatches 1	Indels 0	Gaps 0

Qy	2	TTTTCAGGGAATCCG	16
	1		11
	2		11
	3	TTTTCAGGGAATCCG	17
Db			

RESULT 11			
AR043393/c			
LOCUS	AR043393	21 bp	DNA
DEFINITION	Sequence 10 from patent US 5814482.		linear
			PAT 29-SEP-1999

VERSION	AR043393.1	GI:5964401
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 21)	Dubensky, T.W. Jr., Polo, J.M., Jolly, D.J. and Driver, D.A.	Eukaryotic layered vector initiation systems	Patent: US 5814482-A, 10-29-SEP-1998; Foskett/duffy/00-3142

BASE COUNT	/organism="unknown"							
ORIGIN	5	a	5	c	8	g	3	t

Query Match	67.0%	Score 13.4	DB 6	Length 21
Best Local Similarity	93.3%	Pred. No. 4.6e+04		
Matches 14	Conservative 0	Mismatches 1	Indels 0	Gaps 0

Qy	2	TTTTCAGGGAAATCCG	16
Db	19	TTTTCAGGGAAATCCG	5

RESULT 12		
AR062307		
LOCUS		
DEFINITION	Sequence 9 from patent US 5843723.	21 bp DNA
		Linear
		PAT 29-SEP-1999

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.

REFERENCE  
AUTHORS

1 (bases 1 to 21)  
Dubensky, T.W. Jr.,  
Jolly, D.J., Driver, D.A.  
Polo, J.M., Ibanez, C.E., Chang, S.M.W.,  
Jolly, D.J., Driver, D.A. and Belli, B.A.

FEATURES	Location/Qualifiers
source	1. .21
BASE COUNT	/organism="unknown"
ORIGIN	3 a 8 c 5 g 5 t



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Query Match          67.0%; Score 13.4; DB 6; Length 21;
Best Local Similarity 93.3%; Pred. No. 4.6e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTTTCAGGCGATCCG 16
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DB 3 TTTTCAGGCGATCCG 17

RESULT 13
AR062308/AR062308 21 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5843723.
ACCESSION AR062308
VERSION AR062308.1 GI:5989999
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W.,
          Jolly,D.J., Driver,D.A. and Belli,B.A.
TITLE Alphavirus vector constructs
JOURNAL Patent: US 5843723-A 10 01-DEC-1998;
FEATURES
    source
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BASE COUNT 5 a 5 c 8 g 3 t
ORIGIN

Query Match          67.0%; Score 13.4; DB 6; Length 21;
Best Local Similarity 93.3%; Pred. No. 4.6e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTTTCAGGCGATCCG 16
    ||||| |||||
DB 19 TTTTCAGGCGATCCG 5

RESULT 14
ARI83766
LOCUS ARI83766 21 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 9 from patent US 6342372.
ACCESSION ARI83766
VERSION ARI83766.1 GI:20227735
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dubensky,T.W. Jr., Polo,J.M. and Driver,D.A.
TITLE Eukaryotic layered vector initiation systems for production of
        recombinant proteins
JOURNAL Patent: US 6342372-A 9 29-JAN-2002;
FEATURES
    source
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            /organism="unknown"
BASE COUNT 3 a 8 c 5 g 5 t
ORIGIN

Query Match          67.0%; Score 13.4; DB 6; Length 21;
Best Local Similarity 93.3%; Pred. No. 4.6e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTTTCAGGCGATCCG 16
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DB 3 TTTTCAGGCGATCCG 17

RESULT 15
ARI83767/C
LOCUS ARI83767 21 bp DNA linear PAT 20-APR-2002

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DEFINITION Sequence 10 from patent US 6342372.
ACCESSION ARI83767
VERSION ARI83767.1 GI:20227736
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dubensky,T.W. Jr., Polo,J.M. and Driver,D.A.
TITLE Eukaryotic layered vector initiation systems for production of
        recombinant proteins
JOURNAL Patent: US 6342372-A 10 29-JAN-2002;
FEATURES
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            /organism="unknown"
BASE COUNT 5 a 5 c 8 g 3 t
ORIGIN

Query Match          67.0%; Score 13.4; DB 6; Length 21;
Best Local Similarity 93.3%; Pred. No. 4.6e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTTTCAGGCGATCCG 16
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DB 19 TTTTCAGGCGATCCG 5

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(Without alignments)  
439.108 Million cell updates/sec

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Perfect score: 20  
Sequence: 1 ttttcagggaatccggggg 20

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- 11: /cgn2\_6/ptodata/2/pubpna/US10\_PUB\_PUB.seq:\*\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_PUB\_PUB.seq:\*\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	12.6	63.0	23	10	US-09-303-510-40
2	12.6	63.0	23	10	US-09-303-040-40
3	12.6	63.0	69	10	US-09-785-632A-44
4	12.2	61.0	36	10	US-09-749-234A-27
5	12.2	61.0	87	10	US-09-923-876-6135
6	12.2	61.0	88	10	US-09-783-590-4956
7	12.2	61.0	88	10	US-09-783-590-7099
8	12.2	61.0	89	10	US-09-878-574-6486
9	12.2	61.0	100	10	US-09-864-761-24917
10	12.2	60.0	40	10	US-09-759-143-850
11	12.2	60.0	40	10	US-09-780-669-850
12	12.2	60.0	40	10	US-09-822-827-850
13	12.2	60.0	84	10	US-09-864-761-32573
14	12.2	60.0	86	10	US-09-864-761-32016
15	11.8	59.0	26	10	US-09-736-169-2
16	11.8	59.0	26	12	US-10-055-174-2
17	11.8	59.0	69	10	US-09-764-847-367
18	11.8	59.0	97	10	US-09-294-093B-2105
19	11.6	58.0	31	10	US-09-870-122-8

C	20	11.6	58.0	36	10	US-09-006-298-2	Sequence 2, Appl
C	21	11.6	58.0	45	10	US-09-781-802-59	Sequence 59, Appl
C	22	11.6	58.0	48	5	US-09-900-425A-29	Sequence 29, Appl
C	23	11.6	58.0	50	10	US-09-892-864A-26	Sequence 26, Appl
C	24	11.6	58.0	50	10	US-09-996-561-27	Sequence 27, Appl
C	25	11.6	58.0	68	10	US-09-783-590-1427	Sequence 1427, Ap
C	26	11.6	58.0	74	10	US-09-974-300-4065	Sequence 4065, Ap
C	27	11.6	58.0	85	10	US-09-864-761-31082	Sequence 31082, A
C	28	11.4	57.0	18	10	US-09-789-556A-41	Sequence 41, Appl
C	29	11.4	57.0	31	10	US-09-801-274-141	Sequence 141, App
C	30	11.4	57.0	32	10	US-09-769-864-50	Sequence 50, Appl
C	31	11.4	57.0	38	10	US-09-972-331-7	Sequence 7, Appl
C	32	11.4	57.0	48	10	US-09-766-378A-15	Sequence 15, Appl
C	33	11.4	57.0	52	10	US-09-978-274A-13	Sequence 13, Appl
C	34	11.4	57.0	55	10	US-09-865-099-41	Sequence 41, Appl
C	35	11.4	57.0	55	12	US-10-051-852-41	Sequence 41, Appl
C	36	11.4	57.0	93	10	US-09-884-663A-28	Sequence 28, Appl
C	37	11.2	56.0	25	10	US-09-784-911-18	Sequence 18, Appl
C	38	11.2	56.0	27	9	US-09-731-449-60	Sequence 60, Appl
C	39	11.2	56.0	31	10	US-09-801-274-505	Sequence 505, App
C	40	11.2	56.0	39	10	US-09-859-214-63	Sequence 63, Appl
C	41	11.2	56.0	42	9	US-09-924-647-5	Sequence 5, Appl
C	42	11.2	56.0	42	9	US-09-905-291A-61	Sequence 61, Appl
C	43	11.2	56.0	42	10	US-09-767-609-5	Sequence 5, Appl
C	44	11.2	56.0	42	10	US-09-909-320-61	Sequence 61, Appl
C	45	11.2	56.0	42	10	US-09-909-088B-61	Sequence 61, Appl

## ALIGNMENTS

RESULT 1  
US-09-303-510-40  
; Sequence 40, Application US/09303510A  
; Patent No. US20020028208A1  
; GENERAL INFORMATION:  
; APPLICANT: Collisson, Ellen W.  
; APPLICANT: Hash, Stephen M.  
; APPLICANT: Choi, InSoo  
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline  
; FILE REFERENCE: 54954  
; CURRENT APPLICATION NUMBER: US/09/303.510A  
; CURRENT FILING DATE: 1999-04-30  
; EARLIER APPLICATION NUMBER: 60/083,869  
; EARLIER FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-303-510-40

Query Match 63.0%; Score 12.6; DB 10; Length 23;  
Best local similarity 78.9%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTTCAGGATCCGGG 19  
Db 5 TTTTTCAGGATCCGGG 23

RESULT 2  
US-09-303-040-40  
; Sequence 40, Application US/09303040  
; Patent No. US20020051792A1  
; GENERAL INFORMATION:  
; APPLICANT: Winslow, Barbara J.  
; APPLICANT: Cochran, Mark D.  
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding

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; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
; FILE OF INVENTION: Feline Interferon-gamma And Uses Thereof
; FILE REFERENCE: 54957-B
; CURRENT APPLICATION NUMBER: US/09/303,040
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,870
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 40
; LENGTH: 23
; TYPE: DNA
; ORGANISM: feline CD86 primer
; US-09-303-040-40

Query Match      63.0%; Score 12.6; DB 10; Length 23;
Best Local Similarity 78.9%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 5 TTTTCAGGTTAGCAGGG 23

RESULT 3
; US-09-785-632A-44
; Sequence 44, Application US/09785632A
; Patent No. US20020061512A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Kwon, Young Do
; APPLICANT: Kim, Hyun-Won
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAINS AND METHODS OF
; FILE OF INVENTION: IDENTIFYING SAME
; FILE REFERENCE: 12279-002001
; CURRENT APPLICATION NUMBER: US/09/785,632A
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(69)
; US-09-785-632A-44

Query Match      63.0%; Score 12.6; DB 10; Length 69;
Best Local Similarity 78.9%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TTTTCAGGGAATCCGGG 20
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DB 5 TTTTCAGGGAATGCGCG 23

RESULT 4
; US-09-749-234A-27/C
; Sequence 27, Application US/09749234A
; Patent No. US2002006817A1
; GENERAL INFORMATION:
; APPLICANT: HOFMANN, Joachim
; APPLICANT: SCHMID, Karlheinz
; APPLICANT: PAULI, Annette
; TITLE OF INVENTION: DICTYOCALUS VIVIPARUS ANTIGEN FOR THE
; DIAGNOSIS OF LUNGWORM INFESTATION AND FOR VACCINATION
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
```

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; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/749,234A
; FILING DATE: 27-Dec-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/403,092
; FILING DATE: 199-10-15
; APPLICATION NUMBER: DE 197 15 586.3
; FILING DATE: 15-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 038311/0103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1..36
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
; US-09-749-234A-27

Query Match      61.0%; Score 12.2; DB 10; Length 36;
Best Local Similarity 82.4%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTTCAGGGAATCCGGG 18
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DB 17 TGTTCAGGGAATCCGG 1

RESULT 5
; US-09-923-876-6135/C
; Sequence 6135, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 6135
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700458438H1
; NAME/KEY: unsure
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LOCATION: 31, 47, 59, 86  
OTHER INFORMATION: a, t, c, g, or other  
US-09-923-876-6135

Query Match 61.0%; Score 12.2; DB 10; Length 87;  
Best Local Similarity 77.8%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TTTCAGGGAATCCGGGG 20  
DB 52 TTTCNCGAATCCGGGG 35

## RESULT 6

US-09-783-590-4956/C  
Sequence 4956, Application US/09783590  
Patent No. US20020110850A1  
GENERAL INFORMATION:  
APPLICANT: Dillon, Patrick J.  
APPLICANT: Haseltine, William A.  
APPLICANT: Li, Haodong  
APPLICANT: Rosen, Craig A.  
APPLICANT: Ruben, Steven M.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
FILE REFERENCE: PO-16.2C1  
CURRENT APPLICATION NUMBER: US/09/783,590  
CURRENT FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 08/420,856  
PRIOR FILING DATE: 1995-04-12  
PRIOR APPLICATION NUMBER: 08/346,731  
PRIOR FILING DATE: 1994-11-21  
NUMBER OF SEQ ID NOS: 12485  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 4956  
LENGTH: 88  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (15)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (86)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-783-590-4956

Query Match 61.0%; Score 12.2; DB 10; Length 88;  
Best Local Similarity 77.8%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTCAAGGAATCCGGG 18  
DB 20 TTTTNNAGCAATCCGGG 3

## RESULT 7

US-09-783-590-7099  
Sequence 7099, Application US/09783590  
Patent No. US20020110850A1  
GENERAL INFORMATION:  
APPLICANT: Dillon, Patrick J.  
APPLICANT: Haseltine, William A.  
APPLICANT: Li, Haodong  
APPLICANT: Rosen, Craig A.  
APPLICANT: Ruben, Steven M.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
FILE REFERENCE: PO-16.2C1  
CURRENT APPLICATION NUMBER: US/09/783,590  
CURRENT FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 08/420,856  
PRIOR FILING DATE: 1995-04-12  
PRIOR APPLICATION NUMBER: 08/346,731  
PRIOR FILING DATE: 1994-11-21

NUMBER OF SEQ ID NOS: 12485  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 7099  
LENGTH: 88  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (53)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-783-590-7099

Query Match 61.0%; Score 12.2; DB 10; Length 88;  
Best Local Similarity 82.4%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTTCAGGGAATCCGGGG 20  
DB 19 TTTCAGGGAATCCGGGG 35

## RESULT 8

US-09-878-574-6486/C  
Sequence 6486, Application US/09878574  
Patent No. US20020110548A1  
GENERAL INFORMATION:  
APPLICANT: Byrum, Joseph R.  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Thompson, Michael D.  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21(15401)B  
CURRENT APPLICATION NUMBER: US/09/878,574  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 09/333,535  
PRIOR FILING DATE: 1999-06-14  
NUMBER OF SEQ ID NOS: 15775  
SEQ ID NO 6486  
LENGTH: 89  
TYPE: DNA  
ORGANISM: Glycine max  
OTHER INFORMATION: Clone ID: 701098483H1  
US-09-878-574-6486

Query Match 61.0%; Score 12.2; DB 10; Length 89;  
Best Local Similarity 82.4%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTCAGGGAATCCGGG 18  
DB 84 TTGTCTGGAATCCGGG 68

## RESULT 9

US-09-864-761-24917/C  
Sequence 24917, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03

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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24917
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL133163.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
; OTHER INFORMATION: SWISSPROT HIT: Q90UW9, EVALUATE 9.00e-13
; OTHER INFORMATION: EST HUMAN HIT: BE797925.1, EVALUATE 3.00e-35
; OTHER INFORMATION: NT HIT: X59417.1, EVALUATE 2.00e-35
; US-09-864-761-24917

Query Match      61.0%; Score 12.2; DB 10; Length 100;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      1 TTTTTCAGGAATCCGG 17
        ||||| |||| | ||
Db      55 TTTTTCAGGAAGCTGG 39

```

```

RESULT 10
US-09-759-143-850/c
; Sequence 850, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; US-09-780-669-850

```

```

; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 850
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
; US-09-759-143-850

Query Match      60.0%; Score 12; DB 10; Length 40;
Best Local Similarity 75.0%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy      1 TTTTTCAGGAATCCGGGG 20
        |||| | || | || ||
Db      36 TTTTACGCGATTCTCGGG 17

```

## RESULT 11

```

US-09-780-669-850/c
; Sequence 850, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurlal, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 850
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
; US-09-780-669-850

```

Query Match 60.0%; Score 12; DB 10; Length 40;  
Best Local Similarity 75.0%; Pred. No. 2.5e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 TTTTCAGGGAATCCGGGG 20  
|||||  
Db 36 TTTTACGCGATTTCGTGG 17

RESULT 12  
US-09-822-827-850/c  
; Sequence 850, Application US/09822827  
; Patent No. US20020081680A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.534C1  
; CURRENT APPLICATION NUMBER: US/09/822,827  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 982  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 850  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-09-822-827-850

Query Match 60.0%; Score 12; DB 10; Length 40;  
Best Local Similarity 75.0%; Pred. No. 2.5e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 TTTTCAGGGAATCCGGGG 20  
|||||  
Db 36 TTTTACGCGATTTCGTGG 17

RESULT 13  
US-09-864-761-32573  
; Sequence 32573, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecmlca-x-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 32573  
; LENGTH: 84  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AP000169.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76  
; OTHER INFORMATION: NT HIT: AFI68106.1, EVALU6 3.70e-02  
US-09-864-761-32573

Query Match 60.0%; Score 12; DB 10; Length 84;  
Best Local Similarity 75.0%; Pred. No. 2.7e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 TTTTCAGGGAATCCGGGG 20  
|||||  
Db 13 TGTTCAGCGATTCCAGAG 32

RESULT 14  
US-09-864-761-32016  
; Sequence 32016, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecmlca-x-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30

```
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32016
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000054.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.66
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.62
; OTHER INFORMATION: SWISSPROT HIT: P17525, EVALU 4.10e+00
; OTHER INFORMATION: NT HIT: AF092047.1, EVALU 2.80e+00
US-09-864-761-32016
```

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Query Match          60.0%; Score 12; DB 10; Length 86;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY 1 TTTTCAGGAGATCCGGGG 20
    ||| ||| ||| ||| |||
Db 37 TCTTGAGGAGATCCAGAG 56
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```
RESULT 15
US-09-736-169-2/c
; Sequence 2, Application US/09736169
; Patent No. US20010018055A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Robert E.
; APPLICANT: Tatum, Fred M.
; TITLE OF INVENTION: LKTA Deletion Mutant of P. haemolytica
; FILE REFERENCE: 00295.75997
; CURRENT APPLICATION NUMBER: US/09/736,169
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/280,852
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Pasteurella cf. haemolytica
US-09-736-169-2
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Query Match          59.0%; Score 11.8; DB 10; Length 26;
Best Local Similarity 86.7%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
OY 3 TTTCAGGAGATCCGG 17
    ||| ||| ||| ||| |||
Db 15 TTTCAGGAGATCCGG 1
```

Search completed: November 23, 2002, 06:42:04  
Job time : 18.25 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 25, 2002, 09:10:06 : Search time 755.55 Seconds  
(without alignments)  
428.707 Million cell updates/sec

Title: US-09-296-264-5  
Perfect score: 20  
Sequence: 1 ttttcagggaatccggggg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlmu:\*  
5: em\_estlov:\*  
6: em\_estlpi:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estcl:\*  
10: gb\_estcl2:\*  
11: gb\_hlc:\*  
12: gb\_estcl3:\*  
13: gb\_estcl4:\*  
14: gb\_estcl5:\*  
15: em\_estlun:\*  
16: em\_estlom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_tod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	74.0	79	9	AI925202 wmp9h04.x
2	14.8	74.0	96	14	F26680 HSPD14248 H
3	13.8	69.0	49	9	AI756242 Etesrea41
4	13.8	69.0	64	14	H41671 y006f01.s1
5	13.6	68.0	43	17	AZ346730 1M0082A11
6	13.6	68.0	67	9	AI799398 tw56a01.x

C	7	13.6	68.0	70	9	AI356377
C	8	13.6	68.0	85	14	AA584921
C	9	13.6	68.0	88	14	C01948
C	10	13.6	68.0	90	10	AM102784
C	11	13.6	68.0	100	12	B672884
C	12	13.4	67.0	63	14	T68724
C	13	13.4	67.0	50	9	AA140294
C	14	13.2	66.0	79	9	AI107883
C	15	13.2	66.0	67	9	AU014487
C	16	13.2	66.0	73	14	R62624
C	17	13.2	66.0	76	9	AA918583
C	18	13.2	66.0	77	17	A2769484
C	19	13.2	66.0	79	9	AA411778
C	20	13.2	66.0	82	12	BEB02294
C	21	13.2	66.0	97	9	A1649260
C	22	13.2	66.0	100	13	B0534085
C	23	13	65.0	91	17	A2623789
C	24	12.8	64.0	37	9	AA992758
C	25	12.8	64.0	50	9	AU107657
C	26	12.8	64.0	76	14	T86922
C	27	12.8	64.0	91	14	T91269
C	28	12.8	64.0	94	13	BM507198
C	29	12.6	63.0	34	9	A1632285
C	30	12.6	63.0	41	9	AU269153
C	31	12.6	63.0	46	10	AV671661
C	32	12.6	63.0	53	17	B01982
C	33	12.6	63.0	57	9	AU259067
C	34	12.6	63.0	69	17	BH625831
C	35	12.6	63.0	77	17	AL759161
C	36	12.6	63.0	85	14	B0821331
C	37	12.6	63.0	87	9	A1173945
C	38	12.6	63.0	89	10	AM248154
C	39	12.6	63.0	90	10	AMS49193
C	40	12.6	63.0	94	9	A1188318
C	41	12.6	63.0	94	17	A2424250
C	42	12.6	63.0	94	17	BH642503
C	43	12.6	63.0	95	17	A2853253
C	44	12.6	63.0	97	9	AA864216
C	45	12.6	63.0	97	13	BM513037

## ALIGNMENTS

RESULT 1  
AI925202  
LOCUS wmp9h04.x1 NCI-CGAP ut2 Homo sapiens CDNA clone IMAGE:244419 3'  
DEFINITION similar to SW-BAT2\_HUMAN P48634 LARGE PROLINE-RICH PROTEIN BAT2 ;,  
mRNA sequence.

ACCESSION AI925202  
VERSION AI925202.1 GI:5661166

KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 79)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncilogap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/dbcp/image/image.html](http://www-bio.llnl.gov/dbcp/image/image.html)





Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGGG 20  
||||| ||||||| |||||  
Db 4 TTTTCGGGGAATCCAGGGG 23

RESULT 6  
A1799398/c 67 bp mRNA linear EST 15-DEC-1999  
LOCUS t56a01.x1 NCI CGAP UT3 Homo sapiens cDNA clone IMAGE:2263656 3'  
DEFINITION similar to SW:PRM\_HUMAN P10161 SALIVARY PROLINE-RICH PROTEIN PO  
;contains element MSRI repetitive element;; mRNA sequence.

ACCESSION A1799398 GI:5364870  
VERSION A1799398  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 67)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/dbrrp/image/image.html

FEATURES  
source  
1..67  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2263656"  
/clone\_lib="NCI-CGAP UT3"  
/tissue\_type="poorly-differentiated endometrial  
adenocarcinoma; 2 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.45 kb. Life Technologies catalog #: 11541-018"

BASE COUNT 20 a 22 c 25 g 0 t

ORIGIN  
Query Match 68.0%; Score 13.6; DB 9; Length 67;  
Best Local Similarity 80.0%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGGG 20  
||||| ||||| |||||  
Db 50 TTTTCGGGCGGCCCGGGG 31

RESULT 7  
A1356377/c 70 bp mRNA linear EST 16-FEB-1999  
LOCUS q221d04.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2027527 3'  
DEFINITION similar to TR:Q64306 Q64306 PROLINE-RICH PROTEIN.; contains element  
MSRI repetitive element;; mRNA sequence.

ACCESSION A1356377 GI:4107998  
VERSION A1356377

KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 70)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,  
M.D., Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/dbrrp/image/image.html

FEATURES  
source  
1..70  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2027527"  
/clone\_lib="NCI-CGAP CLL1"  
/tissue\_type="B-cell, chronic lymphocytic leukemia"  
/lab\_host="DH10B"  
/note="Vector: pRT73D-Pac (Pharmacia) with a modified  
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer 15'  
TGTTCACATCTGAGATGGAGCGGCGCGCATTCCTTTTCTTTTCTTTT  
T 3'; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pRT73 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 21 a 27 c 13 g 9 t

ORIGIN  
Query Match 68.0%; Score 13.6; DB 9; Length 70;  
Best Local Similarity 80.0%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGGG 20  
||||| ||||||| |||||  
Db 51 TTTTCGGGGAATCCGGGG 32

RESULT 8  
AAB54921 85 bp mRNA linear EST 04-JAN-1999  
LOCUS aJ78h10.s1 Soares-parathyroid tumor NBHPA Homo sapiens cDNA clone  
DEFINITION IMAGE:1402627 3' similar to TR:Q92801 Q92801 HYPOTHETICAL 28.3 KD  
PROTEIN;; mRNA sequence.

ACCESSION AAB54921 GI:2942459  
VERSION AAB54921  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 85)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
 , Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bdrp/image/image.html

Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Insert Length: 1001 Std Error: 0.00  
 Seq primer: -40mb1 fwd. ET from Amersham  
 High quality sequence stop: 1.

## FEATURES

Location/Qualifiers

1..85  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1402627"  
 /clone\_lib="Soares-parathyroid\_tumor\_NbHPA"  
 /issue\_type="parathyroid tumor"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: parathyroid gland; Vector: pT73D (pharmacia  
 ) with a modified polylinker; Site:1: Not I; Site:2: Eco  
 RI; 1st strand cDNA was primed with a Not I - oligo(OT)  
 primer  
 [5'-TGTTACCAATCTGACGTGGAGCGCCGACCAATTTTGTGTGTGTGT  
 TTTT-3'] double-stranded cDNA was size selected, ligated  
 to Eco RI adapters (Pharmacia), digested with Not I and  
 cloned into the Not I and Eco RI sites of a modified pT73  
 vector (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid  
 adenomas was kindly provided by Dr. Stephen Marx, National  
 Institute of Diabetes and Digestive and Kidney Diseases,  
 NIH."

BASE COUNT 14 a 19 c 25 g 27 t  
 ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 85;  
 Best Local Similarity 80.0%; Pred. No. 3.4e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTTTTCAGGCAATCCGGGGG 20  
 ||||| ||||| ||||| |||||  
 Db 30 TTTTTCAGGCAATCCGGGGG 49

RESULT 9  
 LOCUS C01948 88 bp mRNA linear EST 23-JUL-1996  
 DEFINITION HMG50003954 Human adult (K.Okubo) Homo sapiens CDNA, mRNA  
 sequence.  
 ACCESSION C01948  
 VERSION C01948.1 GI:1434178  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 88)  
 Okubo, K.  
 BodyMap: human gene expression database  
 Unpublished (1995)  
 Contact: Okubo, K.  
 Institute for Molecular and Cellular Biol  
 Osaka University  
 1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan  
 Tel: 06-877-5111(ex.3315)  
 Email: kousakueimcb.osaka-u.ac.jp  
 Human Gene Signature, 3'-directed cDNA sequence. We are not  
 submitting the same cDNA sequence redundantly to DDBJ since 1993.

REFERENCE 9  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

## FEATURES

For the abundance information of clones with this sequence in this  
 library and as well as in other 3'-directed libraries, see  
 http://www.imcb.osaka-u.ac.jp/bodymap/. The sequences of the clones  
 represented by this GS sequence is also found there.  
 Location/Qualifiers

1..88  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Human adult (K.Okubo)"  
 /dev\_stage="adult"  
 /note="Organ: blood; Vector: 1-qt-11; Site:1: Eco-RI;  
 Monocytes were prepared from blood by ficoll-hypaque,  
 percoll and T cell rosetting purification steps (purity:  
 96 %). mRNA was prepared from activated monocytes from a  
 patient with rheumatoid arthritis. mRNA was reverse  
 transcribed with MuLV. Using Eco-RI linkers cDNA was  
 cloned into 1-qt-11 vector arms. The cDNA library was  
 screened by differential hybridization using radioactively  
 marked ss-cDNA from activated and non-activated  
 monocytes."

BASE COUNT 28 a 15 c 12 g 33 t  
 ORIGIN

Query Match 68.0%; Score 13.6; DB 14; Length 88;  
 Best Local Similarity 80.0%; Pred. No. 3.4e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTTTTCAGGCAATCCGGGGG 20  
 ||||| ||||| ||||| |||||  
 Db 25 TTTTTCAGGCAATCCGGGGG 44

RESULT 10  
 LOCUS AM102784 90 bp mRNA linear EST 19-OCT-1999  
 DEFINITION xg38a06.x1 NCI-CGAP\_Ov23 Homo sapiens CDNA clone IMAGE:2596018 3',  
 mRNA sequence.  
 ACCESSION AM102784  
 VERSION AM102784.1 GI:6073397  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 90)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bdrp/image/image.html  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 73.

## FEATURES

Location/Qualifiers

1..90  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2596018"  
 /clone\_lib="NCI-CGAP\_Ov23"  
 /issue\_type="tumor, 5 pooled (see description)"  
 /lab\_host="DH10B"  
 /note="Organ: ovary; Vector: PCMV-SPORT6; Site:1: SalI;  
 Site:2: NotI; Cloned unidirectionally. Primer: oligo dT.  
 Average insert size 1.35 kb. Tumor types include: mixed  
 Mullerian tumor, papillary serous, clear cell, spindle

cell. All are primary tumors, metastasis positive. Life  
Technologies catalog #: 11534-013"

BASE COUNT 17 a 16 c 18 g 39 t

ORIGIN

Query Match 68.0%; Score 13.6; DB 10; Length 90;

Best Local Similarity 80.0%; Pred. No. 3.4e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTTTTCAGGGAATCCGGGG 20

Db 38 TTTTAAAGGAACCGAGG 57

RESULT 11

LOCUS BG672884/c 100 bp mRNA linear EST 30-APR-2001

DEFINITION DRNAOHO8 Rat DRG Library Rattus norvegicus cDNA clone DRNAOHO8

ACCESSION BG672884

VERSION BG672884.1 GI:13894983

KEYWORDS EST.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 100)

Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C., Yang,L.

, Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D., Zhang

,X., Chen,Z., Han,Z.G. and Zhang,X.

Identification of gene expression profile of dorsal root ganglion

in the rat peripheral axotomy model of neuropathic pain

Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)

22056133

Contact: Zhang Xu

Laboratory of Sensory System

Institute of Neuroscience

320 Yue Yang Road, Shanghai 200031, P.R.China

Tel: 86-21-64748700-121

Fax: 86-21-64713446

Email: xu.zhang@ion.ac.cn

This clone is also available at Chinese National Human Genome

Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,

Pudong New Area, P.R.China. Please contact with Zhang Xu

(xu.zhang@ion.ac.cn) or Han Zeguang (hanzegu@sh.sh.cn)

PCR Primers

FORWARD: T7

BACKWARD: T7

Seq primer: T7

POLYA-No.

FEATURES

source

1. 100

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="DRNAOHO8"

/clone\_lib="Rat DRG Library"

/sex="male"

/tissue\_type="dorsal root ganglion"

/dev\_stage="adult"

/note="Total RNA was isolated from hypothalamus and

transcribed into cDNA, which was then used as template in

PCR. The PCR products were separated on sequencing gel.

The differential bands were cut, reamplified, cloned into

PMD18-T vector and confirmed by Northern blot."

BASE COUNT 38 a 16 c 17 g 28 t 1 others

ORIGIN

Query Match 68.0%; Score 13.6; DB 12; Length 100;

Best Local Similarity 80.0%; Pred. No. 3.4e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTTTTCAGGGAATCCGGGG 20

Db 95 TTTTTCAGGGAATCCGGGG 76

RESULT 12

LOCUS T68724

DEFINITION

T68724 63 bp mRNA linear EST 22-FEB-1995

Yc29d01.s1 stratagene liver (#937224) Homo sapiens cDNA clone

IMAGE:82081 3' similar to gb:X02162 APOLIPORPROTEIN A-I PRECURSOR

(HUMAN);, mRNA sequence.

T68724.1 GI:679872

EST.

VERSION T68724.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 63)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chapell,B.,

Chisoe,S., Dietrich,N., Dubuque,T., Favell,A., Gish,W., Hawkins

,M., Hultman,M., Kucaba,F., Lacy,M., Le,M., Le,N., Mardis,E., Moore

,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,

Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,

Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -21m13

High quality sequence stop: 1.

FEATURES

source

1. 63

/organism="Homo sapiens"

/db\_xref="GDB:499138"

/db\_xref="taxon:9606"

/clone="IMAGE:82081"

/clone\_lib="Stratagene liver (#937224)"

/sex="male"

/dev\_stage="49 years old"

/lab\_host="SOLR cells (kanamycin resistant)"

/note="Organ: liver; Vector: pBluescript SK; Site: 1; Score

17. Hepatectomy from normal male caucasian. Average insert

size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'

GAATTCGGCAGAG 3' -3' adaptor sequence: 5'

CTCGAGTGTGTGTGTGTGTGTGT 3'

BASE COUNT 8 a 18 c 11 g 19 t 7 others

ORIGIN

Query Match 67.0%; Score 13.4; DB 14; Length 63;

Best Local Similarity 93.3%; Pred. No. 4.2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTTTCAGGGAATCC 15

Db 36 TTTTTCAGGGAATCC 50

RESULT 13

LOCUS AA140294/c

AA140294 79 bp mRNA linear EST 11-FEB-1997

DEFINITION m83c12.r1 Stratogene mouse heart (#937316) Mus musculus cDNA clone  
IMAGE:604054.5' similar to SW:IDHG\_RAT P41565 ISOCITRATE  
DEHYDROGENASE ;, mRNA sequence.

ACCESSION AA140294  
VERSION AA140294.1 GI:1702550  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 79)

REFERENCE 1 (bases 1 to 79)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisler,S., Kucab,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Thelsting,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.  
The Washu-HHMI Mouse EST Project  
Unpublished (1996)

JOURNAL COMMENT  
Washu-HHMI Mouse EST Project  
Contact: Marra M/Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (Info@image.llnl.gov) for further information.  
MG:369486  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28m13 rev1 ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source  
1..79  
/organism="Mus musculus"  
/strain="NIH Swiss"  
/db\_xref="taxon:10090"  
/clone="IMAGE:604054"  
/clone\_1lb="Stratogene mouse heart (#937316)"  
/sex="pooled"  
/tissue\_type="heart"  
/dev\_stage="13 day embryos"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="organ: heart; Vector: pBlueScript SK-; Site: 1;  
ECORI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.  
Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5';  
adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor  
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

BASE COUNT 20 a 16 c 20 g 23 t  
ORIGIN

Query Match 67.0%; Score 13.4; DB 9; Length 79;  
Best Local Similarity 93.3%; Pred. NO. 4.2e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 TTCACGGAATCCGGG 18  
|||||  
Db 59 TTCAGCAACCCGGG 45

RESULT 14  
AU107883 50 bp mRNA linear EST 30-AUG-2001  
LOCUS AU107883 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION ZR61130, mRNA sequence.  
ACCESSION AU107883  
VERSION AU107883.1 GI:13557405  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)  
Suzuki,Y., Talra,H., Tsunoda,T., Mizushima-Sugano,J., Seese,J., Hata  
H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL MEDLINE  
21270072

COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanebashi, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ms.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers

FEATURES  
source  
1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="ZR61130"  
/clone\_1lb="Sugano Homo sapiens cDNA library"  
/note="Differential display comparison of untreated and  
dimethylfumarate treated U937 cells"

BASE COUNT 8 a 13 c 12 g 16 t 1 others  
ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 50;  
Best Local Similarity 83.3%; Pred. NO. 5.3e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTTTCAGGAATCCGGG 19  
|||||  
Db 32 TTCACGCAACCCGGG 49

RESULT 15  
AU014487 67 bp mRNA linear EST 03-AUG-1998  
LOCUS AU014487 Schizosaccharomyces pombe late log phase cDNA  
DEFINITION Schizosaccharomyces pombe cDNA clone spc09929, mRNA sequence.  
ACCESSION AU014487  
VERSION AU014487.1 GI:3369278  
KEYWORDS EST.  
SOURCE fission yeast.  
ORGANISM Schizosaccharomyces pombe  
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
Schizosaccharomycetales; Schizosaccharomycetaceae;  
Schizosaccharomycetes.  
1 (bases 1 to 67)  
Moriyomo,M. and Mita,K.  
Identification of expressed sequence tags of Schizosaccharomyces  
pombe  
Unpublished (1998)

JOURNAL COMMENT  
Contact: Mitsuki Moriyomo  
Genome Research Group  
National Institute of Radiological Sciences  
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
Email: moriyomo@nirs.go.jp.  
Location/Qualifiers

FEATURES  
source  
1..67  
/organism="Schizosaccharomyces pombe"  
/strain="972"  
/db\_xref="taxon:4896"  
/clone="spc09929"  
/clone\_1lb="Schizosaccharomyces pombe late log phase cDNA"  
/sex="h minus"  
/note="Vector: M13mp19; The cDNA library of  
Schizosaccharomyces pombe was prepared by cloning cDNA  
into the SmaI site of M13mp19 DNA and the direction of DNA  
sequences was not always from 5' to 3'. The cDNA data of  
Schizosaccharomyces pombe are available for searching on  
the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 27 a 1 c 11 g 28 t  
ORIGIN

## Query Match

66.0%; Score 13.2; DB 9; Length 67;

Best Local Similarity 83.3%; Pred. No. 5.3e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 TTTTTCAGGGAATCCGGG 18  
||||||| |||  
Db 10 TTTTTCAGGGAATATGGG 27

Search completed: November 26, 2002, 04:07:03  
Job time : 768.8 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2002, 14:46:40 ; Search time 302.2 Seconds

(without alignments)  
1926.063 Million cell updates/sec

Title: US-09-296-264-6

Perfect score: 20

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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

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Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

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31: em.htg.in:\*

32: em.htg.other:\*

33: em.htg.mu:\*

34: em.htg.pln:\*

35: em.htg.rod:\*

36: em.htg.mam:\*

37: em.htg.vrt:\*

38: em.sy:\*

39: em.htgo.hum:\*

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41: em.htgo.other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	51	6	AX158137
2	14.2	71.0	75	1	ECOTRNABV
3	14.2	71.0	95	6	AX088789
4	14.2	71.0	96	6	AX088790
5	13.6	68.0	63	6	E27556
6	13.6	68.0	76	1	ECOTRNAPHE
7	13.4	67.0	42	6	AR104424
8	13.4	67.0	63	6	AR127588
9	13.4	67.0	63	6	I75257
10	13.2	66.0	73	6	I13478
11	13.2	66.0	28	6	I67871
12	13.2	66.0	51	6	AX199369
13	13.2	66.0	51	6	AX199370
14	12.8	64.0	21	6	AR148748
15	12.8	64.0	40	6	AX025223
16	12.8	64.0	48	6	AR031652
17	12.8	64.0	48	6	I90270
18	12.8	64.0	76	1	ECOTRN
19	12.8	64.0	77	1	ECOTRN1
20	12.8	64.0	87	1	ECOTRN2
21	12.8	64.0	87	1	ECOTRN3A
22	12.8	64.0	87	1	ECOTRN3B
23	12.6	63.0	32	6	AX026032
24	12.6	63.0	36	6	AX452383
25	12.6	63.0	40	9	HS274584
26	12.6	63.0	45	6	AX417920
27	12.6	63.0	48	6	AX014267
28	12.6	63.0	51	6	AX003711
29	12.6	63.0	51	6	AX158138
30	12.6	63.0	51	6	AX256314
31	12.6	63.0	60	6	AX100154
32	12.6	63.0	60	6	AX100155
33	12.6	63.0	60	6	AX100156
34	12.6	63.0	60	6	AX100157
35	12.6	63.0	63	6	AX190431
36	12.6	63.0	64	6	AX003715
37	12.6	63.0	64	6	AX023351
38	12.6	63.0	68	6	AX100153
39	12.6	63.0	75	6	AX353451
40	12.6	63.0	76	1	BACTRF
41	12.6	63.0	79	6	AX003726
42	12.6	63.0	79	6	AX003727
43	12.6	63.0	80	6	AX018524
44	12.6	63.0	80	6	AX018528
45	12.6	63.0	80	6	AX018555

#### ALIGNMENTS

RESULT 1

AX158137/c

LOCUS AX158137

DEFINITION Sequence 1465 from Patent WO0140521.

ACCESSION AX158137

VERSION AX158137.1 GI:14539468

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 51)

AUTHORS Shimkets,R.A. and Leach,M.

TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0140521-A 1465 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
source 1..51  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
misc\_feature 26  
/note="1 of 2 allelic variants (1466 is other entry)  
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OY 1 GGCTAGTTCAGCGGGAGC 19  
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DB 28 GGCTGTTCAGCGGGAGC 10

RESULT 2  
ECCTRNAB 75 bp mRNA linear BCT 16-JUN-1993  
DEFINITION E.coli gene for chimeric transfer RNA-Val.  
ACCESSION X70451  
VERSION X70451.1 GI:312130  
KEYWORDS chimeric; transfer RNA-Val.  
SOURCE Escherichia coli.  
ORGANISM Escherichia coli.  
REFERENCE 1 (bases 1 to 75)  
AUTHORS Meinel,T., Mechulam,Y., Lazennec,C., Bianquet,S. and Fayat,G.  
TITLE Critical role of the acceptor stem of tRNA(Met) in their  
JOURNAL aminoacylation by Escherichia coli methionyl-tRNA synthetase  
MEDLINE J. Mol. Biol. 229 (1), 26-36 (1993)  
PUBMED 93132797  
FEATURES 8421312  
source Location/Qualifiers  
1..75  
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/db\_xref="taxon:562"  
tRNA 1..75  
/product="tRNA-Val"

BASE COUNT 12 a 26 c 26 g 9 t 2 others  
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Best Local Similarity 80.0%; Pred. No. 2.6e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGCTAGTTCAGCGGGAGC 20  
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DB 5 GGCTAGTTCAGCGGGAGC 24

RESULT 3  
AX088789 95 bp DNA linear PAT 17-MAR-2001  
LOCUS AX088789  
DEFINITION Sequence 115 from Patent WO0114416.  
ACCESSION AX088789  
VERSION AX088789.1 GI:13397585  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 95)  
AUTHORS Neeper,M.P., McClements,W.L., Jansen,K.U., Schultz,L.D., Chen,L.  
and Wang,X.M.  
TITLE Synthetic human papillomavirus genes  
JOURNAL Patent: WO 0114416-A 115 01-MAR-2001;  
Merck & Co., Inc. (US)

FEATURES Location/Qualifiers  
source 1..95  
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/note="Codon-Optimized HPV6 E2 fragment"  
BASE COUNT 23 a 36 c 23 g 13 t  
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Best Local Similarity 84.2%; Pred. No. 2.6e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 92 GATCGTTCAGCGGTAGCG 74

RESULT 4  
AX088790 96 bp DNA linear PAT 17-MAR-2001  
LOCUS AX088790  
DEFINITION Sequence 116 from Patent WO0114416.  
ACCESSION AX088790  
VERSION AX088790.1 GI:13397586  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 96)  
AUTHORS Neeper,M.P., McClements,W.L., Jansen,K.U., Schultz,L.D., Chen,L.  
and Wang,X.M.  
TITLE Synthetic human papillomavirus genes  
JOURNAL Patent: WO 0114416-A 116 01-MAR-2001;  
Merck & Co., Inc. (US)  
FEATURES Location/Qualifiers  
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGCTAGTTCAGCGGGAGC 20  
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DB 73 GATCGTTCAGCGGTAGCG 91

RESULT 5  
E27556 63 bp DNA linear PAT 18-JUN-2001  
LOCUS E27556  
DEFINITION Isolation and cloning of nucleic acid molecule by using hairpin  
E27556 loop nucleic acid probe molecule.  
ACCESSION E27556  
VERSION E27556.1 GI:13018221  
KEYWORDS JP 1999206381-A/4.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 63)  
AUTHORS Jun,F. and Koji,S.  
TITLE Isolation and cloning of nucleic acid molecule by using hairpin  
JOURNAL loop nucleic acid probe molecule  
PATENT: JP 1999206381-A 4 03-AUG-1999;  
COMMENT OS Unidentified  
OS JP 1999206381-A/4  
PD 03-AUG-1999  
PF 29-JAN-1998 JP 1998016987  
PR  
PI JUN FUJIMURA,KOJI SHIGEMORI

PC C12N15/09, C1201/68, C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..63  
FT /organism='Unidentified'.  
FEATURES  
source 1..63  
location/Qualifiers  
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Best Local Similarity 80.0%; Pred. No. 5.3e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGGTAGTTCAGCGCGGAGCG 20  
Db 30 GGGCAGGTCAGCGCGCGCG 49

RESULT 6  
LOCUS ECOTRNAPHE 76 bp tRNA linear BCT 15-APR-1994  
DEFINITION E. coli transfer RNA-Phe.  
ACCESSION M24882.1 GI:290481  
VERSION M24882.1 GI:290481  
KEYWORDS transfer RNA-Phe.  
SOURCE Escherichia coli tRNA.  
ORGANISM Escherichia coli  
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
Escherichia.  
REFERENCE 1 (bases 1 to 76)  
AUTHORS Kitchingman, G.R. and Fournier, M.J.  
TITLE Modification-deficient transfer ribonucleic acids from relaxed control Escherichia coli: structures of the major unmodified phenylalanine and leucine transfer RNAs produced during leucine starvation  
JOURNAL Biochemistry 16 (10), 2213-2220 (1977)  
MEDLINE 77182103  
PUBMED 324516  
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location/Qualifiers  
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/db\_xref='taxon:562'  
/product='tRNA-Phe'  
/note='codon recognized: UUC'  
BASE COUNT 15 a 21 c 24 g 13 t 3 others  
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Best Local Similarity 75.0%; Pred. No. 5.2e+04;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 GCGTAGTTCAGCGCGGAGCG 20  
Db 5 GGATAGCTCAGCGCGDAGAG 24

RESULT 7  
LOCUS AR104424 42 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 9 from patent US 6093573.  
ACCESSION AR104424  
VERSION AR104424.1 GI:12817132  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 42)  
AUTHORS Beamer, L.J., Carroll, S.F. and Eisenberg, D.

TITLE Three-dimensional structure of bactericidal/permeability-increasing protein (BPI)  
JOURNAL Patent: US 6093573-A 9 25-JUL-2000;  
FEATURES  
source 1..42  
location/Qualifiers  
BASE COUNT 11 a 8 c 18 g 5 t  
ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 42;  
Best Local Similarity 93.3%; Pred. No. 6.8e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 GTTCAGCGCGGAGCG 20  
Db 3 GTTCAGCGCGGAGCG 17

RESULT 8  
LOCUS AR127588 63 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 6 from patent US 6180774.  
ACCESSION AR127588  
VERSION AR127588.1 GI:14114183  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 63)  
AUTHORS Brown, S. Marie., Dean, D. Allen., Fromm, M. Ernest. and Sanders, P. Rigden.  
TITLE Synthetic DNA sequences having enhanced expression in monocotyledonous plants and method for preparation thereof  
JOURNAL Patent: US 6180774-A 6 30-JAN-2001;  
FEATURES  
source 1..63  
location/Qualifiers  
BASE COUNT 14 a 20 c 15 g 14 t  
ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 63;  
Best Local Similarity 93.3%; Pred. No. 6.6e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 AGTTCAGCGCGGAGCG 19  
Db 26 AGTTCAGCGCGGAGCG 40

RESULT 9  
LOCUS I75257 63 bp DNA linear PAT 03-APR-1998  
DEFINITION Sequence 6 from patent US 5689052.  
ACCESSION I75257  
VERSION I75257.1 GI:3011398  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 63)  
AUTHORS Brown, S. Marie., Dean, D. Allen., Fromm, M. Ernest. and Sanders, P. Rigden.  
TITLE Synthetic DNA sequences having enhanced expression in monocotyledonous plants and method for preparation thereof  
JOURNAL Patent: US 5689052-A 6 18-NOV-1997;  
FEATURES  
source 1..63  
location/Qualifiers  
BASE COUNT 14 a 20 c 15 g 14 t  
ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 63;  
Best Local Similarity 93.3%; Pred. No. 6.6e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 AGTTCAGCGCGGAGC 19  
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Db 26 AGTTCAGCGCGGAGC 40

RESULT 10  
LOCUS 113478 73 bp DNA linear PAT 26-JUL-1995  
DEFINITION Sequence 12 from patent US 5436391.  
ACCESSION 113478  
VERSION 113478.1 GI:910819  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 73)  
AUTHORS Fujimoto,H., Ito,K., Yamamoto,M. and Shumamoto,K.  
TITLE Synthetic insecticidal gene, plants of the genus oryza transformed with the gene, and production thereof  
JOURNAL Patent: US 5436391-A 12-25-JUL-1995;  
FEATURES  
source 1..73  
/organism="unknown"  
BASE COUNT 15 a 25 c 21 g 12 t  
ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 73;  
Best Local Similarity 93.3%; Pred. No. 6.5e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 AGTTCAGCGCGGAGC 19  
|||||  
Db 29 AGTTCAGCGCGGAGC 43

RESULT 11  
LOCUS 167871 28 bp DNA linear PAT 04-FEB-1998  
DEFINITION Sequence 7 from patent US 5674683.  
ACCESSION 167871  
VERSION 167871.1 GI:2829993  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Kool,E.T.  
TITLE Stem-loop and circular oligonucleotides and method of using  
JOURNAL Patent: US 5674683-A 7-07-OCT-1997;  
FEATURES  
source 1..28  
/organism="unknown"  
BASE COUNT 4 a 4 c 16 g 4 t  
ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 28;  
Best Local Similarity 83.3%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGTAGTTCAGCGCGGAGC 18  
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Db 6 GGTGTCTCAGGAGGAGC 23

RESULT 12  
AX199369 51 bp DNA linear PAT 29-AUG-2001  
LOCUS AX199369/c  
DEFINITION Sequence 299 from Patent WO0151670.  
ACCESSION AX199369  
VERSION AX199369.1 GI:15389759  
KEYWORDS

SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 51)  
AUTHORS Shinkets,R.A. and Leach,M.D.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0151670-A 299 19-JUL-2001;  
FEATURES  
source 1..51  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
misc\_feature 26  
/note="1 of 2 allelic variants (300 is other entry)  
Accession number cg43973526"  
BASE COUNT 10 a 17 c 16 g 8 t  
ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 51;  
Best Local Similarity 83.3%; Pred. No. 8.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGTAGTTCAGCGCGGAGC 19  
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Db 19 GGGATTACAGCGCGGAGC 2

RESULT 13  
AX199370 51 bp DNA linear PAT 29-AUG-2001  
LOCUS AX199370/c  
DEFINITION Sequence 300 from Patent WO0151670.  
ACCESSION AX199370  
VERSION AX199370.1 GI:15389761  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 51)  
AUTHORS Shinkets,R.A. and Leach,M.D.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0151670-A 300 19-JUL-2001;  
FEATURES  
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/db\_xref="taxon:9606"  
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Accession number cg43973526"  
BASE COUNT 10 a 16 c 16 g 9 t  
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Best Local Similarity 83.3%; Pred. No. 8.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 19 GGGATTACAGCGCGGAGC 2

RESULT 14  
ARI48748 21 bp DNA linear PAT 08-AUG-2001  
LOCUS ARI48748/c  
DEFINITION Sequence 105 from patent US 6225451.  
ACCESSION ARI48748  
VERSION ARI48748.1 GI:15112838  
KEYWORDS  
SOURCE Unknown.

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ORGANISM      Unknown.
REFERENCE      Unclassified.
                1 (bases 1 to 21)
AUTHORS        Ballinger,D.G., Ding,W., Wagner,S. and Hese,M.A.
TITLE          Chromosome 11-linked coronary heart disease susceptibility gene
JOURNAL        CHDI
FEATURES       Patent: US 6225451-A 105 01-MAY-2001;
                Location/Qualifiers
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RESULT 15
AX025223/c    AX025223      40 bp      DNA      linear      PAT 16-SEP-2000
LOCUS         Sequence 6 from Patent DE19849348.
DEFINITION    AX025223
ACCESSION     AX025223
VERSION       AX025223.1 GI:10186937
KEYWORDS
SOURCE
ORGANISM      rhesus monkey.
                Macaca mulatta
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
                Cercopitheciinae; Macaca.
REFERENCE      1 (bases 1 to 40)
AUTHORS        Schmidt,M. and Kalle,C.V.
JOURNAL        Patent: DE 19849348-A 6 27-APR-2000;
                UNIV LUDWIGS ALBERT (DE)
FEATURES       Location/Qualifiers
                source      1..40
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                /db_xref="taxon:9544"
                31..40
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Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db       40 GGGTCTTCAGCGCGG 25

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Job time : 309.2 secs

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GenCore version 5.1.3  
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## OM nucleic - nucleic search, using sw model

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(without alignments)  
457.027 Million cell updates/sec

Title: US-09-296-264-6  
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Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2390332

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Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	20	100.0	20	21	AAZ31436
2	18	90.0	30	22	AAE83316
3	14.2	71.0	51	22	AAI74524
4	14.2	71.0	65	24	ABN52875
5	14.2	71.0	95	22	AAE75497
6	14.2	71.0	96	22	AAE75498
7	13.6	68.0	30	24	ABK53798
8	13.6	68.0	63	20	AAZ09153
9	13.6	68.0	76	24	ABK87514

10	13.6	68.0	76	24	ABK87515
11	13.6	68.0	76	24	ABK87516
12	13.6	68.0	76	24	ABK87517
13	13.6	68.0	76	24	ABK87518
14	13.6	68.0	76	24	ABK87519
15	13.6	68.0	76	24	ABK87520
16	13.4	67.0	63	19	AAV00294
17	13.4	67.0	63	19	AAE73212
18	13.2	66.0	28	17	AAE73026
19	13.2	66.0	28	17	AAE73026
20	13.2	66.0	33	16	AAE73026
21	13.2	66.0	33	16	AAE73026
22	13.2	66.0	33	16	AAE73026
23	13.2	66.0	33	16	AAE73026
24	13.2	66.0	33	16	AAE73026
25	13.2	66.0	33	16	AAE73026
26	13.2	66.0	33	16	AAE73026
27	13.2	66.0	33	16	AAE73026
28	13.2	66.0	33	16	AAE73026
29	13.2	66.0	33	16	AAE73026
30	13.2	66.0	33	16	AAE73026
31	13.2	66.0	33	16	AAE73026
32	13.2	66.0	33	16	AAE73026
33	13.2	66.0	33	16	AAE73026
34	12.8	64.0	40	21	AAE26930
35	12.8	64.0	40	21	AAE26930
36	12.8	64.0	40	21	AAE26930
37	12.8	64.0	40	21	AAE26930
38	12.8	64.0	40	21	AAE26930
39	12.8	64.0	40	21	AAE26930
40	12.8	64.0	40	21	AAE26930
41	12.8	64.0	40	21	AAE26930
42	12.8	64.0	40	21	AAE26930
43	12.8	64.0	40	21	AAE26930
44	12.8	64.0	40	21	AAE26930
45	12.6	63.0	25	22	AAH74723

## ALIGNMENTS

RESULT 1

ID AAZ31436 standard; DNA: 20 BP.

AAZ31436:

07-FEB-2000 (first entry)

Human neuropilin mRNA specific antisense oligo GRI3606.

Neuropilin: human; growth; metastasis; tumor; neovascularisation; cancer; papilloma; diabetic retinopathy; antisense; ss.

Synthetic.

OS Homo sapiens.

XX W09955855-A2.

04-NOV-1999.

23-APR-1999; 99WO-CA00324.

23-APR-1998; 98US-0082791.

(GENE-) GENESENSE TECHNOLOGIES INC.

Wright JA, Young AH, Lee YS.

WPI: 2000-023357/02.

Antisense oligonucleotides that inhibit neuropilin expression, useful for treating cancer -

XX Claim 4; Page 16; 57pp; English.  
XX  
CC Sequences AAF83316-460 represent antisense oligonucleotides which  
CC inhibit human neuropilin expression. The antisense oligonucleotides can  
CC be used to inhibit the growth or metastasis of a mammalian tumor and  
CC inhibit neovascularisation. The oligonucleotides may be used to treat  
CC various forms of cancers or tumors, such as sarcomas, melanomas,  
CC adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell  
CC carcinomas of the mouth, throat, larynx and lung, genitourinary cancers  
CC such as cervical and bladder cancer, hematopoietic cancers, colon cancer,  
CC breast cancer, pancreatic cancer, renal cancer, brain cancer, skin  
CC cancer, liver cancer, head and neck cancers, and nervous system cancers,  
CC as well as benign lesions such as papillomas. The methods may be used to  
CC treat neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration.  
XX  
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 other;  
Query Match 100.0%; Score 20; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGTAGTTCAGCGCGGAGCG 20  
1 GGGTAGTTCAGCGCGGAGCG 20  
Db 1 GGGTAGTTCAGCGCGGAGCG 20  
RESULT 2  
AAF83316/c  
ID AAF83316 standard; DNA: 30 BP.  
XX  
AC AAF83316;  
XX  
DT 09-JUL-2001 (first entry)  
XX  
DE Human neuropilin-1 (NP-1) DNA amplifying sense primer BTL-259.  
XX  
KM Receptor protein; vascular endothelial growth factor receptor-2; NP-1;  
KM VEGFR-2; neuropilin-1; co-receptor; human; angiogenic; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200131346-A2.  
XX  
PD 03-MAY-2001.  
XX  
PF 26-OCT-2000; 2000WO-US29579.  
XX  
PR 28-OCT-1999; 99US-0162367.  
XX  
PA (PROC ) PROCTER & GAMBLE CO.  
XX  
PI Rosenbaum JS, Whitaker GB, Limberg BJ;  
XX WPI; 2001-308686/32.  
XX  
DR  
XX  
XX Determining compounds which bind to a complex comprising vascular  
PT endothelial growth factor receptor-2 and Neuropilin-1 to provide  
PT superior pro- and anti-angiogenic agents  
XX  
XX Example 1; Fig 3; 82pp; English.  
XX  
CC The invention relates to determining whether a compound is capable of  
CC binding to a receptor protein complex comprising a vascular endothelial  
CC growth factor receptor-2 (VEGFR-2) receptor protein and a neuropilin-1  
CC (NP-1) receptor protein. One method comprises introducing a sample  
CC comprising the compound to the receptor protein and allowing the  
CC compound to bind to the complex. Signaling through VEGFR-2 is enhanced  
CC in the presence of the NP-1 co-receptor. The methods of the invention  
CC can be used for identifying novel pro- and anti-angiogenic compounds.  
CC Sequences AAF83314-16 represents PCR primers used for isolating human  
CC NP-1 DNA.

XX Sequence 30 BP; 5 A; 11 C; 8 G; 6 T; 0 other;  
SQ  
Query Match 90.0%; Score 18; DB 22; Length 30;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 3 GTACTCAGCGCGGAGCG 20  
3 GTACTCAGCGCGGAGCG 13  
Db 30 GTACTCAGCGCGGAGCG 13  
RESULT 3  
AAI74524/c  
ID AAI74524 standard; DNA: 51 BP.  
XX  
AC AAI74524;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ.1465.  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KM protein therapy; vaccine; probe; diagnostic assay; detection;  
KM quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200140521-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 30-NOV-2000; 2000WO-US32758.  
XX  
PR 30-NOV-1999; 99US-0168138.  
PR 29-NOV-2000; 2000US-0726173.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shinkets RA, Leach M;  
XX WPI; 2001-356160/37.  
XX  
DR Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy -  
XX  
XX Claim 1; Page 502; 2653pp; English.  
XX  
CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides.  
CC For example, (I) may be used to treat disorders by rectifying mutations  
CC or deletions in a patient's genome that affect the activity of  
CC polypeptides by expressing inactive proteins or to supplement the  
CC patients own production of polypeptide. Additionally, (I) and its  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays to detect and quantitate the presence of similar nucleic acids  
CC in samples, and therefore which patients may be in need of restorative  
CC therapy. The polypeptides encoded by (I) may be used as antigens in the  
CC production of antibodies specific for polymorphic polypeptides. The  
CC antibodies may also be used to down regulate expression and activity.  
CC The antibodies may also be used as diagnostic agents for detecting the  
CC presence of polymorphic polypeptides in samples.  
XX  
SQ Sequence 51 BP; 10 A; 19 C; 10 G; 12 T; 0 other;  
Query Match 71.0%; Score 14.2; DB 22; Length 51;  
Best Local Similarity 84.2%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;



OY 1 GGGTAGTTCAGCGGAGC 19  
|||||  
DB 28 GGGTGTACAGCGGAGC 10

RESULT 4  
ABN52875/C  
ID ABN52875 standard; DNA: 65 BP.  
XX  
XX ABN52875;  
XX  
XX

DT 15-JUL-2002 (first entry)  
XX

DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25623.

XX Human: mouse; rat; splice transcript; detection; RNA transcript;  
KM splice variant; transcriptome; oligonucleotide library; ss.  
XX

OS Mus musculus.

PN WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001MO-IB01903.

PR 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

PA (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX MPI; 2002-257383/30.

PT New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of  
PT a genome, useful for detecting tissue-, pathology-, and  
PT developmental-specific genes -  
XX  
XX

PS Example 1: SEQ ID 25623; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting  
XX messenger RNAs that populate a (sub-)transcriptome, where the  
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
XX transcription units that populate a genome. The library comprises  
XX several oligonucleotides, each capable of hybridizing selectively to a  
XX set of messenger RNAs transcribed from a given transcription unit of  
XX the genome, which encodes one or more messenger RNA splice variants.  
XX The oligonucleotide libraries are useful for detecting mRNAs from a  
XX biological sample, in expression profiling studies, in qualitatively or  
XX quantitatively characterizing the corresponding transcriptome, and in  
XX detecting RNA transcripts and splice variants of human or animal  
XX transcriptomes. The libraries may also be used as specialised mini  
XX libraries to detect transcripts of a sub-transcriptome under a  
XX particular biological or pathological state, and so allowing the  
XX detection of tissue- and pathology-specific genes such as those genes  
XX only expressed in specific tissue under a specific pathological  
XX condition; to detect developmental specific genes; and to detect RNA  
XX transcripts and splice variants of a transcriptome of a patient suffering  
XX from a particular disorder. ABN27253 to ABN59589 represent  
XX oligonucleotide sequences from rats, humans and mice, which are used in  
XX the exemplification of the present invention.  
XX N.B. The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.

SO Sequence 65 BP; 19 A; 19 C; 13 G; 14 T; 0 other;

Query Match 71.0%; Score 14.2; DB 24; Length 65;  
Best Local Similarity 84.2%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGTAGTTCAGCGGAGCG 20  
|||||  
DB 65 GGTAGTTCGTGTGGAGCG 47

RESULT 5  
AAF75497/C  
ID AAF75497 standard; DNA: 95 BP.  
XX  
XX AAF75497;  
XX  
XX

DT 14-MAY-2001 (first entry)  
XX

DE Codon-optimised HPV6 E2 fragment 6M.

XX Human papillomavirus; HPV; HPV16; HPV6a; HPV18; L1; E2; E7; E1;  
KM antiviral; immunostimulant; vaccine; immunogen; infection; ss.  
XX

OS Human papillomavirus.

PN WO200114416-A2.

PD 01-MAR-2001.

PF 21-AUG-2000; 2000MO-US22932.

PR 25-AUG-1999; 99US-0150728.

PR 07-JUN-2000; 2000US-0210143.

PA (MERI) MERCK & CO INC.

PI Neepier MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;

XX MPI; 2001-218428/22.

PT Novel synthetic polynucleotide encoding human papillomavirus (HPV)  
PT protein or mutated HPV protein useful as anti-HPV vaccines, comprises  
PT optimized-codons for expression of the viral proteins in human host  
PT cells -  
XX  
XX

PS Example 6: Fig 23; 119pp; English.

XX The present sequence is an oligomer which was used in the assembly of  
XX one of a number of synthetic polynucleotides that encode a human  
XX papillomavirus (HPV) protein, or a mutated form of a HPV protein. The  
XX mutated HPV proteins have reduced protein function as compared to wild  
XX type proteins but maintain immunogenicity. The proteins comprise codons  
XX for optimised expression in humans. The polynucleotides are useful as a  
XX vaccine which provides effective immunoprophylaxis against  
XX papillomavirus infection through stimulation of neutralising antibody  
XX and cell-mediated immunity.

SO Sequence 95 BP; 23 A; 36 C; 23 G; 13 T; 0 other;

Query Match 71.0%; Score 14.2; DB 22; Length 95;  
Best Local Similarity 84.2%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGTAGTTCAGCGGAGCG 20  
|||||  
DB 92 GATCGTTCAGCGGAGCG 74

RESULT 6  
AAF75498  
ID AAF75498 standard; DNA: 96 BP.  
XX  
XX AAF75498;  
XX

DT 14-MAY-2001 (first entry)  
XX

DE	Codon-optimised HPV6 E2 fragment 6N.
XX	
KM	Human papillomavirus; HPV; HPV16; HPV6a; HPV18; L1, E2, E7; E1;
KW	antiviral; immunostimulant; vaccine; immunogen; infection; ss.
XX	
OS	Human papillomavirus.
XX	
PN	Synthetic.
XX	
MO200114416-A2.	
PD	
01-MAR-2001.	
XX	
PE	21-AUG-2000; 2000WO-US22932.
XX	
PR	25-AUG-1999; 99US-0150728.
XX	
PR	07-JUN-2000; 2000US-0210143.
XX	
PA	(MERI ) MERCK & CO INC.
XX	
PI	Neeper MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;
DR	WPI; 2001-218428/22.
XX	
PT	Novel synthetic polynucleotide encoding human papillomavirus (HPV)
XX	protein or mutated HPV protein useful as anti-HPV vaccines, comprises
PT	optimized-codons for expression of the viral proteins in human host
PS	cells -
XX	
Example 6; Fig 23; 119pp; English.	
XX	
CC	The present sequence is an oligomer which was used in the assembly of
CC	one of a number of synthetic polynucleotides that encode a human
CC	Papillomavirus (HPV) protein, or a mutated form of a HPV protein. The
CC	mutated HPV proteins have reduced protein function as compared to wild
CC	type proteins but maintain immunogenicity. The proteins comprise codons
CC	for optimised expression in humans. The polynucleotides are useful as a
CC	vaccine which provides effective immunoprophylaxis against
CC	papillomavirus infection through stimulation of neutralising antibody
XX	and cell-mediated immunity.
XX	
SQ	Sequence 96 BP; 13 A; 23 C; 40 G; 20 T; 0 other;
Query Match	71.0%; Score 14.2; DB 22; Length 96;
Best Local Similarity	84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
OY	2 GGTAAGTCAGCGGAGCG 20           Db 73 GATCGTCAAGCGGAGCG 91
RESULT 7	
ABK53798	
ID	ABK53798 standard; DNA; 30 BP.
XX	
AC	ABK53798;
XX	
Df	05-JUN-2002 (first entry)
DE	DMS:acceptor oxidoreductase, PCR primer #44.
XX	
KW	DMS:acceptor oxidoreductase; dimethyl sulphide; sulphoxide;
RW	prochiral organic nucleotide; sulphoxide enantiomer; primer;
KW	chiral drug production; optically-active functional drug; ss.
OS	
XX	Rhodovulum sulfidophilum.
XX	
MO200216570-A1.	
XX	
PD	28-FEB-2002.
XX	
PF#	21-AUG-2001; 2001WO-AU01033.
XX	

BR	21-AUG-2000; 2000AU-0009559.
XX	
PA	(UYQU ) UNIV QUEENSLAND.
XX	
PI	McDevitt CA, McEwan AG;
XX	
DR	WPI; 2002-280922/32.
XX	
PT	New recombinant dimethyl sulphide:acceptor oxidoreductase or its
PT	subunits, useful for oxidising prochiral organic sulphides to form
PT	sulphoxide enantiomers for chiral drug synthesis -
PS	Claim 15; Page 47; 66pp; English.
XX	
CC	The invention relates to a recombinant dimethyl sulphide (DMS):acceptor
CC	oxidoreductase (I) or its subunit selected from recombinant alpha,
CC	beta, delta and gamma subunits. (I) is useful for oxidising prochiral
CC	organic sulphides to form sulfoxide enantiomers for chiral drug
CC	synthesis. (I) is expressed in a transformed bacterium. The
CC	enantiomer formed is useful for producing a chiral drug. (1) is useful
CC	for synthesis of optically-active functional groups of drug. DNA encoding
CC	(1) is useful for producing a strain of DMS:acceptor oxidoreductase-
CC	deficient Rhodovulum sulfidophilum, which is useful in whole-cell
CC	reaction, where DMS:acceptor oxidoreductase activity is unwanted.
CC	AAB53751:AAB53805 represent R. sulfidophilum DMS:acceptor oxidoreductase
CC	subunit coding sequences and PCR primers of the invention.
XX	
SQ	Sequence 30 BP; 3 A; 9 C; 12 G; 6 T; 0 other;
	Query Match            68.0%; Score 13.6; DB 24; Length 30;
	Best Local Similarity   80.0%; Pred. No. 2.2e+03;
	Matches   16; Conservative   0; Mismatches   4; Indels   0; Gaps   0
QY	1 GGGTAGTTCAGCGGGGACGC 20
Db	6 GGGTACTCTCAGCGGGTTCG 25
RESULT 8	
ID	AAZ09153 standard; DNA; 63 BP.
XX	
AC	AAZ09153;
XX	
DT	18-OCT-1999 (first entry)
XX	
DE	Hairpin type nucleic acid probe 4.
XX	
KM	Hairpin; probe; separation; autocomplementary stem loop; marker; ss.
OS	Synthetic.
XX	
JN	JF11206381-A.
XX	
PD	03-AUG-1999.
XX	
PE	29-JAN-1998; 98JP-0016987.
XX	
PR	29-JAN-1998; 98JP-0016987.
XX	
PA	(AISH-) AISHIN COSMOS KENKYUSHO KK.
XX	
DR	WPI; 1999-486357/41.
XX	
PT	Use of hairpin type nucleic acid probe - useful for detecting and
PT	isolating nucleic acid in short time free from denaturation or
PT	mutation
XX	
PS	Disclosure; Page 13; 15pp; Japanese.
XX	
CC	This invention describes the use of a hairpin type nucleic acid probe
CC	molecule for separation of a target nucleic acid having a desired
CC	nucleotide sequence composed of a 1st nucleotide part having an

```
CC autocomplementary stem loop structure, a 2nd nucleotide part, especially
CC composed of at least 15 bases, having a single stranded structure
CC extended from one terminal of the 1st nucleotide part and a marker for
CC the separation, especially biotin or digoxigenin, being contained in the
CC 1st and/or 2nd part(s) and at least partially complementary to the above
CC mentioned nucleotide sequences and further the marker for separation is
CC capable of specific binding with a particular substance. Detection and
CC isolation of an intact target nucleic acid is available in a short
CC period of time free from denaturation or mutation, without requiring
CC construction of DNA library or its screening. AA209150-209155 are DNA
CC probes used in the method of the invention.
XX
SO Sequence 63 BP; 4 A; 20 C; 25 G; 14 T; 0 other;

Query Match 68.0%; Score 13.6; DB 20; Length 63;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGAGTTCAGCGCGGAGCG 20
   ||| ||| ||| ||| ||| |||
DB 30 GGGCAGCTCAGCGCGCGC 49

RESULT 9
ABK87514
ID ABK87514 standard; RNA; 76 BP.
XX
AC ABK87514;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human immunodeficiency virus (HIV) transfer RNA (tRNA)Lys1,2.
XX
XX Transfer RNA; tRNA; transfer ribonucleic acid; retrovirus;
KW reverse transcriptase priming; human immunodeficiency virus; HIV;
KW simian immunodeficiency virus; tRNALys3; aminoacyl tRNA synthetase;
KW LysRS; tRNALys1,2; ss.
XX
OS Human immunodeficiency virus type 1.
XX
FH Key Location/Qualifiers
FT stem_loop 10..25 /*tag- a
FT modified_base 10 /*tag- b
FT /*tag- b /mod_base- G
FT /*note- "2-methyl Guanine"
FT stem_loop 27..43 /*tag- c
FT modified_base 46 /*tag- d
FT /*tag- d /mod_base- G
FT /*note- "7-methyl Guanine"
FT modified_base 48 /*tag- e
FT /*tag- e /mod_base- C
FT /*note- "5-methyl Cytosine"
FT modified_base 49 /*tag- f
FT /*tag- f /mod_base- C
FT /*note- "5-methyl Cytosine"
FT modified_base 58 /*tag- g
FT /*tag- g /mod_base- A
FT /*note- "1-methyl Adenine"
FT stem_loop 49..65 /*tag- h
FT /*tag- h
XX
PN HQ200244349-A2.
XX
XX 06-JUN-2002.
XX
XX 27-NOV-2001; 2001MO-CA01700.

XX
XX 28-NOV-2000; 2000US-253146P.
XX
XX (UYMC-) UNITV MCGILL.
XX
XX Cen S, Kleiman L;
XX
XX WPI; 2002-508511/54.
XX
XX
XX Modulating incorporation of tRNA involved in reverse transcriptase
PT priming into retrovirus e.g. human immunodeficiency virus tRNA-Lys3
PT comprises modulating activity and/or level of cognate aminoacyl tRNA
PT synthetase
XX
PS Disclosure: Fig 6; 121pp; English.
XX
XX The invention describes a method of modulating incorporation of transfer
CC ribonucleic acid (tRNA) involved in reverse transcriptase priming into
CC retroviral virion such as human immunodeficiency virus or simian
CC immunodeficiency virus, e.g. tRNA(Lys3). The method comprises modulating
CC the activity and/or level of cognate aminoacyl tRNA synthetase e.g.
CC LysRS, where the level positively correlates with an incorporation of the
CC tRNA into the virion. The invention also describes a method useful for
CC targeting a molecule into HIV by providing the molecule linked to a
CC sufficient number of aminoacyl tRNA synthetases, preferably LysRS. The
CC invention also describes a method useful for screening and selecting an
CC agent that modulates the incorporation of tRNA (tRNA(Lys), preferably
CC tRNA(Lys3)) and/or cognate aminoacyl tRNA synthetase (preferably Lys)
CC into a retroviral virion such as HIV or related viruses. The invention
CC describes the use of a molecule for interfering with incorporation of
CC native tRNA (preferably tRNA(Lys), more preferably tRNA(Lys3)) involved
CC in reverse transcriptase (RT) priming and/or its native cognate aminoacyl
CC tRNA synthetase (preferably LysRS) into a retroviral virion such as HIV
CC or related viruses, preferably HIV-1. This sequence represents the human
CC immunodeficiency virus type 1 (HIV-1) Isoacceptor tRNA Lys1,2, the
CC function of which is not yet known.
XX
SO Sequence 76 BP; 11 A; 23 C; 26 G; 7 U; 9 other;

Query Match 68.0%; Score 13.6; DB 24; Length 76;
Best Local Similarity 65.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGAGTTCAGCGCGGAGCG 20
   || :|| :|| :|| :|| :||
DB 5 GGCUCGCUACGCGGAGAG 24

RESULT 10
ABK87515
ID ABK87515 standard; RNA; 76 BP.
XX
AC ABK87515;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human immunodeficiency virus (HIV) transfer RNA (tRNA)Lys3.
XX
XX Transfer RNA; tRNA; transfer ribonucleic acid; retrovirus;
KW reverse transcriptase priming; human immunodeficiency virus; HIV;
KW simian immunodeficiency virus; tRNALys3; aminoacyl tRNA synthetase;
KW LysRS; tRNALys3; ss.
XX
OS Human immunodeficiency virus type 1.
XX
FH Key Location/Qualifiers
FT stem_loop 10..25 /*tag- a
FT modified_base 10 /*tag- b
FT /*tag- b /mod_base- G
FT /*note- "2-methyl Guanine"
FT stem_loop 27..43
```

```
FT      modified_base      /*tag= c
FT      46
FT      /*tag= d
FT      /mod_base= g
FT      /note= "7-methyl Guanine"
FT      48
FT      modified_base      /*tag= e
FT      /mod_base= c
FT      /note= "5-methyl Cytosine"
FT      49
FT      /*tag= f
FT      /mod_base= c
FT      /note= "5-methyl Cytosine"
FT      58
FT      modified_base      /*tag= g
FT      /mod_base= A
FT      /note= "1-methyl Adenine"
FT      49.65
FT      stem_loop          /*tag= h
FT
FT      WO200244349-A2.
FT
FT      06-JUN-2002.
FT
FT      27-NOV-2001; 2001WO-CA01700.
FT
FT      28-NOV-2000; 2000US-253146P.
FT
FT      (UYMC-) UNIV MCGILL.
FT
FT      Cen S, Kleiman L;
FT
FT      WPI: 2002-508511/54.
FT
FT      Modulating incorporation of tRNA involved in reverse transcriptase
PT      printing into retrovirus e.g. human immunodeficiency virus tRNA-Lys3
PT      comprises modulating activity and/or level of cognate aminoacyl tRNA
PT      synthetase -
PT
PT      Disclosure: Fig 6; 121pp; English.
PS
PS
XX      The invention describes a method of modulating incorporation of transfer
CC      ribonucleic acid (tRNA) involved in reverse transcriptase priming into
CC      retroviral virion such as human immunodeficiency virus or simian
CC      immunodeficiency virus, e.g. tRNA(Lys3). The method comprises modulating
CC      the activity and/or level of cognate aminoacyl tRNA synthetase e.g.
CC      LysRS, where the level positively correlates with an incorporation of the
CC      tRNA into the virion. The invention also describes a method useful for
CC      targeting a molecule into HIV by providing the molecule linked to a
CC      sufficient number of aminoacyl tRNA synthetases, preferably LysRS. The
CC      invention also describes a method useful for screening and selecting an
CC      agent that modulates the incorporation of tRNA (tRNA(Lys), preferably
CC      tRNA(Lys3)) and/or cognate aminoacyl tRNA synthetase (preferably Lys)
CC      into a retroviral virion such as HIV or related viruses. The invention
CC      describes the use of a molecule for interfering with incorporation of
CC      native tRNA (preferably tRNA(Lys), more preferably tRNA(Lys3)) involved
CC      in reverse transcriptase (RT) priming and/or its native cognate aminoacyl
CC      tRNA synthetase (preferably LysRS) into a retroviral virion such as HIV
CC      or related viruses, preferably HIV-1. This sequence represents the Human
CC      immunodeficiency virus type 1 (HIV-1) isoacceptor tRNA Lys3, used as the
CC      primer for reverse transcriptase catalysed synthesis of minus strand DNA.
XX
XX      Sequence 76 BP; 14 A; 20 C; 23 G; 10 U; 9 other;
```

```
Query Match      68.0%; Score 13.6; DB 24; Length 76;
Best Local Similarity 65.0%; Pred. NO. 2.3e+03;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 GGGTAGTTCAGCGGAGGCG 20
      11 : 11 : 11 : 11 : 11 : 1
DB      5 GGAUAGCUCACGCGGAGAG 24
```

```
RESULT 11
ABR87516
ID      ABR87516 standard; RNA; 76 BP.
XX
XX      ABR87516;
XX
XX      24-SEP-2002 (first entry)
XX
XX      Human immunodeficiency virus (HIV) transfer RNA 35(tRNA)Lys3.
DE
XX
XX      Transfer RNA; tRNA; transfer ribonucleic acid; retrovirus;
XX      reverse transcriptase priming; human immunodeficiency virus; HIV;
XX      simian immunodeficiency virus; tRNA(Lys3); aminoacyl tRNA synthetase;
XX      LysRS; tRNA(Lys3; mutant; ss.
XX
XX      Human immunodeficiency virus type 1.
OS
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
FH      mutation      replace(35,U)
FT      /*tag= a
FT
FT      WO200244349-A2.
FT
FT      06-JUN-2002.
FT
FT      27-NOV-2001; 2001WO-CA01700.
FT
FT      28-NOV-2000; 2000US-253146P.
FT
FT      (UYMC-) UNIV MCGILL.
FT
FT      Cen S, Kleiman L;
FT
FT      WPI: 2002-508511/54.
FT
FT      Modulating incorporation of tRNA involved in reverse transcriptase
PT      priming into retrovirus e.g. human immunodeficiency virus tRNA-Lys3
PT      comprises modulating activity and/or level of cognate aminoacyl tRNA
PT      synthetase -
PT
PT      Example 4; Page -: 121pp; English.
PS
PS
XX      The invention describes a method of modulating incorporation of transfer
CC      ribonucleic acid (tRNA) involved in reverse transcriptase priming into
CC      retroviral virion such as human immunodeficiency virus or simian
CC      immunodeficiency virus, e.g. tRNA(Lys3). The method comprises modulating
CC      the activity and/or level of cognate aminoacyl tRNA synthetase e.g.
CC      LysRS, where the level positively correlates with an incorporation of the
CC      tRNA into the virion. The invention also describes a method useful for
CC      targeting a molecule into HIV by providing the molecule linked to a
CC      sufficient number of aminoacyl tRNA synthetases, preferably LysRS. The
CC      invention also describes a method useful for screening and selecting an
CC      agent that modulates the incorporation of tRNA (tRNA(Lys), preferably
CC      tRNA(Lys3)) and/or cognate aminoacyl tRNA synthetase (preferably Lys)
CC      into a retroviral virion such as HIV or related viruses. The invention
CC      describes the use of a molecule for interfering with incorporation of
CC      native tRNA (preferably tRNA(Lys), more preferably tRNA(Lys3)) involved
CC      in reverse transcriptase (RT) priming and/or its native cognate aminoacyl
CC      tRNA synthetase (preferably LysRS) into a retroviral virion such as HIV
CC      or related viruses, preferably HIV-1. This sequence represents a mutant
CC      of the Human immunodeficiency virus type 1 (HIV-1) isoacceptor tRNA Lys3,
CC      used as the primer for reverse transcriptase catalysed synthesis of minus
CC      strand DNA.
CC      Note: This sequence does not appear in the specification but has been
CC      created using the wild type sequence shown in ABR87515 using information
CC      given in the specification.
XX
XX      Sequence 76 BP; 14 A; 20 C; 24 G; 9 U; 9 other;
```

```
Query Match      68.0%; Score 13.6; DB 24; Length 76;
Best Local Similarity 65.0%; Pred. NO. 2.3e+03;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

OY 1 GCGTACTTCAGCGCGGAGCG 20  
 11 : 11 : 11 : 11 : 11 : 11 :  
 DB 5 GGAUAGCUCAGDCGGDAGAG 24

RESULT 12  
 ABK87517  
 ID ABK87517 standard; RNA: 76 BP.  
 XX  
 XX  
 AC ABK87517;  
 XX  
 DT 24-SEP-2002 (first entry)  
 XX

Human immunodeficiency virus (HIV) transfer RNA 34, 35(tRNA)Lys3.

XX Transfer RNA: tRNA; transfer ribonucleic acid; retrovirus;  
 KM reverse transcriptase priming; human immunodeficiency virus; HIV;  
 KM simian immunodeficiency virus; tRNA(Lys3); aminoacyl tRNA synthetase;  
 KM LysRS; tRNA(Lys3); mutant; ss.  
 XX

OS Human immunodeficiency virus type 1.  
 OS Synthetic.  
 XX

PH Key Location/Qualifiers  
 FT mutation replace(34,S)  
 FT /\*tag= a  
 FT replace(35,U)  
 FT mutation /\*tag= b  
 XX

PN W0200244349-A2.  
 XX

PD 06-JUN-2002.  
 XX

PF 27-NOV-2001; 2001MO-CA01700.  
 XX

PR 28-NOV-2000; 2000US-253146P.  
 XX

PA (UYMC-) UNIV MCGILL.  
 XX

PI Gen S, Kleiman L;  
 XX

DR WPI; 2002-508511/54.  
 XX

XX The invention describes a method of modulating incorporation of transfer  
 CC ribonucleic acid (tRNA) involved in reverse transcriptase priming into  
 CC retroviral virion such as human immunodeficiency virus or simian  
 CC immunodeficiency virus, e.g. tRNA(Lys3). The method comprises modulating  
 CC the activity and/or level of cognate aminoacyl tRNA synthetase e.g.  
 CC LysRS, where the level positively correlates with an incorporation of the  
 CC tRNA into the virion. The invention also describes a method useful for  
 CC targeting a molecule into HIV by providing the molecule linked to a  
 CC sufficient number of aminoacyl tRNA synthetases, preferably LysRS. The  
 CC invention also describes a method useful for screening and selecting an  
 CC agent that modulates the incorporation of tRNA (tRNA(Lys), preferably  
 CC tRNA(Lys3)) and/or cognate aminoacyl tRNA synthetase (preferably Lys)  
 CC into a retroviral virion such as HIV or related viruses. The invention  
 CC describes the use of a molecule for interfering with incorporation of  
 CC native tRNA (preferably tRNA(Lys), more preferably tRNA(Lys3)) involved  
 CC in reverse transcriptase (RT) priming and/or its native cognate aminoacyl  
 CC tRNA synthetase (preferably LysRS) into a retroviral virion such as HIV  
 CC or related viruses, preferably HIV-1. This sequence represents a mutant  
 CC of the Human immunodeficiency virus type 1 (HIV-1) isocceptor tRNA Lys3,  
 CC used as the primer for reverse transcriptase catalysed synthesis of minus  
 CC strand DNA.  
 CC Note: This sequence does not appear in the specification but has been

CC created using the wild type sequence shown in ABK87515 using information  
 CC given in the specification.  
 CC  
 SQ Sequence 76 BP; 14 A; 21 C; 24 G; 9 U; 8 other;

Query Match 68.0%; Score 13.6; DB 24; Length 76;  
 Best Local Similarity 65.0%; Pred. No. 2.3e+03;  
 Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 GCGTACTTCAGCGCGGAGCG 20  
 11 : 11 : 11 : 11 : 11 : 11 :  
 DB 5 GGAUAGCUCAGDCGGDAGAG 24

RESULT 13  
 ABK87518  
 ID ABK87518 standard; RNA: 76 BP.  
 XX  
 XX  
 AC ABK87518;  
 XX  
 DT 24-SEP-2002 (first entry)  
 XX

Human immunodeficiency virus (HIV) transfer RNA 35, 36(tRNA)Lys3.

XX Transfer RNA: tRNA; transfer ribonucleic acid; retrovirus;  
 KM reverse transcriptase priming; human immunodeficiency virus; HIV;  
 KM simian immunodeficiency virus; tRNA(Lys3); aminoacyl tRNA synthetase;  
 KM LysRS; tRNA(Lys3); mutant; ss.  
 XX

OS Human immunodeficiency virus type 1.  
 OS Synthetic.  
 XX

PH Key Location/Qualifiers  
 FT mutation replace(35,U)  
 FT /\*tag= a  
 FT replace(36,U)  
 FT mutation /\*tag= b  
 XX

PN W0200244349-A2.  
 XX

PD 06-JUN-2002.  
 XX

PF 27-NOV-2001; 2001MO-CA01700.  
 XX

PR 28-NOV-2000; 2000US-253146P.  
 XX

PA (UYMC-) UNIV MCGILL.  
 XX

PI Gen S, Kleiman L;  
 XX

DR WPI; 2002-508511/54.  
 XX

XX The invention describes a method of modulating incorporation of transfer  
 CC ribonucleic acid (tRNA) involved in reverse transcriptase priming into  
 CC retroviral virion such as human immunodeficiency virus or simian  
 CC immunodeficiency virus, e.g. tRNA(Lys3). The method comprises modulating  
 CC the activity and/or level of cognate aminoacyl tRNA synthetase e.g.  
 CC LysRS, where the level positively correlates with an incorporation of the  
 CC tRNA into the virion. The invention also describes a method useful for  
 CC targeting a molecule into HIV by providing the molecule linked to a  
 CC sufficient number of aminoacyl tRNA synthetases, preferably LysRS. The  
 CC invention also describes a method useful for screening and selecting an  
 CC agent that modulates the incorporation of tRNA (tRNA(Lys), preferably  
 CC tRNA(Lys3)) and/or cognate aminoacyl tRNA synthetase (preferably Lys)  
 CC into a retroviral virion such as HIV or related viruses. The invention  
 CC describes the use of a molecule for interfering with incorporation of

CC native tRNA (preferably tRNA(Lys), more preferably tRNA(Lys3)) involved  
CC in reverse transcriptase (RT) priming and/or its native cognate aminoacyl  
CC tRNA synthetase (preferably LysRS) into a retroviral virion such as HIV  
CC or related viruses, preferably HIV-1. This sequence represents a mutant  
CC of the Human immunodeficiency virus type 1 (HIV-1) isoacceptor tRNA Lys3,  
CC used as the primer for reverse transcriptase catalysed synthesis of minus  
CC strand DNA.  
CC Note: This sequence does not appear in the specification but has been  
CC created using the wild type sequence shown in ABK87515 using information  
CC given in the specification.  
SQ Sequence 76 BP; 15 A; 20 C; 24 G; 8 U; 9 other;  
Query Match 68.0%; Score 13.6; DB 24; Length 76;  
Best Local Similarity 65.0%; Pred. No. 2.3e+03;  
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGTAGTTCAGCGGAGCG 20  
DB 5 GGAUAGCUCACGCGDAGAG 24  
RESULT 14  
ABK87519  
ID ABK87519 standard; RNA; 76 BP.  
XX  
AC ABK87519;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
XX Human immunodeficiency virus (HIV) transfer RNA 34, 35, 36(tRNA)Lys3.  
DE  
XX Transfer RNA; tRNA; transfer ribonucleic acid; retrovirus;  
KM reverse transcriptase priming; human immunodeficiency virus; HIV;  
KM simian immunodeficiency virus; tRNA(Lys3); aminoacyl tRNA synthetase;  
KM LysRS; tRNA(Lys3); mutant; ss.  
XX  
OS Human immunodeficiency virus type 1.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT mutation /tag= a  
FT mutation replace(34,S)  
FT mutation /tag= a  
FT mutation replace(35,U)  
FT mutation /tag= a  
FT mutation replace(36,U)  
FT mutation /tag= b  
XX  
PN WO200244349-A2.  
XX  
PD 06-JUN-2002.  
XX  
PF 27-NOV-2001; 2001WO-CA01700.  
XX  
PR 28-NOV-2000; 2000US-253146P.  
XX  
PA (UYMC-) UNIV MCGILL.  
PI Cen S, Kleiman L;  
XX  
DR WPI; 2002-508511/54.  
XX  
XX Modulating incorporation of tRNA involved in reverse transcriptase  
PT priming into retrovirus e.g. human immunodeficiency virus tRNA-Lys3  
PT comprises modulating activity and/or level of cognate aminoacyl tRNA  
PT synthetase -  
XX  
XX Example 4; Page -; 121pp; English.  
XX  
CC The invention describes a method of modulating incorporation of transfer  
CC ribonucleic acid (tRNA) involved in reverse transcriptase priming into  
CC retroviral virion such as human immunodeficiency virus or simian  
CC immunodeficiency virus, e.g. tRNA(Lys3). The method comprises modulating

CC the activity and/or level of cognate aminoacyl tRNA synthetase e.g.  
CC LysRS, where the level positively correlates with an incorporation of the  
CC tRNA into the virion. The invention also describes a method useful for  
CC targeting a molecule into HIV by providing the molecule linked to a  
CC sufficient number of aminoacyl tRNA synthetases, preferably LysRS. The  
CC invention also describes a method useful for screening and selecting an  
CC agent that modulates the incorporation of tRNA (tRNA(Lys), preferably  
CC tRNA(Lys3)) and/or cognate aminoacyl tRNA synthetase (preferably Lys  
CC into a retroviral virion such as HIV or related viruses. The invention  
CC describes the use of a molecule for interfering with incorporation of  
CC native tRNA (preferably tRNA(Lys), more preferably tRNA(Lys3)) involved  
CC in reverse transcriptase (RT) priming and/or its native cognate aminoacyl  
CC tRNA synthetase (preferably LysRS) into a retroviral virion such as HIV  
CC or related viruses, preferably HIV-1. This sequence represents a mutant  
CC of the Human immunodeficiency virus type 1 (HIV-1) isoacceptor tRNA Lys3,  
CC used as the primer for reverse transcriptase catalysed synthesis of minus  
CC strand DNA.  
CC Note: This sequence does not appear in the specification but has been  
CC created using the wild type sequence shown in ABK87515 using information  
CC given in the specification.  
SQ Sequence 76 BP; 15 A; 21 C; 24 G; 8 U; 8 other;  
Query Match 68.0%; Score 13.6; DB 24; Length 76;  
Best Local Similarity 65.0%; Pred. No. 2.3e+03;  
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGTAGTTCAGCGGAGCG 20  
DB 5 GGAUAGCUCACGCGDAGAG 24  
RESULT 15  
AAC09858/C  
ID AAC09858 standard; cDNA; 88 BP.  
XX  
AC AAC09858;  
XX  
DT 06-OCT-2000 (first entry)  
XX  
XX Human secreted protein 5' EST, SEQ ID NO: 13933.  
DE  
XX Human: 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KM gene therapy; chromosome mapping; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1033401-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 21-FEB-2000; 2000EP-0200610.  
XX  
PR 26-FEB-1999; 99US-0122487.  
XX  
PA (GEST ) GENSET.  
PI Dumas Milne Edwards J, Duclert A, Giordano J;  
XX  
DR WPI; 2000-500381/45.  
XX  
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX  
PS Claim 1; SEQ ID 13933; 71pp + CD-ROM; English.  
XX  
CC The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
CC identified within the present sequence. The 5' ESTs were prepared from  
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
CC of the mRNA because they are often obtained from oligo-dT primed cDNA

CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
CC derived from the 5' ends of mRNAs and even in those cases where longer  
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
CC They are used to obtain upstream regulatory sequences and to design  
CC expression and secretion vectors.

XX  
SQ Sequence 88 BP; 11 A; 33 C; 24 G; 20 T; 0 other;

Query Match

Best Local Similarity 68.0%; Score 13.6; DB 21; Length 88;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGCTAGTTCAGCGGAGCG 20

DB 85 GCGAGATTTCAGAGGAGCG 66

Search completed: November 23, 2002, 06:28:44  
Job time : 101.6 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2002, 05:53:51 ; Search time 21.55 Seconds  
(without alignments)  
284.619 Million cell updates/sec

Title: US-09-296-264-6

Perfect score: 20

Sequence: 1 gggtagtcagcgagcgagcg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15333831 residues

687286

687286

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

- 1: /cgn2\_6/prodata/1/lna/5A\_COMB.seq:\*
- 2: /cgn2\_6/prodata/1/lna/5B\_COMB.seq:\*
- 3: /cgn2\_6/prodata/1/lna/5A\_COMB.seq:\*
- 4: /cgn2\_6/prodata/1/lna/5B\_COMB.seq:\*
- 5: /cgn2\_6/prodata/1/lna/5A\_COMB.seq:\*
- 6: /cgn2\_6/prodata/1/lna/5B\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.4	67.0	42	3	US-08-879-565-9
2	13.4	67.0	63	1	US-08-530-492-6
3	13.4	67.0	63	4	US-08-906-517-6
4	13.4	67.0	73	1	US-07-982-712-12
5	13.2	66.0	28	1	US-08-408-656-7
6	13.2	66.0	28	5	PCT-US95-03602-7
7	13.2	66.0	33	4	US-08-432-871C-14
8	13.2	66.0	33	4	US-09-270-956-14
9	12.8	64.0	21	4	US-09-262-773-105
10	12.8	64.0	48	1	US-08-391-000-11
11	12.8	64.0	48	2	US-08-741-931-11
12	12.4	62.0	24	2	US-08-508-088-5
13	12.4	62.0	24	2	US-09-009-925-5
14	12.4	62.0	27	4	US-09-314-847A-13
15	12.4	62.0	65	1	US-08-453-104-11
16	12.4	62.0	65	2	US-08-694-824-11
17	12.4	62.0	73	1	US-08-453-104-20
18	12.4	62.0	73	2	US-08-694-824-20
19	12.2	61.0	20	4	US-09-344-529-15
20	12.2	61.0	20	4	US-09-907-843-30
21	12.2	61.0	25	2	US-08-412-376-3
22	12.2	61.0	25	2	US-08-859-998-1021
23	12.2	61.0	25	3	US-08-646-273-32
24	12.2	61.0	25	4	US-09-225-928-1021
25	12.2	61.0	31	5	PCT-US92-10792-29
26	12.2	60.0	21	1	US-08-009-263C-84
27	12.2	60.0	21	3	US-08-838-715B-84

#### ALIGNMENTS

c 28	12	60.0	31	1	US-08-706-037-2	Sequence 2, Appl1
c 29	12	60.0	31	2	US-09-005-397-2	Sequence 2, Appl1
c 30	12	60.0	44	4	US-08-918-288-66	Sequence 66, Appl1
c 31	12	60.0	44	4	US-09-282-357-66	Sequence 66, Appl1
c 32	12	60.0	67	2	US-08-400-115-19	Sequence 19, Appl1
c 33	12	60.0	71	2	US-08-400-115-18	Sequence 18, Appl1
c 34	12	60.0	76	1	US-08-345-623-3	Sequence 3, Appl1
c 35	12	60.0	76	4	US-08-866-116A-19	Sequence 19, Appl1
c 36	12	60.0	76	4	US-08-866-116A-20	Sequence 20, Appl1
c 37	12	60.0	84	2	US-08-400-115-20	Sequence 20, Appl1
c 38	12	60.0	87	4	US-08-866-116A-3	Sequence 3, Appl1
c 39	12	60.0	92	5	PCT-US91-05808-1	Sequence 1, Appl1
c 40	12	60.0	92	6	5168053-2	Patent No. 5168053
c 41	11.8	59.0	21	4	US-09-345-217-12	Sequence 12, Appl1
c 42	11.8	59.0	22	1	US-08-510-696-14	Sequence 1, Appl1
c 43	11.8	59.0	22	3	US-09-035-220-24	Sequence 24, Appl1
c 44	11.8	59.0	22	5	PCT-US96-12455-1	Sequence 1, Appl1
c 45	11.8	59.0	27	3	US-09-035-220-4	Sequence 4, Appl1

#### RESULT 1

US-08-879-565-9  
Sequence 9, Application US/08879565A  
Patent No. 6093573  
GENERAL INFORMATION:  
APPLICANT: Beamer, Lesa J.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Eisenberg, David  
TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF  
FILE REFERENCE: 1103/110340S01  
CURRENT FILING DATE: US/08/879, 565A  
NUMBER OF SEQ. ID NOS.: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
OTHER INFORMATION: Oligonucleotide complementary to SEQ ID NO:8

Query Match 67.0%; Score 13.4; DB 3; Length 42;  
Best Local Similarity 93.3%; Pred. No. 4.1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GTTCAGCGGAGCG 20  
Db 3 GTTCAGCGGAGCG 17

#### RESULT 2

US-08-530-492-6  
Sequence 6, Application US/08530492  
Patent No. 5689052  
GENERAL INFORMATION:  
APPLICANT: Brown, Sherri M.  
APPLICANT: Dean, Duff A.  
APPLICANT: Fromm, Michael E.  
APPLICANT: Sanders, Patricia R.  
TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced  
TITLE OF INVENTION: Expression in Monocytoidous Plants and Method For  
TITLE OF INVENTION: Preparation Thereof  
NUMBER OF SEQUENCES: 164  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF  
STREET: 700 Chesterfield Parkway No. 5689052th  
CITY: St. Louis  
STATE: Missouri

COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/530,492  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/172,333  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(10605)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6099  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (synthetic)  
US-08-530-492-6

Query Match 67.0%; Score 13.4; DB 1; Length 63;  
Best Local Similarity 93.3%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTTCAGCGCGGAGC 19  
|||||  
DB 26 AGTTCAGCGCGGAGC 40

RESULT 3  
US-08-906-517-6  
Sequence 6, Application US/08906517  
Patent No. 6180774  
GENERAL INFORMATION:  
APPLICANT: Brown, Sherri M.  
APPLICANT: Dean, Duff A.  
APPLICANT: Fromm, Michael E.  
TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced  
TITLE OF INVENTION: Expression in Monocotyledonous Plants and Method For  
NUMBER OF SEQUENCES: 164  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/906,517  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: MBST-170  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000  
TELEFAX: 512-474-7577  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-906-517-6

Query Match 67.0%; Score 13.4; DB 4; Length 63;  
Best Local Similarity 93.3%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTTCAGCGCGGAGC 19  
|||||  
DB 26 AGTTCAGCGCGGAGC 40

RESULT 4  
US-07-982-712-12  
Sequence 12, Application US/07982712  
Patent No. 5436391  
GENERAL INFORMATION:  
APPLICANT: Hideya FUJIMOTO, Kimiko ITOH  
APPLICANT: Mikihiro YAMAMOTO, and Ko SHIMAMOTO  
TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous  
TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 144 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/982,712  
FILING DATE: 19921127  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 73 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-07-982-712-12

Query Match 67.0%; Score 13.4; DB 1; Length 73;  
Best Local Similarity 93.3%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTTCAGCGCGGAGC 19  
|||||  
DB 29 AGTTCAGCGCGGAGC 43

RESULT 5  
US-08-408-656-7  
Sequence 7, Application US/08408656  
Patent No. 5674683  
GENERAL INFORMATION:  
APPLICANT: KOOL, Eric T.  
TITLE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/408,656  
FILING DATE: 21-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9373  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
US-08-408-656-7  
Query Match 66.0%; Score 13.2; DB 1; Length 28;  
Best Local Similarity 83.3%; Pred. No. 5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 GGGTAGTTCAGCGGGAG 18  
||||| 11 1111 11111  
Db 6 GGGTGTCTCAGAGGAG 23  
RESULT 6  
PCT-US95-03602-7  
Sequence 7, Application PC/TUS9503602  
GENERAL INFORMATION:  
APPLICANT: Research Corporation Technologies, Inc.  
TITLE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03602  
FILING DATE: 21-MAR-1995  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9373  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
PCT-US95-03602-7  
Query Match 66.0%; Score 13.2; DB 5; Length 28;  
Best Local Similarity 83.3%; Pred. No. 5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 GGGTAGTTCAGCGGGAG 18  
||||| 11 1111 11111  
Db 6 GGGTGTCTCAGAGGAG 23  
RESULT 7  
US-08-432-871C-14/C  
Sequence 14, Application US/08432871C  
Patent No. 5877010  
GENERAL INFORMATION:  
APPLICANT: Loeb, Lawrence A.  
APPLICANT: Loeb, Margaret E.  
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,871C  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 240052.409C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..33  
US-08-432-871C-14  
Query Match 66.0%; Score 13.2; DB 2; Length 33;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGCGAG 18  
||||| ||||| |||||  
DB 26 GGGTAGCACAGAGGAG 9

## RESULT 8

US-09-270-956-14/C  
; Sequence 14, Application US/09270956  
; Patent No. 6451571  
; GENERAL INFORMATION:  
; APPLICANT: Loeb, Lawrence A.  
; APPLICANT: Black, Margaret E.  
; TITLE OF INVENTION: THYMIDINE KINASE MUTANTS  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/270,956  
; FILING DATE: 17-MAR-1999  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 240052.409C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; TELEX: 3723836  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: join(1..33)  
; US-09-270-956-14

Query Match 66.0%; Score 13.2; DB 4; Length 33;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGCGAG 18  
||||| ||||| |||||  
DB 26 GGGTAGCACAGAGGAG 9

RESULT 9  
US-09-262-773-105/C  
; Sequence 105, Application US/09262773  
; Patent No. 6225451  
; GENERAL INFORMATION:  
; APPLICANT: Ballinger, Dennis G.  
; APPLICANT: Ding, Wei  
; APPLICANT: Wagner, Susanne  
; APPLICANT: Hess, Mark A.  
; TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE  
; FILE REFERENCE: Myriad 3  
; CURRENT APPLICATION NUMBER: US/09/262,773  
; CURRENT FILING DATE: 1999-03-04  
; NUMBER OF SEQ ID NOS: 210

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 105  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: primer  
US-09-262-773-105

Query Match 64.0%; Score 12.8; DB 4; Length 21;  
Best Local Similarity 87.5%; Pred. No. 7.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TAGTTCAGCGCGAG 18  
||||| ||||| |||||  
DB 19 GTAGTCAGCGAGAG 4

## RESULT 10

US-08-391-000-11/C  
; Sequence 11, Application US/08391000  
; Patent No. 5723752  
; GENERAL INFORMATION:  
; APPLICANT: HOUTZ, Robert L.  
; TITLE OF INVENTION: CLONING AND DEVELOPMENTAL EXPRESSION OF  
; TITLE OF INVENTION: PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,000  
; FILING DATE: 21-FEB-1995  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 028750-123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 48 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-391-000-11

Query Match 64.0%; Score 12.8; DB 1; Length 48;  
Best Local Similarity 87.5%; Pred. No. 8.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TAGTTCAGCGCGAGC 19  
||||| ||||| |||||  
DB 17 TAGTTCAGCGCGTAGC 2

RESULT 11  
US-08-741-931-11/C  
; Sequence 11, Application US/08741931  
; Patent No. 5866394  
; GENERAL INFORMATION:  
; APPLICANT: HOUTZ, Robert L.

TITLE OF INVENTION: CLONING AND DEVELOPMENTAL EXPRESSION OF  
TITLE OF INVENTION: PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE  
TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/741,931  
FILING DATE: 31-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/391,000  
FILING DATE: 21-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Neuh, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 028750-123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-741-931-11

Query Match 64.0%; Score 12.8; DB 2; Length 48;  
Best Local Similarity 87.5%; Pred. No. 8.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TAGTCAGCGGAGC 19  
DB 17 TAGTCAGCGGAGC 2

RESULT 12  
US-08-508-088-5/C  
Sequence 5, Application US/08508088  
Patent No. 5851826  
GENERAL INFORMATION:  
APPLICANT: FRAEDEL, Corneli  
APPLICANT: GELLER, Alfred  
APPLICANT: LIM, Fliid  
TITLE OF INVENTION: HELPER VIRUS-FREE HERPESVIRUS VECTOR PACKAGING SYSTEM  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02019  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/508,088  
FILING DATE: 26-JUL-1995

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: DAVID, RESNICK S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45485  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: 200291 STRE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-508-088-5

Query Match 62.0%; Score 12.4; DB 2; Length 24;  
Best Local Similarity 92.9%; Pred. No. 1.2e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTAGTCAGCGG 15  
DB 24 GGTAGTCAGCGG 11

RESULT 13  
US-09-009-925-5/C  
Sequence 5, Application US/09009925  
Patent No. 5998208  
GENERAL INFORMATION:  
APPLICANT: CHILDREN'S MEDICAL CENTER CORPORATION  
TITLE OF INVENTION: HELPER VIRUS-FREE HERPESVIRUS VECTOR PACKAGING SYSTEM  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02019  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,925  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12033  
FILING DATE: 22-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/508,088  
FILING DATE: 26-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DAVID, RESNICK S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45485-CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-09-009-925-5

Query Match 62.0%; Score 12.4; DB 2; Length 24;  
Best Local Similarity 92.9%; Pred. No. 1.2e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGTAGTTCAGGCGG 15  
DB 24 GGTAGTTCAGGCGG 11

## RESULT 14

US-09-314-847A-13/C  
Sequence 13, Application US/09314847A  
Patent No. 6365410  
GENERAL INFORMATION:  
APPLICANT: Schellenberger, Volker  
APPLICANT: Liu, Amy D.  
APPLICANT: Selfanova, Olga V.  
TITLE OF INVENTION: Directed Evolution of Microorganisms  
FILE REFERENCE: GC560  
CURRENT APPLICATION NUMBER: US/09/314,847A  
CURRENT FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 13  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer  
US-09-314-847A-13

Query Match 62.0%; Score 12.4; DB 4; Length 27;  
Best Local Similarity 92.9%; Pred. No. 1.2e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGTAGTTCAGGCGG 15  
DB 14 GGTAGTTCAGTGG 1

## RESULT 15

US-08-453-104-11  
Sequence 11, Application US/08453104  
Patent No. 5633446  
GENERAL INFORMATION:  
APPLICANT: CORNELISSEN, Marc  
APPLICANT: SOETAERT, Piet  
APPLICANT: STAM, Maïke  
APPLICANT: DOCKX, Jan  
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS  
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: George Mason Bldg., Washington & Prince Sts.  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/453,104  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,869  
FILING DATE: 16-DEC-1992  
APPLICATION NUMBER: GB 90401055.0  
FILING DATE: 18-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Rea, Teresa S  
REGISTRATION NUMBER: 30,427  
REFERENCE/DOCKET NUMBER: 010830-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 65 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-453-104-11

Query Match 62.0%; Score 12.4; DB 1; Length 65;  
Best Local Similarity 92.9%; Pred. No. 1.3e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 AGTTCAGGCGGAG 18  
DB 31 AGTTCAGGAGGAG 44

Search completed: November 23, 2002, 06:36:05  
Job time : 23.55 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: November 23, 2002, 05:54:41 : Search time 17.25 Seconds  
(Without alignments)  
439.108 Million cell updates/sec

Title: US-09-296-264-6

Perfect score: 20  
Sequence: 1 gggtagtcagcgagcgagcg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 195614

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published\_Applications\_NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCr\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/PCrUS\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.2	66.0	94	10	US-09-783-590-6963
2	12.6	63.0	36	12	US-10-001-879-17
3	12.6	63.0	38	9	US-09-771-035A-42
4	12.2	61.0	70	10	US-09-871-579-2
5	12.2	61.0	70	10	US-09-871-579-14
6	12.2	61.0	72	10	US-09-871-579-7
7	12.2	60.0	27	10	US-09-822-698A-15
8	12.2	60.0	43	9	US-10-027-806-94
9	12.2	60.0	69	10	US-09-822-698A-16
10	11.8	59.0	21	10	US-09-845-129-12
11	11.8	59.0	33	10	US-09-828-447-29
12	11.6	58.0	21	9	US-10-032-495-40
13	11.6	58.0	60	10	US-09-734-188-24
14	11.6	58.0	69	10	US-09-790-417-254
15	11.6	58.0	89	10	US-09-764-869-2114
16	11.6	58.0	89	10	US-09-764-877-3966
17	11.6	58.0	92	10	US-09-761-288-33
18	11.6	58.0	92	10	US-09-761-288-37
19	11.6	58.0	94	10	US-09-761-288-41

20	11.6	58.0	94	10	US-09-761-288-48	Sequence 48, Appl
21	11.6	58.0	97	10	US-09-783-590-4948	Sequence 948, Ap
22	11.6	58.0	99	10	US-09-783-590-9868	Sequence 9868, Ap
23	11.4	57.0	18	10	US-09-969-373-3867	Sequence 3867, Ap
24	11.4	57.0	18	10	US-09-969-373-3869	Sequence 3869, Ap
25	11.4	57.0	69	9	US-09-944-413-22	Sequence 22, Appl
26	11.4	57.0	69	9	US-09-944-403-22	Sequence 22, Appl
27	11.4	57.0	69	9	US-09-944-896-22	Sequence 22, Appl
28	11.4	57.0	69	10	US-09-866-028-22	Sequence 22, Appl
29	11.4	57.0	69	10	US-09-944-449-22	Sequence 22, Appl
30	11.4	57.0	69	10	US-09-944-457-22	Sequence 22, Appl
31	11.4	57.0	69	10	US-09-945-587-22	Sequence 22, Appl
32	11.4	57.0	69	10	US-09-945-015-22	Sequence 22, Appl
33	11.4	57.0	69	10	US-09-944-396-22	Sequence 22, Appl
34	11.4	57.0	69	10	US-09-944-097-22	Sequence 22, Appl
35	11.4	57.0	69	10	US-09-944-432-22	Sequence 22, Appl
36	11.4	57.0	69	10	US-09-943-762-22	Sequence 22, Appl
37	11.4	57.0	69	10	US-09-943-654-22	Sequence 22, Appl
38	11.4	57.0	69	10	US-09-943-851A-22	Sequence 1169, Ap
39	11.4	57.0	96	10	US-09-969-373-1169	Sequence 1169, Ap
40	11.2	56.0	18	10	US-09-969-373-2268	Sequence 2268, Ap
41	11.2	56.0	19	10	US-09-725-752A-11	Sequence 11, Appl
42	11.2	56.0	31	10	US-09-801-274-994	Sequence 994, App
43	11.2	56.0	89	10	US-09-764-877-2438	Sequence 2438, Ap
44	11.2	56.0	94	10	US-09-864-761-32576	Sequence 32576, A
45	11.2	56.0	96	10	US-09-864-761-25922	Sequence 25922, A

#### ALIGNMENTS

RESULT 1  
US-09-783-590-6963/C  
Sequence 6963, Application US/09783590  
Patent No. US20020110850A1  
GENERAL INFORMATION:  
APPLICANT: Dillon, Patrick J.  
APPLICANT: Haseltine, William A.  
APPLICANT: Li, Haodong  
APPLICANT: Rosen, Craig A.  
APPLICANT: Ruben, Steven M.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
FILE REFERENCE: PO-16,2C1  
CURRENT APPLICATION NUMBER: US/09/783,590  
CURRENT FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 08/420,856  
PRIOR FILING DATE: 1995-04-12  
PRIOR APPLICATION NUMBER: 08/346,731  
PRIOR FILING DATE: 1994-11-21  
NUMBER OF SEQ ID NOS: 12485  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6963  
LENGTH: 94  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (83)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-783-590-6963  
Query Match 66.0% Score 13.2; DB 10; Length 94;  
Best Local Similarity 83.3% Pred. No. 8e+02; 3; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 GTAGTTCAGCGGCGAGCG 20  
DB 42 GTAGTTCAGCGGCGAGCG 25  
RESULT 2  
US-10-001-879-17  
Sequence 17, Application US/10001879

```
; Patent No. US20020127237A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Caferkey, Robert
; APPLICANT: All, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0281
; CURRENT APPLICATION NUMBER: US/10/001,879
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,188
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-879-17
```

```
Query Match 63.0%; Score 12.6; DB 12; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 1 GGGTAGTTCAGCGCGGAGC 19
    ||| ||| ||| ||| |||
DB 4 GCGGATTACAGCGCTGAGC 22
```

```
RESULT 3
US-09-771-035A-42/c
; Sequence 42, Application US/09771035A
; Patent No. US20020165370A1
; GENERAL INFORMATION:
; APPLICANT: KUMAGAI, Monto H.
; APPLICANT: ROBERTS, Peter D.
; APPLICANT: VAETHONGS, Andy A.
; TITLE OF INVENTION: CYTOPLASMIC GENE INHIBITION OR GENE
; TITLE OF INVENTION: EXPRESSION IN TRANSFECTED PLANTS BY TOBRAVIRAL VECTOR
; FILE REFERENCE: 008010137CPUS04
; CURRENT APPLICATION NUMBER: US/09/771,035A
; CURRENT FILING DATE: 2001-01-21
; PRIOR APPLICATION NUMBER: 09/359,301
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/ US 00/20261
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Nicotiana benthamiana
US-09-771-035A-42
```

```
Query Match 63.0%; Score 12.6; DB 9; Length 38;
Best Local Similarity 78.9%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 1 GGGTAGTTCAGCGCGGAGC 19
    ||| ||| ||| ||| |||
DB 28 GCGTAGTTCAGCGCGCGC 10
```

```
RESULT 4
US-09-871-579-2/c
; Sequence 2, Application US/09871579
; Patent No. US20020061541A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Eng, Charis
```

```
; TITLE OF INVENTION: Diagnosis of Endometrial Precancers
; FILE REFERENCE: B0801/7220 (JRV)
; CURRENT APPLICATION NUMBER: US/09/871,579
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: US 60/208,542
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/289,449
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-871-579-2
```

```
Query Match 61.0%; Score 12.2; DB 10; Length 70;
Best Local Similarity 82.4%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 4 TAGTTCAGCGCGGAGCG 20
    ||| ||| ||| ||| |||
DB 45 TATTTCGGCGCGGCGCG 29
```

```
RESULT 5
US-09-871-579-14/c
; Sequence 14, Application US/09871579
; Patent No. US20020061541A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Eng, Charis
; TITLE OF INVENTION: Diagnosis of Endometrial Precancers
; FILE REFERENCE: B0801/7220 (JRV)
; CURRENT APPLICATION NUMBER: US/09/871,579
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: US 60/208,542
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/289,449
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-871-579-14
```

```
Query Match 61.0%; Score 12.2; DB 10; Length 70;
Best Local Similarity 82.4%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 4 TAGTTCAGCGCGGAGCG 20
    ||| ||| ||| ||| |||
DB 45 TATTTCGGCGCGGCGCG 29
```

```
RESULT 6
US-09-871-579-7/c
; Sequence 7, Application US/09871579
; Patent No. US20020061541A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Eng, Charis
; TITLE OF INVENTION: Diagnosis of Endometrial Precancers
; FILE REFERENCE: B0801/7220 (JRV)
; CURRENT APPLICATION NUMBER: US/09/871,579
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: US 60/208,542
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/289,449
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 20
```



SOFTWARE: PatentIn version 3.0  
SEQ ID NO 7  
LENGTH: 72  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-871-579-7

Query Match 61.0%; Score 12.2; DB 10; Length 72;  
Best Local Similarity 82.4%; Pred. No. 2.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TAGTTCAGCGCGGAGCG 20  
DB 45 TATTTCCGCGCGGCGGCG 29

RESULT 7  
US-09-822-698A-15  
Sequence 15, Application US/09822698A  
Patent No. US20020146750A1  
GENERAL INFORMATION:  
APPLICANT: Hoogenboom, Hendricus R.J.M.  
APPLICANT: Henderikx, Maria P.G.  
TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
FILE REFERENCE: DXX-015.1 US  
CURRENT APPLICATION NUMBER: US/09/822,698A  
CURRENT FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: US 09/538,913  
PRIOR FILING DATE: 2000-03-30  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: Microsoft Word  
SEQ ID NO 15  
LENGTH: 27  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: nucleotide sequence coding for a  
US-09-822-698A-15

Query Match 60.0%; Score 12; DB 10; Length 27;  
Best Local Similarity 75.0%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 GCGTAGTTCAGCGCGGAGCG 20  
DB 3 GGGTGATCAGCGCGGCGGCG 22

RESULT 8  
US-10-027-806-94/C  
Sequence 94, Application US/10027806  
Patent No. US20020160476A1  
GENERAL INFORMATION:  
APPLICANT: Swanson, Ronald V.  
APPLICANT: Feldman, Robert A.  
APPLICANT: Schleper, Christa  
TITLE OF INVENTION: NOCUTIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM  
FILE REFERENCE: DORP.002A  
CURRENT APPLICATION NUMBER: US/10/027,806  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 94  
LENGTH: 43  
TYPE: DNA  
ORGANISM: Cenarchaeum symbiosum  
FEATURE:  
NAME/KEY: TATA\_signal  
LOCATION: (11)...(16)  
US-10-027-806-94

Query Match 60.0%; Score 12; DB 9; Length 43;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GTTCAGCGCGGA 17  
DB 28 GTTCAGCGCGGA 17

RESULT 9  
US-09-822-698A-16  
Sequence 16, Application US/09822698A  
Patent No. US20020146750A1  
GENERAL INFORMATION:  
APPLICANT: Hoogenboom, Hendricus R.J.M.  
APPLICANT: Henderikx, Maria P.G.  
TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
FILE REFERENCE: DXX-015.1 US  
CURRENT APPLICATION NUMBER: US/09/822,698A  
CURRENT FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: US 09/538,913  
PRIOR FILING DATE: 2000-03-30  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: Microsoft Word  
SEQ ID NO 16  
LENGTH: 69  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: PH1-IL-2 backward primer  
US-09-822-698A-16

Query Match 60.0%; Score 12; DB 10; Length 69;  
Best Local Similarity 75.0%; Pred. No. 3e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 GCGTAGTTCAGCGCGGAGCG 20  
DB 24 GGGTGATCAGCGCGGCGGCG 43

RESULT 10  
US-09-845-129-12/C  
Sequence 12, Application US/09845129  
Patent No. US20020146700A1  
GENERAL INFORMATION:  
APPLICANT: DUFF, GORDON W.  
APPLICANT: COX, ANGELA  
APPLICANT: CAMP, NICOLA J.  
APPLICANT: DIGIOVINE, FRANCESCO S.  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED  
FILE REFERENCE: MSA-010.02  
CURRENT APPLICATION NUMBER: US/09/845,129  
CURRENT FILING DATE: 2001-04-27  
PRIOR APPLICATION NUMBER: 09/345,217  
PRIOR FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: PCT/GB98/01481  
PRIOR FILING DATE: 1998-05-21  
PRIOR APPLICATION NUMBER: 9711040.7  
PRIOR FILING DATE: 1997-05-29  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-845-129-12

Query Match 59.0%; Score 11.8; DB 10; Length 21;

Best Local Similarity 86.7%; Pred. No. 3.7e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 TAGTTCAGCGGAGC 18  
|||||  
DB 19 TAGTTCAGGTGGTAG 5

## RESULT 11

US-09-828-447-29/C  
; Sequence 29, Application US/09828447  
; Patent No. US20020069432A1  
; GENERAL INFORMATION:  
; APPLICANT: COSTA E SILVA, OSWALDO DA  
; APPLICANT: BOHNETT, HANS J.  
; APPLICANT: VAN THIELEN, NOCHA  
; APPLICANT: CHEN, ROUYING  
; APPLICANT: ISHITANI, MANABU  
; TITLE OF INVENTION: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS  
; FILE REFERENCE: 16313-0037  
; CURRENT APPLICATION NUMBER: US/09/828,447  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 60/196,001  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-828-447-29

Query Match 59.0%; Score 11.8; DB 10; Length 33;  
Best Local Similarity 86.7%; Pred. No. 3.7e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 AGTTCAGCGGAGC 19  
|||||  
DB 19 AGTTCAGCGTGGAGC 5

RESULT 12  
US-10-032-495-40  
; Sequence 40, Application US/10032495  
; Patent No. US20020155601A1  
; GENERAL INFORMATION:  
; APPLICANT: YAN, WEN LIANG  
; TITLE OF INVENTION: METHOD FOR PRODUCING A POPULATION OF HOMOZYGOUS STEM  
; TITLE OF INVENTION: CELLS HAVING A PRE-SELECTED IMMUNOTYPE AND/OR GENOTYPE,  
; TITLE OF INVENTION: CELLS SUITABLE FOR TRANSPLANT DERIVED THEREFROM, AND  
; TITLE OF INVENTION: MATERIALS AND METHODS USING SAME  
; FILE REFERENCE: 0249-000205  
; CURRENT APPLICATION NUMBER: US/10/032,495  
; CURRENT FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: 60/258,881  
; PRIOR FILING DATE: 2001-01-02  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-10-032-495-40

Query Match 58.0%; Score 11.6; DB 9; Length 21;  
Best Local Similarity 77.8%; Pred. No. 4.6e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GGTACTTCAGCGGAGC 19  
|||||  
DB 1 GGGATTACAGCGAGGAGC 18

## RESULT 13

US-09-734-188-24/C  
; Sequence 24, Application US/09734188  
; Patent No. US20020106645A1  
; GENERAL INFORMATION:  
; APPLICANT: Richardson Ph.D., Mary Ann  
; APPLICANT: Goldman, Assistant Counsel, Robin A.  
; APPLICANT: New York State Office of Mental Health  
; APPLICANT: Nathan S. Kline Institute for Psychiatric Research  
; TITLE OF INVENTION: PAH  
; FILE REFERENCE: Kline Inst.  
; CURRENT APPLICATION NUMBER: US/09/734,188  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 09/253,025  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-734-188-24

Query Match 58.0%; Score 11.6; DB 10; Length 60;  
Best Local Similarity 77.8%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 GTAATTCAGCGGAGCG 20  
|||||  
DB 46 GTAATCCGGCGGCGGCG 29

RESULT 14  
US-09-790-417-254/C  
; Sequence 254, Application US/09790417  
; Patent No. US20010031470A1  
; GENERAL INFORMATION:  
; APPLICANT: Shultz, John W.  
; APPLICANT: Lewis, Martin K.  
; APPLICANT: Lieppe, Donna  
; APPLICANT: Mandrekari, Michelle  
; APPLICANT: Kephart, Daniel  
; APPLICANT: Rhodes, Richard B.  
; APPLICANT: Andrews, Christine A.  
; APPLICANT: Hartnett, James R.  
; APPLICANT: Gu, Trent  
; APPLICANT: Olson, Ryan J.  
; APPLICANT: Wood, Keith W.  
; APPLICANT: Welch, Roy  
; TITLE OF INVENTION: Nucleic Acid Detection  
; FILE REFERENCE: Pro-103 6868/75528  
; CURRENT APPLICATION NUMBER: US/09/790,417  
; CURRENT FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 09/358,972  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: 09/042,287  
; PRIOR FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 254  
; LENGTH: 69  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Probe to A1u  
US-09-790-417-254



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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2002, 09:10:06 : Search time 755.55 Seconds  
(without alignments)  
428.707 Million cell updates/sec

Title: US-09-296-264-6  
Perfect score: 20  
Sequence: 1 gggtagtcagcgagcgagcg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues  
Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estdb:\*  
2: em\_esthm:\*  
3: em\_estln:\*  
4: em\_estm:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vtc:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rnd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	97	9	AA406204 zu65d04.s
2	14.2	71.0	97	17	CNS020YXN
3	13.8	69.0	99	14	T72387
4	13.6	68.0	32	17	A2377853
5	13.6	68.0	61	17	A2920486
6	13.6	68.0	92	17	BH412029

Result 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AA406204/c	AA406204	zu65d04.s1 Soares, testis_NHT Homo sapiens CDNA clone IMAGE:742855	AA406204	AA406204	GI:2064185	EST.	human.	1 (bases 1 to 97)	Haller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.	Washu-Merck EST Project 1997	Unpublished (1997)	Contact: Wilson R Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand

## ALIGNMENTS

Result 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AA406204	AA406204	zu65d04.s1 Soares, testis_NHT Homo sapiens CDNA clone IMAGE:742855	AA406204	AA406204	GI:2064185	EST.	human.	1 (bases 1 to 97)	Haller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.	Washu-Merck EST Project 1997	Unpublished (1997)	Contact: Wilson R Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand



Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTAAGTTCAGCGGAGCG 20  
 11 11111 111 111  
 Db 49 GCGAGTTCATGCGGNGCG 31

## RESULT 4

AZ377853 32 bp DNA linear GSS 02-OCT-2000  
 LOCUS 1M0132E21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0132E21 F, DNA sequence.

ACCESSION AZ377853  
 VERSION AZ377853.1 GI:10491553  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 32)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0132 row: E column: 21  
 Seq primer: CGTTGTAACGACGCGCCACT  
 Class: plasmid ends  
 High quality sequence stop: 32.  
 Location/Qualifiers

## FEATURES

## source

1. 32  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0132E21"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMDA2nv. Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g1147321141pb/AP129072.1) a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN

Query Match 68.0%; Score 13.6; DB 17; Length 32;  
 Best Local Similarity 80.0%; Pred. No. 4.3e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGTAGTTCAGCGCGGAGCG 20  
 11 11 1111111111111111  
 Db 20 GGATAGACCGACGCGGAGCG 1

## RESULT 5

AZ920486 61 bp DNA linear GSS 17-DEC-2001  
 LOCUS 1006020A02.x1 1006 - RescueMu Grid G Zea mays genomic, DNA  
 DEFINITION sequence.

ACCESSION AZ920486  
 VERSION AZ920486.1 GI:13391189  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays

REFERENCE 1 (bases 1 to 61)  
 AUTHORS Walbot,V.  
 TITLE Maize genomic sequences found using engineered RescueMu transposon  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Sequence was trimmed at very probable ligation site. Post-ligation  
 sequence submitted separately.  
 Plate: 1006020 row: 38  
 Class: transposon-tagged.  
 Location/Qualifiers

## FEATURES

## source

1. 61  
 /organism="Zea mays"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 /clone\_lib="1006 - RescueMu Grid G"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: leaf; Vector: RescueMu (engineered from  
 pBluescript backbone); Site\_1: BamHI; Site\_2: BglII;  
 RescueMu is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on RescueMu, go to the web  
 site 'www.zmdb.lastate.edu' and follow the links for  
 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was  
 extracted from leaf punches, double digested using BamHI  
 and BglII, and ligated to form circular plasmids. DH10B  
 cells were transformed and then screened on LB plates with  
 ampicillin."

BASE COUNT 6 a 27 c 19 g 9 t

## ORIGIN

Query Match 68.0%; Score 13.6; DB 17; Length 61;  
 Best Local Similarity 80.0%; Pred. No. 4.6e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGTAGTTCAGCGCGGAGCG 20  
 11111111 1111 111  
 Db 61 GCGTAGTTTGGCGGCGGCGG 42

RESULT 6  
 BH412029/c

LOCUS BH412029 92 bp DNA linear GSS 12-DEC-2001  
 DEFINITION 1007024H03.y1 1007 - RescueMu Grid H Zea mays genomic, DNA  
 sequence.

ACCESSION BH412029  
VERSION BH412029.1 GI:17584839  
KEYWORDS GSS.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 92)  
AUTHORS Walbot,V.  
TITLE Maize genomic sequences found using engineered Rescuenu transposon  
JOURNAL Unpublished (2001)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Very probable ligation site of ends cut by single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1007024 column: 14  
Class: transposon-tagged.  
FEATURES  
source  
Location/Qualifiers  
1..92  
/organism="Zea mays"  
/cultivar="mixed background W23/A188/873"  
/db\_xref="taxon:4577"  
/clone\_lib="1007 - Rescuenu Grid H"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: leaf; Vector: Rescuenu (engineered from pBluescript backbone); Site.1: BamHI; Site.2: BglII; Rescuenu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuenu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuenu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 13 a 41 c 26 g 12 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 17; Length 92;  
Best Local Similarity 80.0%; Pred. No. 4.8e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGCTAGTCAGCGCGGAGCG 20  
||| |||| |||| |||| ||||  
Db 49 GGGGCTTCACAGCGGAGCG 30

RESULT 7  
AZ440246/c 38 bp DNA linear GSS 03-OCT-2000  
LOCUS AZ440246  
DEFINITION 1M0231A18F mouse 10kb plasmid UGCC1M library Mus musculus genomic  
ACCESSION AZ440246  
VERSION AZ440246.1 GI:10564259  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 38)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0231 Row: A Column: 18  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 38.  
FEATURES  
source  
Location/Qualifiers  
1..38  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0231A18"  
/clone\_lib="Mouse 10kb plasmid UGCC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1147321419b1AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 9 a 14 c 5 g 10 t  
ORIGIN

Query Match 66.0%; Score 13.2; DB 17; Length 38;  
Best Local Similarity 83.3%; Pred. No. 6.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGTAGTTCAGCGCGGAGCG 19  
|||| |||| |||| ||||  
Db 30 GGTAATTTCAGCGGAGCG 13

RESULT 8  
A1033458 51 bp mRNA linear EST 28-AUG-1998  
LOCUS A1033458  
DEFINITION ow94h01.s1 Soares-fetal\_liver\_spleen\_JINR5.S1 Homo sapiens cDNA  
SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN); mRNA  
sequence.  
ACCESSION A1033458  
VERSION A1033458.1 GI:3254411  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 51)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),



JOURNAL  
COMMENT

Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: c9apds-remail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (infoimage.lnl.gov) for further information.  
Trace considered overall poor quality  
Insert length: 400 Std Error: 0.00  
Seq primer: -40m13 fwd. RT from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source

1. 51  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1554513"  
/clone\_1lb="Soares\_fetal\_liver\_spleen\_INFLS\_S1"  
/sex="male"  
/dev\_stage="20 week post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)  
with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI;  
This is a subtracted version of the original Soares fetal  
liver spleen INFLS library. 1st strand cDNA was primed  
with a Pac I - 01190(OT) primer (5'  
AAGTGAAGATTATTAAGATCTTTTTTTTTTTTTTTT 3').  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Pac I and cloned into the Pac I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT  
ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 51;  
Best Local Similarity 83.3%; Pred. No. 6.7e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Gy 3 GTAGTCAGCGGAGCG 20  
||||| ||||| |||||  
Db 33 GTAGTCAGCGTGCAGTG 50

RESULT 9  
BM431597/c 51 bp mRNA linear EST 31-JAN-2002  
LOCUS BM431597  
DEFINITION BM431597.1 Bos taurus Duodenum #1 library Bos taurus cDNA, mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 51)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Senses, C.W., Gordon  
, P.M.K. and Moore, S.S.  
Gene Expression Profiling of the Bovine Gastrointestinal Tract  
Unpublished (2002)  
Contact: Dr. Stephen Moore  
Dept of AFNS, University of Alberta  
410 Agri/For. Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
Tel: 780 492 0169  
Fax: 780 492 4265  
Email: smoores@afns.ualberta.ca  
Insert Length: 51 Std Error: 0.00  
POLYA-No.

FEATURES  
source

1. 51  
Location/Qualifiers  
/organism="Bos taurus"  
/db\_xref="taxon:9913"

/clone\_1lb="Bos taurus Duodenum #1 library"  
/tissue\_type="Smooth muscle"  
/cell\_type="Simple columnar epithelial"  
/dev\_stage="Young adult"  
/lab\_host="XLI-BlueMR" strain  
/note="Organ: Intestine/duodenum; Vector: Uni-ZAPXR;  
Site\_1: EcoRI; Site\_2: Xho I"  
BASE COUNT  
ORIGIN

Query Match 66.0%; Score 13.2; DB 13; Length 51;  
Best Local Similarity 83.3%; Pred. No. 6.7e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Gy 2 GGTAGTCAGCGGAGC 19  
||| ||||| |||||  
Db 27 GGGGTTTCAGCGCGAGC 10

RESULT 10  
CNS02V1M/c 60 bp DNA linear GSS 15-MAY-2000  
LOCUS CNS02V1M  
DEFINITION Tetradon nigroviridis genome survey sequence PUC-Ort end of clone  
173124 of library G from Tetradon nigroviridis, genomic survey  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AT215203.1 GI:7874022  
GSS: genome survey sequence.  
Tetradon nigroviridis.  
Tetradon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes;  
Tetradontidae; Tetradon.  
1 (bases 1 to 60)  
Roest-Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,  
Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F.,  
Saurin, W. and Weissenbach, J.  
Human gene number estimate provided by genome wide analysis using  
Tetradon nigroviridis DNA sequence

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Unpublished  
2 (bases 1 to 60)  
Roest-Crolius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,  
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and  
Weissenbach, J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetradon nigroviridis  
Unpublished  
3 (bases 1 to 60)  
Genoscope.  
Direct Submission  
Submitted (12-APR-2000)  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetradon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/tetradon>.

FEATURES  
source

1. 60  
/organism="Tetradon nigroviridis"  
/db\_xref="taxon:99883"  
/clone="173124"  
/clone\_1lb="G"  
/note="Genoscope sequence ID: CONG173BE12SP1-end :  
PUC-Ort"  
BASE COUNT  
ORIGIN

Query Match 66.0%; Score 13.2; DB 17; Length 60;  
Best Local Similarity 83.3%; Pred. No. 6.8e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Gy 2 GGTAGTCAGCGGAGC 19  
||||| ||| ||||| |||

Db 40 GGTAAGTACGACGGAGC 23

RESULT 11  
LOCUS CINS02VVD 65 bp DNA linear GSS 15-MAY-2000  
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone  
175608 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
AL216274.1 GI:7875093  
ACCESSION AL216274.1 GI:7875093  
KEYWORDS GSS: genome survey sequence.  
SOURCE Tetraodon nigroviridis.  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.  
1 (bases 1 to 65)  
Roest-Crollius,H., Jallou,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished  
2 (bases 1 to 65)  
Roest-Crollius,H., Jallou,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Unpublished  
3 (bases 1 to 65)  
Genoscope.  
Direct Submission  
Submitted (12-APR-2000)  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/Tetraodon>.  
location/Qualifiers  
1..65  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone="175608"  
/clone.lib="G"  
/note="Genoscope sequence ID : C0AG175BD04LPI-end : T7"  
BASE COUNT 14 a 16 c 30 g 4 t 1 others  
ORIGIN

Query Match 66.0%; Score 13.2; DB 17; Length 65;  
Best Local Similarity 83.3%; Pred. No. 6.9e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGTAAGTACGACGGAGC 19  
||||| 1 11 ||||| 11  
Db 6 GGTAAGTACGACGGAGC 23

RESULT 12  
LOCUS BM398474 23 bp mRNA linear EST 17-JAN-2002  
DEFINITION 5009-0-45-G04.t.1 Chllicoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
BM398474  
ACCESSION BM398474.1 GI:18198527  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila.  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
1 (bases 1 to 23)  
Turkewitz,A.P., Kairer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel

TITLE 'J. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
JOURNAL Contact: Turkewitz AP  
COMMENT Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: 73.  
location/Qualifiers  
1..23  
/organism="Tetrahymena thermophila"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone.lib="Chllicoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chllicoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."  
BASE COUNT 3 a 7 c 9 g 4 t  
ORIGIN

Query Match 64.0%; Score 12.8; DB 13; Length 23;  
Best Local Similarity 87.5%; Pred. No. 9e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 AGTCAGCGCGGAGCG 20  
||||| 11 ||||| 11 ||||| 11  
Db 4 AGTCAGCGCGGAGCG 19

RESULT 13  
LOCUS L32042 25 bp mRNA linear EST 02-AUG-1995  
DEFINITION HDXMP2E8A Human placenta Homo sapiens cDNA clone XP2E8A, mRNA  
sequence.  
L32042  
ACCESSION L32042.1 GI:557153  
VERSION L32042.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 25)  
Lee,C.-C., Yazdani,A., Wehnert,M., Bailey,J., Couch,T., Xiong,M.,  
Coolbaugh,M.I., Chinnault,C.A., Baldini,A., Lindsay,E.A., Zhao,Z.-Y.  
and Caskey,C.T.H.  
Isolation of chromosome-specific genes by reciprocal probing of  
arrayed cDNAs and cosmid libraries  
Hum. Mol. Genet. 4, 1373-1380 (1995)  
Contact: Caskey,C.T.H.  
location/Qualifiers  
1..25  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/map="xp22.1"  
/clone="XP2E8A"  
/clone.lib="Human placenta"  
/note="Arrayed cDNAs and cosmid libraries from human  
placental tissue"  
BASE COUNT 6 a 4 c 10 g 5 t  
ORIGIN

Query Match 64.0%; Score 12.8; DB 14; Length 25;  
Best Local Similarity 87.5%; Pred. No. 9.1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GGTAAGTACGACGGAGA 17  
||||| 11 ||||| 11 ||||| 11  
Db 1 GGTAAGTACGACGGAGA 16

RESULT 14  
 A2650453/c 42 bp DNA linear GSS 14-DEC-2000  
 LOCUS TA126F030  
 DEFINITION T. brucei sheared genomic DNA clone 126f03, reverse sequence,  
 genome survey sequence.  
 ACCESSION AL463415  
 VERSION AL463415.1 GI:11893925  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei.  
 ORGANISM Trypanosoma brucei.  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.  
 1 (bases 1 to 77)  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
 Direct Submission  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and  
 nhl@sanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v+1 method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
 source  
 1. .42  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U06C1M0520F10"  
 /clone\_lib="Mouse 10kb plasmid U06C1M library"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: pMDA2nv. Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (glt47321149pAR129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 10 a 15 c 5 g 12 t  
 ORIGIN

Query Match 64.0% Score 12.8; DB 17; Length 42;  
 Best Local Similarity 87.5% Pred. No. 9.7e+04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GGAGTTCAGCGGGA 17  
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 DB 36 GGAGTTCAGCGGGA 21

RESULT 15  
 TA126F030 77 bp DNA linear GSS 13-DEC-2000  
 LOCUS TA126F030  
 DEFINITION T. brucei sheared genomic DNA clone 126f03, reverse sequence,  
 genome survey sequence.  
 ACCESSION AL463415  
 VERSION AL463415.1 GI:11893925  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei.  
 ORGANISM Trypanosoma brucei.  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.  
 1 (bases 1 to 77)  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
 Direct Submission  
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 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
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 nhl@sanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v+1 method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nelsayed@tigr.org  
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 at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
 source  
 1. .77  
 Location/Qualifiers  
 /organism="Trypanosoma brucei"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="126f03"  
 /clone\_lib="126f03"

BASE COUNT 30 a 12 c 18 g 17 t  
 ORIGIN

Query Match 64.0% Score 12.8; DB 17; Length 77;  
 Best Local Similarity 87.5% Pred. No. 1e+05;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 AGTCAGCGGAGCG 20  
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 DB 51 AGTCAGCGGAGCG 66

Search completed: November 26, 2002, 04:07:14  
 Job time : 766.8 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2002, 14:46:40 : Search time 302.2 Seconds

(Without alignments)  
1926.063 Million cell updates/sec

Title: US-09-296-264-7

Perfect score: 20  
Sequence: 1 aatgcgcctctgtcccgca 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenBml: \*  
1: gb\_da: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_cm: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sy: \*  
12: gb\_un: \*  
13: gb\_vl: \*  
14: gb\_da: \*  
15: em\_fun: \*  
16: em\_hum: \*  
17: em\_in: \*  
18: em\_mu: \*  
19: em\_mu: \*  
20: em\_mu: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_ph: \*  
24: em\_pat: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htg\_mus: \*  
34: em\_htg\_pln: \*  
35: em\_htg\_rtd: \*  
36: em\_htg\_man: \*  
37: em\_htg\_vrt: \*  
38: em\_sy: \*  
39: em\_htgo\_hum: \*  
40: em\_htgo\_mus: \*  
41: em\_htgo\_other: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	25	6	AR184007
2	14.2	71.0	25	6	I68645
3	13.8	69.0	44	6	AX027575
4	13.8	69.0	45	6	AX027576
5	13.6	68.0	30	6	AX278367
6	13.4	67.0	78	3	AF090124
7	13.2	66.0	20	6	AR163949
8	13.2	66.0	20	6	AX326934
9	13.2	66.0	34	6	A60217
10	13.2	66.0	34	6	AR122293
11	13.2	66.0	40	6	AR135209
12	13.2	66.0	40	6	AR146705
13	13.2	66.0	40	6	AR152276
14	13.2	66.0	40	6	AR157814
15	13.2	66.0	45	9	HS4403877
16	13.2	66.0	77	9	HSRGS08
17	13.2	66.0	79	6	A50092
18	13.2	65.0	31	6	AX248740
19	12.8	64.0	21	6	AR120005
20	12.8	64.0	21	6	AR120068
21	12.8	64.0	21	6	I13801
22	12.8	64.0	21	6	I13864
23	12.8	64.0	21	6	I33435
24	12.8	64.0	53	6	A84386
25	12.8	64.0	53	6	AX427285
26	12.8	64.0	78	3	URDRR05
27	12.6	63.0	65	6	AR064497
28	12.6	63.0	72	9	S80783
29	12.6	63.0	72	9	S80785
30	12.4	62.0	51	6	AX160189
31	12.4	62.0	51	6	AX165134
32	12.2	61.0	20	6	AR136418
33	12.2	61.0	25	6	AX196730
34	12.2	61.0	28	6	AX040164
35	12.2	61.0	30	10	MMHNE113B
36	12.2	61.0	32	9	S81153
37	12.2	61.0	39	6	AX097394
38	12.2	61.0	40	6	I07950
39	12.2	61.0	41	6	AX135990
40	12.2	61.0	41	6	AX136047
41	12.2	61.0	41	6	BD006882
42	12.2	61.0	45	6	AX027573
43	12.2	61.0	45	6	AX027574
44	12.2	61.0	45	10	MMF12RNA
45	12.2	61.0	51	6	AX157611

#### ALIGNMENTS

RESULT 1  
LOCUS AR184007  
DEFINITION Sequence 10 from patent US 6342483.  
ACCESSION AR184007  
VERSION AR184007.1 GI:20227976  
KEYWORDS  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
Holt,J.T., Jensen,R.A., Page,D.L., Obermiller,P.S.,  
Robinson-Benion,C.L. and Thompson,M.E.  
Method for detection and treatment of breast cancer  
Patent: US 6342483-A 10 29-JAN-2002.

FEATURES Location/Qualifiers  
source 1..25  
/organism="unknown"  
BASE COUNT 4 a 8 c 8 g 5 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 25;  
Best Local Similarity 84.2%; Pred. No. 2.3e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ATGGCGCCCTGTGCCGA 20  
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DB 3 ATGGCGCTCTGTACCGA 21

RESULT 2  
168645 168645 25 bp DNA linear PAT 04-FEB-1998  
LOCUS DEFINITION Sequence 10 from patent US 5677125.  
ACCESSION 168645  
VERSION 168645.1 GI:2830767  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Holt,J.T., Jensen,R.A., Page,D.L., Obermiller,P.S. and Robinson-Benion,C.L.  
TITLE Method of detection and diagnosis of pre-invasive cancer  
JOURNAL Patent: US 5677125-A 10 14-OCT-1997;  
FEATURES Location/Qualifiers  
source 1..25  
/organism="unknown"

BASE COUNT 4 a 8 c 8 g 5 t  
ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 25;  
Best Local Similarity 84.2%; Pred. No. 2.3e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ATGGCGCCCTGTGCCGA 20  
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DB 3 ATGGCGCTCTGTACCGA 21

RESULT 3  
AX027575 44 bp DNA linear PAT 16-SEP-2000  
LOCUS DEFINITION Sequence 35 from Patent W00039308.  
ACCESSION AX027575  
VERSION AX027575.1 GI:10188483  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 44)  
AUTHORS Sakai,Y., Hashimoto,Y. and Takemoto,Y.  
TITLE Ik3 kinase  
JOURNAL Patent: WO 0039308-A 35 06-JUL-2000;  
SAKAI YUTAKA (JP) ; GLAXO WELLCOME KABUSHIKI KAISHA (JP) ; HASHIMOTO YASUHIRO (JP) ; TAKEMOTO YOSHIHIRO (JP)  
FEATURES Location/Qualifiers  
source 1..44  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Primer"

BASE COUNT 6 a 14 c 18 g 6 t  
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Query Match 69.0%; Score 13.8; DB 6; Length 44;  
Best Local Similarity 88.2%; Pred. No. 3.4e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGCGCCCTGTGCCGA 20  
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DB 24 GGCGCCCTGTGCCGA 40

RESULT 4  
AX027576/c 45 bp DNA linear PAT 16-SEP-2000  
LOCUS DEFINITION Sequence 36 from Patent W00039308.  
ACCESSION AX027576  
VERSION AX027576.1 GI:10188484  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Sakai,Y., Hashimoto,Y. and Takemoto,Y.  
TITLE Ik3 kinase  
JOURNAL Patent: WO 0039308-A 36 06-JUL-2000;  
SAKAI YUTAKA (JP) ; GLAXO WELLCOME KABUSHIKI KAISHA (JP) ; HASHIMOTO YASUHIRO (JP) ; TAKEMOTO YOSHIHIRO (JP)  
FEATURES Location/Qualifiers  
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/note="Primer"

BASE COUNT 6 a 19 c 14 g 6 t  
ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 45;  
Best Local Similarity 88.2%; Pred. No. 3.4e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGCGCCCTGTGCCGA 20  
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DB 21 GGCGCCCTGTGCCGA 5

RESULT 5  
AX278367 30 bp DNA linear PAT 01-NOV-2001  
LOCUS DEFINITION Sequence 30 from Patent W00177169.  
ACCESSION AX278367  
VERSION AX278367.1 GI:16605376  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Tang,T.Y., Labat,I., Tillinghast,J.S., Sinku,A., Liu,C., Dimanac,R.T., Stache-Crain,B., Dickson,M., Mize,N.K. and Nishikawa,M.  
TITLE Methods and materials relating to novel stem cell growth factor-like polypeptides and polynucleotides  
JOURNAL Patent: WO 0177169-A 30 18-OCT-2001;  
HYSEO, INC. (US) ; KIRIN BEER KABUSHIKI KAISHA (JP)  
FEATURES Location/Qualifiers  
source 1..30  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="PCR primer"

BASE COUNT 5 a 6 c 11 g 8 t  
ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 30;  
Best Local Similarity 80.0%; Pred. No. 4.4e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AATGGCGCCCTGTGCCGA 20  
||||| || |||||  
DB 21 AATGGCGCCCTGTGCCGA 2